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GENES AND MEMES: PART I

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PREFACE

This book belongs to a series of online books summarizing the recent state Topological Geometrodynamics (TGD) and its applications. TGD can be regarded as a unified theory of fundamental interactions but is not the kind of unified theory as so called GUTs constructed by graduate students at seventies and eighties using detailed recipes for how to reduce everything to group theory. Nowadays this activity has been completely computerized and it probably takes only a few hours to print out the predictions of this kind of unified theory as an article in the desired format. TGD is something different and I am not ashamed to confess that I have devoted the last 37 years of my life to this enterprise and am still unable to write The Rules.

If I remember correctly, I got the basic idea of Topological Geometrodynamics (TGD) during autumn 1977, perhaps it was October. What I realized was that the representability of physical space-times as 4-dimensional surfaces of some higher-dimensional space-time obtained by replacing the points of Minkowski space with some very small compact internal space could resolve the conceptual difficulties of general relativity related to the definition of the notion of energy. This belief was too optimistic and only with the advent of what I call zero energy ontology the understanding of the notion of Poincare invariance has become satisfactory. This required also the understanding of the relationship to General Relativity.

It soon became clear that the approach leads to a generalization of the notion of space-time with particles being represented by space-time surfaces with finite size so that TGD could be also seen as a generalization of the string model. Much later it became clear that this generalization is consistent with conformal invariance only if space-time is 4-dimensional and the Minkowski space factor of imbedding space is 4-dimensional. During last year it became clear that 4-D Minkowski space and 4-D complex projective space CP_2 are completely unique in the sense that they allow twistor space with Kähler structure.

It took some time to discover that also the geometrization of also gauge interactions and elementary particle quantum numbers could be possible in this framework: it took two years to find the unique internal space (CP_2) providing this geometrization involving also the realization that family replication phenomenon for fermions has a natural topological explanation in TGD framework and that the symmetries of the standard model symmetries are much more profound than pragmatic TOE builders have believed them to be. If TGD is correct, main stream particle physics chose the wrong track leading to the recent deep crisis when people decided that quarks and leptons belong to same multiplet of the gauge group implying instability of proton.

There have been also longstanding problems.

- Gravitational energy is well-defined in cosmological models but is not conserved. Hence the conservation of the inertial energy does not seem to be consistent with the Equivalence Principle. Furthermore, the imbeddings of Robertson-Walker cosmologies turned out to be vacuum extremals with respect to the inertial energy. About 25 years was needed to realize that the sign of the inertial energy can be also negative and in cosmological scales the density of inertial energy vanishes: physically acceptable universes are creatable from vacuum. Eventually this led to the notion of zero energy ontology (ZEO) which deviates dramatically from the standard ontology being however consistent with the crossing symmetry of quantum field theories. In this framework the quantum numbers are assigned with zero energy states located at the boundaries of so called causal diamonds defined as intersections of future and past directed light-cones. The notion of energy-momentum becomes length scale dependent since one has a scale hierarchy for causal diamonds. This allows to understand the non-conservation of energy as apparent.

  Equivalence Principle as it is expressed by Einstein's equations follows from Poincare invariance once it is realized that GRT space-time is obtained from the many-sheeted space-time of TGD by lumping together the space-time sheets to a regionof Minkowski space and endowing it with an effective metric given as a sum of Minkowski metric and deviations of the metrices of space-time sheets from Minkowski metric. Similar description relates classical gauge potentials identified as components of induced spinor connection to Yang-Mills gauge potentials in GRT space-time. Various topological inhomogenities below resolution scale identified as particles are described using energy momentum tensor and gauge currents.

- From the beginning it was clear that the theory predicts the presence of long ranged classical electro-weak and color gauge fields and that these fields necessarily accompany classical electromagnetic fields.

  It took about 26 years to gain the maturity to admit the obvious: these fields are classical correlates for long range color and weak interactions assignable to dark matter. The only possible conclusion is that TGD physics is a fractal consisting of an entire hierarchy of fractal copies of standard model physics. Also the understanding of electro-weak massivation and screening of weak charges has been a long standing problem, and 32 years was needed to discover that what I call weak form of electric-magnetic duality gives a satisfactory solution of the problem and provides also surprisingly powerful insights to the mathematical structure of quantum TGD.

  The latest development was the realization that the well- definedness of electromagnetic charge as quantum number for the modes of the induced spinors field requires that the CP_2 projection of the region in which they are non-vanishing carries vanishing W boson field and is 2-D. This implies in the generic case their localization to 2-D surfaces: string world sheets and possibly also partonic 2-surfaces. This localization applies to all modes except covariantly constant right handed neutrino generating supersymmetry and mplies that string model in 4-D space-time is part of TGD. Localization is possible only for Kähler-Dirac assigned with Kähler action defining the dynamics of space-time surfaces. One must however leave open the question whether W field might vanish for the space-time of GRT if related to many-sheeted space-time in the proposed manner even when they do not vanish for space-time sheets.

I started the serious attempts to construct quantum TGD after my thesis around 1982. The original optimistic hope was that path integral formalism or canonical quantization might be enough to construct the quantum theory but the first discovery made already during first year of TGD was that these formalisms might be useless due to the extreme non-linearity and enormous vacuum degeneracy of the theory. This turned out to be the case.

- It took some years to discover that the only working approach is based on the generalization of Einstein's program. Quantum physics involves the geometrization of the infinite-dimensional "world of classical worlds" (WCW) identified as 3-dimensional surfaces. Still few years had to pass before I understood that general coordinate invariance leads to a more or less unique solution of the problem and in positive energyontology implies that space-time surfaces are analogous to Bohr orbits. This in positive energy ontology in which space-like 3-surface is basic object. It is not clear whether Bohr orbitology is necessary also in ZEO in which space-time surfaces connect space-like 3-surfaces at the light-like boundaries of causal diamond CD obtained as intersection of future and past directed light-cones (with CP_2 factor included). The reason is that the pair of 3-surfaces replaces the boundary conditions at single 3-surface involving also time derivatives. If one assumes Bohr orbitology then strong correlations between the 3-surfaces at the ends of CD follow. Still a couple of years and I discovered that quantum states of the Universe can be identified as classical spinor fields in WCW. Only quantum jump remains the genuinely quantal aspect of quantum physics.

- During these years TGD led to a rather profound generalization of the space-time concept. Quite general properties of the theory led to the notion of many-sheeted space-time with sheets representing physical subsystems of various sizes. At the beginning of 90s I became dimly aware of the importance of p-adic number fields and soon ended up with the idea that p-adic thermodynamics for a conformally invariant system allows to understand elementary particle massivation with amazingly few input assumptions. The attempts to understand p-adicity from basic principles led gradually to the vision about physics as a generalized number theory as an approach complementary to the physics as an infinite-dimensional spinor geometry of WCW approach. One of its elements was a generalization of the number concept obtained by fusing real numbers and various p-adic numbers along common rationals. The number theoretical trinity involves besides p-adic number fields also quaternions and octonions and the notion of infinite prime.

- TGD inspired theory of consciousness entered the scheme after 1995 as I started to write a book about consciousness. Gradually it became difficult to say where physics ends and

consciousness theory begins since consciousness theory could be seen as a generalization of quantum measurement theory by identifying quantum jump as a moment of consciousness and by replacing the observer with the notion of self identified as a system which is conscious as long as it can avoid entanglement with environment. The somewhat cryptic statement "Everything is conscious and consciousness can be only lost" summarizes the basic philosophy neatly.

The idea about p-adic physics as physics of cognition and intentionality emerged also rather naturally and implies perhaps the most dramatic generalization of the space-time concept in which most points of p-adic space-time sheets are infinite in real sense and the projection to the real imbedding space consists of discrete set of points. One of the most fascinating outcomes was the observation that the entropy based on p-adic norm can be negative. This observation led to the vision that life can be regarded as something in the intersection of real and p-adic worlds. Negentropic entanglement has interpretation as a correlate for various positively colored aspects of conscious experience and means also the possibility of strongly correlated states stable under state function reduction and different from the conventional bound states and perhaps playing key role in the energy metabolism of living matter.

If one requires consistency of Negentropy Mazimization Pronciple with standard measurement theory, negentropic entanglement defined in terms of number theoretic negentropy is necessarily associated with a density matrix proportional to unit matrix and is maximal and is characterized by the dimension n of the unit matrix. Negentropy is positive and maximal for a p-adic unique prime dividing n.

- One of the latest threads in the evolution of ideas is not more than nine years old. Learning about the paper of Laurent Nottale about the possibility to identify planetary orbits as Bohr orbits with a gigantic value of gravitational Planck constant made once again possible to see the obvious. Dynamical quantized Planck constant is strongly suggested by quantum classical correspondence and the fact that space-time sheets identifiable as quantum coherence regions can have arbitrarily large sizes. Second motivation for the hierarchy of Planck constants comes from bio-electromagnetism suggesting that in living systems Planck constant could have large values making macroscopic quantum coherence possible. The interpretation of dark matter as a hierarchy of phases of ordinary matter characterized by the value of Planck constant is very natural.

  During summer 2010 several new insights about the mathematical structure and interpretation of TGD emerged. One of these insights was the realization that the postulated hierarchy of Planck constants might follow from the basic structure of quantum TGD. The point is that due to the extreme non-linearity of the classical action principle the correspondence between canonical momentum densities and time derivatives of the imbedding space coordinates is one-to-many and the natural description of the situation is in terms of local singular covering spaces of the imbedding space. One could speak about effective value of Planck constant $h_{eff} = n \times h$ coming as a multiple of minimal value of Planck constant. Quite recently it became clear that the non-determinism of Kähler action is indeed the fundamental justification for the hierarchy: the integer n can be also interpreted as the integer characterizing the dimension of unit matrix characterizing negentropic entanglement made possible by the many-sheeted character of the space-time surface.

  Due to conformal invariance acting as gauge symmetry the n degenerate space-time sheets must be replaced with conformal equivalence classes of space-time sheets and conformal transformations correspond to quantum critical deformations leaving the ends of space-time surfaces invariant. Conformal invariance would be broken: only the sub-algebra for which conformal weights are divisible by n act as gauge symmetries. Thus deep connections between conformal invariance related to quantum criticality, hierarchy of Planck constants, negentropic entanglement, effective p-adic topology, and non-determinism of Kähler action perhaps reflecting p-adic non-determinism emerges.

  The implications of the hierarchy of Planck constants are extremely far reaching so that the significance of the reduction of this hierarchy to the basic mathematical structure distinguishing between TGD and competing theories cannot be under-estimated.

From the point of view of particle physics the ultimate goal is of course a practical construction recipe for the S-matrix of the theory. I have myself regarded this dream as quite too ambitious taking into account how far reaching re-structuring and generalization of the basic mathematical structure of quantum physics is required. It has indeed turned out that the dream about explicit formula is unrealistic before one has understood what happens in quantum jump. Symmetries and general physical principles have turned out to be the proper guide line here. To give some impressions about what is required some highlights are in order.

- With the emergence of ZEO the notion of S-matrix was replaced with M-matrix defined between positive and negative energy parts of zero energy states. M-matrix can be interpreted as a complex square root of density matrix representable as a diagonal and positive square root of density matrix and unitary S-matrix so that quantum theory in ZEO can be said to define a square root of thermodynamics at least formally. M-matrices in turn bombine to form the rows of unitary U-matrix defined between zero energy states.

- A decisive step was the strengthening of the General Coordinate Invariance to the requirement that the formulations of the theory in terms of light-like 3-surfaces identified as 3-surfaces at which the induced metric of space-time surfaces changes its signature and in terms of space-like 3-surfaces are equivalent. This means effective 2-dimensionality in the sense that partonic 2-surfaces defined as intersections of these two kinds of surfaces plus 4-D tangent space data at partonic 2-surfaces code for the physics. Quantum classical correspondence requires the coding of the quantum numbers characterizing quantum states assigned to the partonic 2-surfaces to the geometry of space-time surface. This is achieved by adding to the modified Dirac action a measurement interaction term assigned with light-like 3-surfaces.

- The replacement of strings with light-like 3-surfaces equivalent to space-like 3-surfaces means enormous generalization of the super conformal symmetries of string models. A further generalization of these symmetries to non-local Yangian symmetries generalizing the recently discovered Yangian symmetry of $\mathcal{N} = 4$ supersymmetric Yang-Mills theories is highly suggestive. Here the replacement of point like particles with partonic 2-surfaces means the replacement of conformal symmetry of Minkowski space with infinite-dimensional superconformal algebras. Yangian symmetry provides also a further refinement to the notion of conserved quantum numbers allowing to define them for bound states using non-local energy conserved currents.

- A further attractive idea is that quantum TGD reduces to almost topological quantum field theory. This is possible if the Kähler action for the preferred extremals defining WCW Kähler function reduces to a 3-D boundary term. This takes place if the conserved currents are so called Beltrami fields with the defining property that the coordinates associated with flow lines extend to single global coordinate variable. This ansatz together with the weak form of electric-magnetic duality reduces the Kähler action to Chern-Simons term with the condition that the 3-surfaces are extremals of Chern-Simons action subject to the constraint force defined by the weak form of electric magnetic duality. It is the latter constraint which prevents the trivialization of the theory to a topological quantum field theory. Also the identification of the Kähler function of WCW as Dirac determinant finds support as well as the description of the scattering amplitudes in terms of braids with interpretation in terms of finite measurement resolution coded to the basic structure of the solutions of field equations.

- In standard QFT Feynman diagrams provide the description of scattering amplitudes. The beauty of Feynman diagrams is that they realize unitarity automatically via the so called Cutkosky rules. In contrast to Feynman's original beliefs, Feynman diagrams and virtual particles are taken only as a convenient mathematical tool in quantum field theories. QFT approach is however plagued by UV and IR divergences and one must keep mind open for the possibility that a genuine progress might mean opening of the black box of the virtual particle.

  In TGD framework this generalization of Feynman diagrams indeed emerges unavoidably. Light-like 3-surfaces replace the lines of Feynman diagrams and vertices are replaced by 2-D partonic 2-surfaces. Zero energy ontology and the interpretation of parton orbits as light-like

"wormhole throats" suggests that virtual particle do not differ from on mass shell particles only in that the four- and three- momenta of wormhole throats fail to be parallel. The two throats of the wormhole contact defining virtual particle would contact carry on mass shell quantum numbers but for virtual particles the four-momenta need not be parallel and can also have opposite signs of energy.

The localization of the nodes of induced spinor fields to 2-D string world sheets (and possibly also to partonic 2-surfaces) implies a stringy formulation of the theory analogous to stringy variant of twistor formalism with string world sheets having interpretation as 2-braids. In TGD framework fermionic variant of twistor Grassmann formalism leads to a stringy variant of twistor diagrammatics in which basic fermions can be said to be on mass-shell but carry non-physical helicities in the internal lines. This suggests the generalization of the Yangian symmetry to infinite-dimensional super-conformal algebras.

TGD based view about quantum consciousness relies on following ideas and inputs.

- TGD inspired theory of consciousness can be seen as a generalization of quantum measurement theory by bringing in conscious observer. The basic new elements are the resolution of the basic problem of the measurement theory by the introduction of ZEO, which brings new elements also to the quantum measurement theory and leads to a view about how the arrow of time and its flow are generated. p-Adic physics brings in the notion of negentropic entanglement and Negentropy Maximization Principle provides the basic variational principle. The possibility of negentropic entanglement predicts evolution as gradual increase of negentropic resources of the Universe.

- The notion of self - at least as effective notion- emerges naturally from negentropic entanglement and from more precise view about sequence of state function reductions which now leaves invariant only the second part of zero energy state but changes the other one. The generation of "Akashic records" defined by negentropically entangled systems are in vital role in the understanding of evolution.

- CDs serve as correlates of selves and a hierarchy of selves is predicted and closely relates to the p-adic hierarchy and hierarchy of Planck constants. Subselves are interpreted as mental images of self and the sharing of mental images by fusion of subselves gives rise to a kind of stereo consciousness.

The following list gives the basic elements of TGD inspire quantum biology.

- Many-sheeted space-time allows the interpretation of the structures of macroscopic world around us in terms of space-time topology. Magnetic/field body acts as intentional agent using biological body as a sensory receptor and motor instrument and controlling biological body and inheriting its hierarchical fractal structure. Fractal hierarchy of EEGs and its variants can be seen as communication and control tools of magnetic body. Also collective levels of consciousness have a natural interpretation in terms of magnetic body. Magnetic body makes also possible entanglement in macroscopic length scales. The braiding of magnetic flux tubes makes possible topological quantum computations and provides a universal mechanism of memory. One can also undersand the real function of various information molecules and corresponding receptors by interpreting the receptors as addresses in quantum computer memory and information molecules as ends of flux tubes which attach to these receptors to form a connection in quantum web.

- Magnetic body carrying dark matter and forming an onion-like structure with layers characterized by large values of Planck constant is the key concept of TGD inspired view about Quantum Mind to biology.. Magnetic body is identified as intentional agent using biological body as sensory receptor and motor instrument. EEG and its fractal variants are identified as a communication and control tool of the magnetic body and a fractal hierarchy of analogs of EEG is predicted. Living system is identified as a kind of Indra's net with biomolecules representing the nodes of the net and magnetic flux tubes connections between then.

  The reconnection of magnetic flux tubes and phase transitions changing Planck constant and therefore the lengths of the magnetic flux tubes are identified as basic mechanisms behind

DNA replication and analogous processes and also behind the phase transitions associated with the gel phase in cell interior. The braiding of magnetic flux makes possible universal memory representation recording the motions of the basic units connected by flux tubes. Braiding also defines topological quantum computer programs updated continually by the flows of the basic units. The model of DNA as topological quantum computer is discussed as an application. In zero energy ontology the braiding actually generalize to 2-braiding for string world sheets in 4-D space-time and brings in new elements.

- Zero energy ontology (ZEO) makes possible the proposed p-adic description of intentions and cognitions and their transformations to action. Time mirror mechanism based on sending of negative energy signal to geometric past would apply to both long term memory recall, remote metabolism, and realization of intentional acting as an activity beginning in the geometric past in accordance with the findings of Libet. ZEO gives a precise content to the notion of negative energy signal in terms of zero energy state for which the arrow of geometric time is opposite to the standard one.

  The associated notion of causal diamond (CD) is essential element and assigns to elementary particles new fundamental time scales which are macroscopic: for electron the time scale is .1 seconds, the fundamental biorhythm. An essentially new element is time-like entanglement which allows to understand among other things the quantum counterparts of Boolean functions in terms of time-like entanglement in fermionic degrees of freedom.

- The assignment of dark matter with a hierarchy of Planck constants gives rise to a hierarchy of macroscopic quantum phases making possible macroscopic and macrotemporal quantum coherence and allowing to understand evolution as a gradual increase of Planck constant. The model for dark nucleons leads to a surprising conclusion: the states of nucleons correspond to DNA, RNA, tRNA, and amino-acids in a natural manner and vertebrate genetic code as correspondence between DNA and amino-acids emerges naturally. This suggests that genetic code is realized at the level of dark hadron physics and living matter in the usual sense provides a secondary representation for it. The hierarchy of Planck constants emerges from basic TGD under rather general assumptions.

- p-Adic physics can be identified as physics of cognition and intentionality. Negentropic entanglement possible for number theoretic entanglement entropy makes sense for rational (and even algebraic) entanglement and leads to the identification of life as something residing in the intersection of real and p-adic worlds. NMP respects negentropic entanglement and the attractive idea is that the experience of understanding and positively colored emotions relate to negentropic entanglement.

- Living matter as conscious hologram is one of the basic ideas of TGD inspired biology and consciousness theory. The basic objection against TGD is that the interference of classical fields is impossible in the standard sense for the reason that that classical fields are not primary dynamical variables in TGD Universe. The resolution is based on the observation that only the interference of the effects caused by these fields can be observed experimentally and that many-sheeted space-time allows to realized the summation of effects in terms of multiple topological condensations of particles to several parallel space-time sheets. One concrete implication is fractality of qualia. Qualia appear in very wide range of scales: our qualia could in fact be those of magnetic body. The proposed mechanism for the generation of qualia realizes the fractality idea.

Various anomalies of living matter have been in vital role in the development of not only TGD view about living matter but also TGD itself.

- TGD approach to living matter was strongly motivated by the findings about strange behavior of cell membrane and of cellular water, and gel behavior of cytoplasm. Also the findings about effects of ELF em fields on vertebrate brain were decisive and led to the proposal of the hierarchy of Planck constants found later to emerge naturally from the non-determinism of Kähler action. Rather satisfactorily, the other manner to introduce the hierarchy of Planck constants is in terms of gravitational Planck constant: at least in microscopic scales the equivalence of these approaches makes sense and leads to highly non-trivial predictions. The basic

testable prediction is that dark photons have cyclotron frequencies inversely proportional to their massess but universal energy spectrum in visible and UV range which corresponds to the transition energies for biomolecules so that they are ideal for biocontrol at the level of both magnetic bodies and at the level of biochemistry.

- Water is in key role in living matter and also in TGD inspired view about living matter. The anomalies of water lead to a model for dark nuclei as dark proton strings with the surprising prediction that DNA, RNA, aninoacids and even tRNA are in one-one correspondence with the resulting 3-quark states and that vertebrate genetic code emerges naturally. This leads to a vision about water as primordial lifeform still playing a vital role in living organisms. The model of water memory and homeopathy in turn generalizes to a vision about how immune system might have evolved.

- Metabolic energy is necessary for conscious information processing in living matter. This suggests that metabolism should be basically tranfer of negentropic entanglement from nutrients to the organism. ATP could be seen as a molecule of consciousness in this picture and high energy phosphate bond would make possible the transfer of negentropy.

What I have said above is strongly biased view about the recent situation in quantum TGD and its applications to biology and consciousness. This vision is single man's view and doomed to contain unrealistic elements as I know from experience. My dream is that young critical readers could take this vision seriously enough to try to demonstrate that some of its basic premises are wrong or to develop an alternative based on these or better premises. I must be however honest and tell that 37 years of TGD is a really vast bundle of thoughts and quite a challenge for anyone who is not able to cheat himself by taking the attitude of a blind believer or a light-hearted debunker trusting on the power of easy rhetoric tricks.

Karkkila, October, 30, Finland

Matti Pitkänen

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Neither TGD nor these books would exist without the help and encouragement of many people. The friendship with Heikki and Raija Haila and their family have been kept me in contact with the everyday world and without this friendship I would not have survived through these lonely 32 years most of which I have remained unemployed as a scientific dissident. I am happy that my children have understood my difficult position and like my friends have believed that what I am doing is something valuable although I have not received any official recognition for it.

During last decade Tapio Tammi has helped me quite concretely by providing the necessary computer facilities and being one of the few persons in Finland with whom to discuss about my work. I have had also stimulating discussions with Samuli Penttinen who has also helped to get through the economical situations in which there seemed to be no hope. The continual updating of fifteen online books means quite a heavy bureaucracy at the level of bits and without a systemization one ends up with endless copying and pasting and internal consistency is soon lost. Pekka Rapinoja has offered his help in this respect and I am especially grateful for him for my Python skills. Also Matti Vallinkoski has helped me in computer related problems.

The collaboration with Lian Sidorov was extremely fruitful and she also helped me to survive economically through the hardest years. The participation to CASYS conferences in Liege has been an important window to the academic world and I am grateful for Daniel Dubois and Peter Marcer for making this participation possible. The discussions and collaboration with Eduardo de Luna and Istvan Dienes stimulated the hope that the communication of new vision might not be a mission impossible after all. Also blog discussions have been very useful. During these years I have received innumerable email contacts from people around the world. In particualr, I am grateful for Mark McWilliams and Ulla Matfolk for providing links to possibly interesting web sites and articles. These contacts have helped me to avoid the depressive feeling of being some kind of Don Quixote of Science and helped me to widen my views: I am grateful for all these people.

In the situation in which the conventional scientific communication channels are strictly closed it is important to have some loop hole through which the information about the work done can at least in principle leak to the publicity through the iron wall of the academic censorship. Without any exaggeration I can say that without the world wide web I would not have survived as a scientist nor as individual. Homepage and blog are however not enough since only the formally published result is a result in recent day science. Publishing is however impossible without a direct support from power holders- even in archives like arXiv.org.

Situation changed for five years ago as Andrew Adamatsky proposed the writing of a book about TGD when I had already got used to the thought that my work would not be published during my life time. The Prespacetime Journal and two other journals related to quantum biology and consciousness - all of them founded by Huping Hu - have provided this kind of loop holes. In particular, Dainis Zeps, Phil Gibbs, and Arkadiusz Jadczyk deserve my gratitude for their kind help in the preparation of an article series about TGD catalyzing a considerable progress in the understanding of quantum TGD. Also the viXra archive founded by Phil Gibbs and its predecessor Archive Freedom have been of great help: Victor Christianto deserves special thanks for doing the hard work needed to run Archive Freedom. Also the Neuroquantology Journal founded by Sultan Tarlaci deserves a special mention for its publication policy. And last but not least: there are people who experience as a fascinating intellectual challenge to spoil the practical working conditions of a person working with something which might be called unified theory: I am grateful for the people who have helped me to survive through the virus attacks, an activity which has taken roughly one month per year during the last half decade and given a strong hue of grey to my hair.

For a person approaching his sixty year birthday it is somewhat easier to overcome the hard

feelings due to the loss of academic human rights than for an inpatient youngster. Unfortunately the economic situation has become increasingly difficult during the twenty years after the economic depression in Finland which in practice meant that Finland ceased to be a constitutional state in the strong sense of the word. It became possible to depose people like me from the society without fear about public reactions and the classification as dropout became a convenient tool of ridicule to circumvent the ethical issues. During last few years when the right wing has held the political power this trend has been steadily strengthening. In this kind of situation the concrete help from individuals has been and will be of utmost importance. Against this background it becomes obvious that this kind of work is not possible without the support from outside and I apologize for not being able to mention all the people who have helped me during these years.

Karkkila, October, 30, 2015 Finland

Matti Pitkänen

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Chapter 1

Introduction

1.1 Basic Ideas Of Topological Geometrodynamics (TGD)

Standard model describes rather successfully both electroweak and strong interactions but sees them as totally separate and contains a large number of parameters which it is not able to predict. For about four decades ago unified theories known as Grand Unified Theories (GUTs) trying to understand electroweak interactions and strong interactions as aspects of the same fundamental gauge interaction assignable to a larger symmetry group emerged. Later superstring models trying to unify even gravitation and strong and weak interactions emerged. The shortcomings of both GUTs and superstring models are now well-known. If TGD - whose basic idea emerged 37 years ago - would emerge now it would be seen as an attempt trying to solve the difficulties of these approaches to unification.

The basic physical picture behind TGD corresponds to a fusion of two rather disparate approaches: namely TGD as a Poincare invariant theory of gravitation and TGD as a generalization of the old-fashioned string model.

1.1.1 Basic Vision Very Briefly

T(opological) G(eometro)D(ynamics) is one of the many attempts to find a unified description of basic interactions. The development of the basic ideas of TGD to a relatively stable form took time of about half decade [K1].

The basic vision and its relationship to existing theories is now rather well understood.

1. Space-times are representable as 4-surfaces in the 8-dimensional imbedding space $H = M^4 \times CP_2$, where M^4 is 4-dimensional (4-D) Minkowski space and CP_2 is 4-D complex projective space (see Appendix).

2. Induction procedure (a standard procedure in fiber bundle theory, see Appendix) allows to geometrize various fields. Space-time metric characterizing gravitational fields corresponds to the induced metric obtained by projecting the metric tensor of H to the space-time surface. Electroweak gauge potentials are identified as projections of the components of CP_2 spinor connection to the space-time surface, and color gauge potentials as projections of CP_2 Killing vector fields representing color symmetries. Also spinor structure can be induced: induced spinor gamma matrices are projections of gamma matrices of H and induced spinor fields just H spinor fields restricted to space-time surface. Spinor connection is also projected. The interpretation is that distances are measured in imbedding space metric and parallel translation using spinor connection of imbedding space.

   The induction procedure applies to octonionic structure and the conjecture is that for preferred extremals the induced octonionic structure is quaternionic: again one just projects the octonion units. I have proposed that one can lift space-time surfaces in H to the Cartesian product of the twistor spaces of M^4 and CP_2, which are the only 4-manifolds allowing twistor space with Kähler structure. Now the twistor structure would be induced in some sense, and should co-incide with that associated with the induced metric. Clearly, the 2-spheres defining

the fibers of twistor spaces of M^4 and CP_2 must allow identification: this 2-sphere defines the S^2 fiber of the twistor space of space-time surface. This poses constraint on the imbedding of the twistor space of space-time surfaces as sub-manifold in the Cartesian product of twistor spaces.

3. Geometrization of quantum numbers is achieved. The isometry group of the geometry of CP_2 codes for the color gauge symmetries of strong interactions. Vierbein group codes for electroweak symmetries, and explains their breaking in terms of CP_2 geometry so that standard model gauge group results. There are also important deviations from standard model: color quantum numbers are not spin-like but analogous to orbital angular momentum: this difference is expected to be seen only in CP_2 scale. In contrast to GUTs, quark and lepton numbers are separately conserved and family replication has a topological explanation in terms of topology of the partonic 2-surface carrying fermionic quantum numbers.

   M^4 and CP_2 are unique choices for many other reasons. For instance, they are the unique 4-D space-times allowing twistor space with Kähler structure. M^4 light-cone boundary allows a huge extension of 2-D conformal symmetries. Imbedding space H has a number theoretic interpretation as 8-D space allowing octonionic tangent space structure. M^4 and CP_2 allow quaternionic structures. Therefore standard model symmetries have number theoretic meaning.

4. Induced gauge potentials are expressible in terms of imbedding space coordinates and their gradients and general coordinate invariance implies that there are only 4 field like variables locally. Situation is thus extremely simple mathematically. The objection is that one loses linear superposition of fields. The resolution of the problem comes from the generalization of the concepts of particle and space-time.

   Space-time surfaces can be also particle like having thus finite size. In particular, space-time regions with Euclidian signature of the induced metric (temporal and spatial dimensions in the same role) emerge and have interpretation as lines of generalized Feynman diagrams. Particle in space-time can be identified as a topological inhomogenuity in background space-time surface which looks like the space-time of general relativity in long length scales.

   One ends up with a generalization of space-time surface to many-sheeted space-time with space-time sheets having extremely small distance of about 10^4 Planck lengths (CP_2 size). As one adds a particle to this kind of structure, it touches various space-time sheets and thus interacts with the associated classical fields. Their effects superpose linearly in good approximation and linear superposition of fields is replaced with that for their effects.

   This resolves the basic objection. It also leads to the understanding of how the space-time of general relativity and quantum field theories emerges from TGD space-time as effective space-time when the sheets of many-sheeted space-time are lumped together to form a region of Minkowski space with metric replaced with a metric identified as the sum of empty Minkowski metric and deviations of the metrics of sheets from empty Minkowski metric. Gauge potentials are identified as sums of the induced gauge potentials. TGD is therefore a microscopic theory from which standard model and general relativity follow as a topological simplification however forcing to increase dramatically the number of fundamental field variables.

5. A further objection is that classical weak fields identified as induced gauge fields are long ranged and should cause large parity breaking effects due to weak interactions. These effects are indeed observed but only in living matter. A possible resolution of problem is implied by the condition that the modes of the induced spinor fields have well-defined electromagnetic charge. This forces their localization to 2-D string world sheets in the generic case having vanishing weak gauge fields so that parity breaking effects emerge just as they do in standard model. Also string model like picture emerges from TGD and one ends up with a rather concrete view about generalized Feynman diagrammatics. A possible objection is that the Kähler-Dirac gamma matrices do not define an integrable distribution of 2-planes defining string world sheet.

An even strong condition would be that the induced classical gauge fields at string world sheet vanish: this condition is allowed by the topological description of particles. The CP_2 projection of string world sheet would be 1-dimensional. Also the number theoretical condition that octonionic and ordinary spinor structures are equivalent guaranteeing that fermionic dynamics is associative leads to the vanishing of induced gauge fields.

The natural action would be given by string world sheet area, which is present only in the space-time regions with Minkowskian signature. Gravitational constant would be present as a fundamental constant in string action and the ratio $\hbar/G/R^2$ would be determined by quantum criticality condition. The hierarchy of Planck constants $h_{eff}/h = n$ assigned to dark matter in TGD framework would allow to circumvent the objection that only objects of length of order Planck length are possible since string tension given by $T = 1/\hbar_{eff}G$ apart from numerical factor could be arbitrary small. This would make possible gravitational bound states as partonic 2-surfaces as structures connected by strings and solve the basic problem of super string theories. This option allows the natural interpretation of M^4 type vacuum extremals with CP_2 projection, which is Lagrange manifold as good approximations for space-time sheets at macroscopic length scales. String area does not contribute to the Kähler function at all.

Whether also induced spinor fields associated with Kähler-Dirac action and de-localized inside entire space-time surface should be allowed remains an open question: super-conformal symmetry strongly suggests their presence. A possible interpretation for the corresponding spinor modes could be in terms of dark matter, sparticles, and hierarchy of Planck constants.

It is perhaps useful to make clear what TGD is not and also what new TGD can give to physics.

1. TGD is *not* just General Relativity made concrete by using imbeddings: the 4-surface property is absolutely essential for unifying standard model physics with gravitation and to circumvent the incurable conceptual problems of General Relativity. The many-sheeted space-time of TGD gives rise only at macroscopic limit to GRT space-time as a slightly curved Minkowski space. TGD is *not* a Kaluza-Klein theory although color gauge potentials are analogous to gauge potentials in these theories.

   TGD space-time is 4-D and its dimension is due to completely unique conformal properties of light-cone boundary and 3-D light-like surfaces implying enormous extension of the ordinary conformal symmetries. Light-like 3-surfaces represent orbits of partonic 2-surfaces and carry fundamental fermions at 1-D boundaries of string world sheets. TGD is *not* obtained by performing Poincare gauging of space-time to introduce gravitation and plagued by profound conceptual problems.

2. TGD is *not* a particular string model although string world sheets emerge in TGD very naturally as loci for spinor modes: their 2-dimensionality makes among other things possible quantum deformation of quantization known to be physically realized in condensed matter, and conjectured in TGD framework to be crucial for understanding the notion of finite measurement resolution. Hierarchy of objects of dimension up to 4 emerge from TGD: this obviously means analogy with branes of super-string models.

   TGD is *not* one more item in the collection of string models of quantum gravitation relying on Planck length mystics. Dark matter becomes an essential element of quantum gravitation and quantum coherence in astrophysical scales is predicted just from the assumption that strings connecting partonic 2-surfaces serve are responsible for gravitational bound states.

   TGD is *not* a particular string model although AdS/CFT duality of super-string models generalizes due to the huge extension of conformal symmetries and by the identification of WCW gamma matrices as Noether super-charges of super-symplectic algebra having a natural conformal structure.

3. TGD is *not* a gauge theory. In TGD framework the counterparts of also ordinary gauge symmetries are assigned to super-symplectic algebra (and its Yangian [A11] [B10, B7, B8]), which is a generalization of Kac-Moody algebras rather than gauge algebra and suffers a

fractal hierarchy of symmetry breakings defining hierarchy of criticalities. TGD is *not* one more quantum field theory like structure based on path integral formalism: path integral is replaced with functional integral over 3-surfaces, and the notion of classical space-time becomes exact part of the theory. Quantum theory becomes formally a purely classical theory of WCW spinor fields: only state function reduction is something genuinely quantal.

4. TGD view about spinor fields is *not* the standard one. Spinor fields appear at three levels. Spinor modes of the imbedding space are analogs of spinor modes charactering incoming and outgoing states in quantum field theories. Induced second quantized spinor fields at space-time level are analogs of stringy spinor fields. Their modes are localized by the well-definedness of electro-magnetic charge and by number theoretic arguments at string world sheets. Kähler-Dirac action is fixed by supersymmetry implying that ordinary gamma matrices are replaced by what I call Kähler-Dirac gamma matrices - this something new. WCW spinor fields, which are classical in the sense that they are not second quantized, serve as analogs of fields of string field theory and imply a geometrization of quantum theory.

5. TGD is in some sense an extremely conservative geometrization of entire quantum physics: *no* additional structures such as gauge fields as independent dynamical degrees of freedom are introduced: Kähler geometry and associated spinor structure are enough. "Topological" in TGD should not be understood as an attempt to reduce physics to torsion (see for instance [B6]) or something similar. Rather, TGD space-time is topologically non-trivial in all scales and even the visible structures of everyday world represent non-trivial topology of space-time in TGD Universe.

6. Twistor space - or rather, a generalization of twistor approach replacing masslessness in 4-D sense with masslessness in 8-D sense and thus allowing description of also massive particles - emerged originally as a technical tool, and its Kähler structure is possible only for $H = M^4 \times CP_2$. It however turned out that much more than a technical tool is in question. What is genuinely new is the infinite-dimensional character of the Kähler geometry making it highly unique, and its generalization to p-adic number fields to describe correlates of cognition. Also the hierarchies of Planck constants $h_{eff} = n \times h$ reducing to the quantum criticality of TGD Universe and p-adic length scales and Zero Energy Ontology represent something genuinely new.

The great challenge is to construct a mathematical theory around these physically very attractive ideas and I have devoted the last41 years for the realization of this dream and this has resulted 24 online books about TGD and nine online books about TGD inspired theory of consciousness and of quantum biology.

1.1.2 Two Visions About TGD And Their Fusion

As already mentioned, TGD can be interpreted both as a modification of general relativity and generalization of string models.

TGD as a Poincare invariant theory of gravitation

The first approach was born as an attempt to construct a Poincare invariant theory of gravitation. Space-time, rather than being an abstract manifold endowed with a pseudo-Riemannian structure, is regarded as a surface in the 8-dimensional space $H = M^4_{\times} CP_2$, where M^4 denotes Minkowski space and $CP_2 = SU(3)/U(2)$ is the complex projective space of two complex dimensions [A21, A25, A17, A24].

The identification of the space-time as a sub-manifold [A22, A31] of $M^4 \times CP_2$ leads to an exact Poincare invariance and solves the conceptual difficulties related to the definition of the energy-momentum in General Relativity.

It soon however turned out that sub-manifold geometry, being considerably richer in structure than the abstract manifold geometry, leads to a geometrization of all basic interactions. First, the geometrization of the elementary particle quantum numbers is achieved. The geometry of CP_2 explains electro-weak and color quantum numbers. The different H-chiralities of H-spinors

correspond to the conserved baryon and lepton numbers. Secondly, the geometrization of the field concept results. The projections of the CP_2 spinor connection, Killing vector fields of CP_2 and of H-metric to four-surface define classical electro-weak, color gauge fields and metric in X^4.

The choice of H is unique from the condition that TGD has standard model symmetries. Also number theoretical vision selects $H = M^4 \times CP_2$ uniquely. M^4 and CP_2 are also unique spaces allowing twistor space with Kähler structure.

TGD as a generalization of the hadronic string model

The second approach was based on the generalization of the mesonic string model describing mesons as strings with quarks attached to the ends of the string. In the 3-dimensional generalization 3-surfaces correspond to free particles and the boundaries of the 3- surface correspond to partons in the sense that the quantum numbers of the elementary particles reside on the boundaries. Various boundary topologies (number of handles) correspond to various fermion families so that one obtains an explanation for the known elementary particle quantum numbers. This approach leads also to a natural topological description of the particle reactions as topology changes: for instance, two-particle decay corresponds to a decay of a 3-surface to two disjoint 3-surfaces.

This decay vertex does not however correspond to a direct generalization of trouser vertex of string models. Indeed, the important difference between TGD and string models is that the analogs of string world sheet diagrams do not describe particle decays but the propagation of particles via different routes. Particle reactions are described by generalized Feynman diagrams for which 3-D light-like surface describing particle propagating join along their ends at vertices. As 4-manifolds the space-time surfaces are therefore singular like Feynman diagrams as 1-manifolds.

Quite recently, it has turned out that fermionic strings inside space-time surfaces define an exact part of quantum TGD and that this is essential for understanding gravitation in long length scales. Also the analog of AdS/CFT duality emerges in that the Kähler metric can be defined either in terms of Kähler function identifiable as Kähler action assignable to Euclidian space-time regions or Kähler action + string action assignable to Minkowskian regions.

The recent view about construction of scattering amplitudes is very "stringy". By strong form of holography string world sheets and partonic 2-surfaces provide the data needed to construct scattering amplitudes. Space-time surfaces are however needed to realize quantum-classical correspondence necessary to understand the classical correlates of quantum measurement. There is a huge generalization of the duality symmetry of hadronic string models. Scattering amplitudes can be regarded as sequences of computational operations for the Yangian of super-symplectic algebra. Product and co-product define the basic vertices and realized geometrically as partonic 2-surfaces and algebraically as multiplication for the elements of Yangian identified as super-symplectic Noether charges assignable to strings. Any computational sequences connecting given collections of algebraic objects at the opposite boundaries of causal diamond (CD) produce identical scattering amplitudes.

Fusion of the two approaches via a generalization of the space-time concept

The problem is that the two approaches to TGD seem to be mutually exclusive since the orbit of a particle like 3-surface defines 4-dimensional surface, which differs drastically from the topologically trivial macroscopic space-time of General Relativity. The unification of these approaches forces a considerable generalization of the conventional space-time concept. First, the topologically trivial 3-space of General Relativity is replaced with a "topological condensate" containing matter as particle like 3-surfaces "glued" to the topologically trivial background 3-space by connected sum operation. Secondly, the assumption about connectedness of the 3-space is given up. Besides the "topological condensate" there could be "vapor phase" that is a "gas" of particle like 3-surfaces and string like objects (counterpart of the "baby universes" of GRT) and the non-conservation of energy in GRT corresponds to the transfer of energy between different sheets of the space-time and possibly existence vapour phase.

What one obtains is what I have christened as many-sheeted space-time (see **Fig.** `http://tgdtheory.fi/appfigures/manysheeted.jpg` or **Fig. ??** in the appendix of this book). One particular aspect is topological field quantization meaning that various classical fields assignable to a physical system correspond to space-time sheets representing the classical fields to that particular

system. One can speak of the field body of a particular physical system. Field body consists of topological light rays, and electric and magnetic flux quanta. In Maxwell's theory system does not possess this kind of field identity. The notion of magnetic body is one of the key players in TGD inspired theory of consciousness and quantum biology.

This picture became more detailed with the advent of zero energy ontology (ZEO). The basic notion of ZEO is causal diamond (CD) identified as the Cartesian product of CP_2 and of the intersection of future and past directed light-cones and having scale coming as an integer multiple of CP_2 size is fundamental. CDs form a fractal hierarchy and zero energy states decompose to products of positive and negative energy parts assignable to the opposite boundaries of CD defining the ends of the space-time surface. The counterpart of zero energy state in positive energy ontology is the pair of initial and final states of a physical event, say particle reaction.

At space-time level ZEO means that 3-surfaces are pairs of space-like 3-surfaces at the opposite light-like boundaries of CD. Since the extremals of Kähler action connect these, one can say that by holography the basic dynamical objects are the space-time surface connecting these 3-surfaces. This changes totally the vision about notions like self-organization: self-organization by quantum jumps does not take for a 3-D system but for the entire 4-D field pattern associated with it.

General Coordinate Invariance (GCI) allows to identify the basic dynamical objects as space-like 3-surfaces at the ends of space-time surface at boundaries of CD: this means that space-time surface is analogous to Bohr orbit. An alternative identification is as light-like 3-surfaces at which the signature of the induced metric changes from Minkowskian to Euclidian and interpreted as lines of generalized Feynman diagrams. Also the Euclidian 4-D regions would have similar interpretation. The requirement that the two interpretations are equivalent, leads to a strong form of General Coordinate Invariance. The outcome is effective 2-dimensionality stating that the partonic 2-surfaces identified as intersections of the space-like ends of space-time surface and light-like wormhole throats are the fundamental objects. That only effective 2-dimensionality is in question is due to the effects caused by the failure of strict determinism of Kähler action. In finite length scale resolution these effects can be neglected below UV cutoff and above IR cutoff. One can also speak about strong form of holography.

1.1.3 Basic Objections

Objections are the most powerful tool in theory building. The strongest objection against TGD is the observation that all classical gauge fields are expressible in terms of four imbedding space coordinates only- essentially CP_2 coordinates. The linear superposition of classical gauge fields taking place independently for all gauge fields is lost. This would be a catastrophe without many-sheeted space-time. Instead of gauge fields, only the effects such as gauge forces are superposed. Particle topologically condenses to several space-time sheets simultaneously and experiences the sum of gauge forces. This transforms the weakness to extreme economy: in a typical unified theory the number of primary field variables is countered in hundreds if not thousands, now it is just four.

Second objection is that TGD space-time is quite too simple as compared to GRT space-time due to the imbeddability to 8-D imbedding space. One can also argue that Poincare invariant theory of gravitation cannot be consistent with General Relativity. The above interpretation allows to understand the relationship to GRT space-time and how Equivalence Principle (EP) follows from Poincare invariance of TGD. The interpretation of GRT space-time is as effective space-time obtained by replacing many-sheeted space-time with Minkowski space with effective metric determined as a sum of Minkowski metric and sum over the deviations of the induced metrices of space-time sheets from Minkowski metric. Poincare invariance suggests strongly classical EP for the GRT limit in long length scales at least. One can consider also other kinds of limits such as the analog of GRT limit for Euclidian space-time regions assignable to elementary particles. In this case deformations of CP_2 metric define a natural starting point and CP_2 indeed defines a gravitational instanton with very large cosmological constant in Einstein-Maxwell theory. Also gauge potentials of standard model correspond classically to superpositions of induced gauge potentials over space-time sheets.

Topological field quantization

Topological field quantization distinguishes between TGD based and more standard - say Maxwellian - notion of field. In Maxwell's fields created by separate systems superpose and one cannot tell which part of field comes from which system except theoretically. In TGD these fields correspond to different space-time sheets and only their effects on test particle superpose. Hence physical systems have well-defined field identifies - field bodies - in particular magnetic bodies.

The notion of magnetic body carrying dark matter with non-standard large value of Planck constant has become central concept in TGD inspired theory of consciousness and living matter, and by starting from various anomalies of biology one ends up to a rather detailed view about the role of magnetic body as intentional agent receiving sensory input from the biological body and controlling it using EEG and its various scaled up variants as a communication tool. Among other thins this leads to models for cell membrane, nerve pulse, and EEG.

1.1.4 P-Adic Variants Of Space-Time Surfaces

There is a further generalization of the space-time concept inspired by p-adic physics forcing a generalization of the number concept through the fusion of real numbers and various p-adic number fields. One might say that TGD space-time is adelic. Also the hierarchy of Planck constants forces a generalization of the notion of space-time but this generalization can be understood in terms of the failure of strict determinism for Kähler action defining the fundamental variational principle behind the dynamics of space-time surfaces.

A very concise manner to express how TGD differs from Special and General Relativities could be following. Relativity Principle (Poincare Invariance), General Coordinate Invariance, and Equivalence Principle remain true. What is new is the notion of sub-manifold geometry: this allows to realize Poincare Invariance and geometrize gravitation simultaneously. This notion also allows a geometrization of known fundamental interactions and is an essential element of all applications of TGD ranging from Planck length to cosmological scales. Sub-manifold geometry is also crucial in the applications of TGD to biology and consciousness theory.

1.1.5 The Threads In The Development Of Quantum TGD

The development of TGD has involved several strongly interacting threads: physics as infinite-dimensional geometry; TGD as a generalized number theory, the hierarchy of Planck constants interpreted in terms of dark matter hierarchy, and TGD inspired theory of consciousness. In the following these threads are briefly described.

The theoretical framework involves several threads.

1. Quantum T(opological) G(eometro)D(ynamics) as a classical spinor geometry for infinite-dimensional WCW, p-adic numbers and quantum TGD, and TGD inspired theory of consciousness and of quantum biology have been for last decade of the second millenium the basic three strongly interacting threads in the tapestry of quantum TGD.

2. The discussions with Tony Smith initiated a fourth thread which deserves the name "TGD as a generalized number theory". The basic observation was that classical number fields might allow a deeper formulation of quantum TGD. The work with Riemann hypothesis made time ripe for realization that the notion of infinite primes could provide, not only a reformulation, but a deep generalization of quantum TGD. This led to a thorough and extremely fruitful revision of the basic views about what the final form and physical content of quantum TGD might be. Together with the vision about the fusion of p-adic and real physics to a larger coherent structure these sub-threads fused to the "physics as generalized number theory" thread.

3. A further thread emerged from the realization that by quantum classical correspondence TGD predicts an infinite hierarchy of macroscopic quantum systems with increasing sizes, that it is not at all clear whether standard quantum mechanics can accommodate this hierarchy, and that a dynamical quantized Planck constant might be necessary and strongly suggested by the failure of strict determinism for the fundamental variational principle. The identification

of hierarchy of Planck constants labelling phases of dark matter would be natural. This also led to a solution of a long standing puzzle: what is the proper interpretation of the predicted fractal hierarchy of long ranged classical electro-weak and color gauge fields. Quantum classical correspondences allows only single answer: there is infinite hierarchy of p-adically scaled up variants of standard model physics and for each of them also dark hierarchy. Thus TGD Universe would be fractal in very abstract and deep sense.

The chronology based identification of the threads is quite natural but not logical and it is much more logical to see p-adic physics, the ideas related to classical number fields, and infinite primes as sub-threads of a thread which might be called "physics as a generalized number theory". In the following I adopt this view. This reduces the number of threads to four.

TGD forces the generalization of physics to a quantum theory of consciousness, and represent TGD as a generalized number theory vision leads naturally to the emergence of p-adic physics as physics of cognitive representations. The eight online books [K54, **?**, K35, K70, K49, K69, K68, K48] about TGD and nine online books about TGD inspired theory of consciousness and of quantum biology [K50, K5, K40, K4, K22, K28, K31, K47, K63] are warmly recommended to the interested reader.

Quantum TGD as spinor geometry of World of Classical Worlds

A turning point in the attempts to formulate a mathematical theory was reached after seven years from the birth of TGD. The great insight was "Do not quantize". The basic ingredients to the new approach have served as the basic philosophy for the attempt to construct Quantum TGD since then and have been the following ones:

1. Quantum theory for extended particles is free(!), classical(!) field theory for a generalized Schrödinger amplitude in the configuration space CH ("world of classical worlds", WCW) consisting of all possible 3-surfaces in H. "All possible" means that surfaces with arbitrary many disjoint components and with arbitrary internal topology and also singular surfaces topologically intermediate between two different manifold topologies are included. Particle reactions are identified as topology changes [A27, A32, A35]. For instance, the decay of a 3-surface to two 3-surfaces corresponds to the decay $A \to B+C$. Classically this corresponds to a path of WCW leading from 1-particle sector to 2-particle sector. At quantum level this corresponds to the dispersion of the generalized Schrödinger amplitude localized to 1-particle sector to two-particle sector. All coupling constants should result as predictions of the theory since no nonlinearities are introduced.

2. During years this naive and very rough vision has of course developed a lot and is not anymore quite equivalent with the original insight. In particular, the space-time correlates of Feynman graphs have emerged from theory as Euclidian space-time regions and the strong form of General Coordinate Invariance has led to a rather detailed and in many respects unexpected visions. This picture forces to give up the idea about smooth space-time surfaces and replace space-time surface with a generalization of Feynman diagram in which vertices represent the failure of manifold property. I have also introduced the word "world of classical worlds" (WCW) instead of rather formal "configuration space". I hope that "WCW" does not induce despair in the reader having tendency to think about the technicalities involved!

3. WCW is endowed with metric and spinor structure so that one can define various metric related differential operators, say Dirac operator, appearing in the field equations of the theory [1]

4. WCW Dirac operator appearing in Super-Virasoro conditions, imbedding space Dirac operator whose modes define the ground states of Super-Virasoro representations, Kähler-Dirac operator at space-time surfaces, and the algebraic variant of M^4 Dirac operator appearing in

[1] There are four kinds of Dirac operators in TGD. The geometrization of quantum theory requires Kähler metric definable either in terms of Kähler function identified as Kähler action for Euclidian space-time regions or as anti-commutators for WCW gamma matrices identified as conformal Noether super-charges associated with the second quantized modified Dirac action consisting of string world sheet term and possibly also Kähler Dirac action in Minkowskian space-time regions. These two possible definitions reflect a duality analogous to AdS/CFT duality.

propagators. The most ambitious dream is that zero energy states correspond to a complete solution basis for the Dirac operator of WCW so that this classical free field theory would dictate M-matrices defined between positive and negative energy parts of zero energy states which form orthonormal rows of what I call U-matrix as a matrix defined between zero energy states. Given M-matrix in turn would decompose to a product of a hermitian square root of density matrix and unitary S-matrix.

M-matrix would define time-like entanglement coefficients between positive and negative energy parts of zero energy states (all net quantum numbers vanish for them) and can be regarded as a hermitian square root of density matrix multiplied by a unitary S-matrix. Quantum theory would be in well-defined sense a square root of thermodynamics. The orthogonality and hermiticity of the M-matrices commuting with S-matrix means that they span infinite-dimensional Lie algebra acting as symmetries of the S-matrix. Therefore quantum TGD would reduce to group theory in well-defined sense.

In fact the Lie algebra of Hermitian M-matrices extends to Kac-Moody type algebra obtained by multiplying hermitian square roots of density matrices with powers of the S-matrix. Also the analog of Yangian algebra involving only non-negative powers of S-matrix is possible and would correspond to a hierarchy of CDs with the temporal distances between tips coming as integer multiples of the CP_2 time.

The M-matrices associated with CDs are obtained by a discrete scaling from the minimal CD and characterized by integer n are naturally proportional to a representation matrix of scaling: $S(n) = S^n$, where S is unitary S-matrix associated with the minimal CD [K60]. This conforms with the idea about unitary time evolution as exponent of Hamiltonian discretized to integer power of S and represented as scaling with respect to the logarithm of the proper time distance between the tips of CD.

U-matrix elements between M-matrices for various CDs are proportional to the inner products $Tr[S^{-n_1} \circ H^i H^j \circ S^{n_2} \lambda]$, where λ represents unitarily the discrete Lorentz boost relating the moduli of the active boundary of CD and H^i form an orthonormal basis of Hermitian square roots of density matrices. $\circ$ tells that S acts at the active boundary of CD only. It turns out possible to construct a general representation for the U-matrix reducing its construction to that of S-matrix. S-matrix has interpretation as exponential of the Virasoro generator L_{-1} of the Virasoro algebra associated with super-symplectic algebra.

5. By quantum classical correspondence the construction of WCW spinor structure reduces to the second quantization of the induced spinor fields at space-time surface. The basic action is so called modified Dirac action (or Kähler-Dirac action) in which gamma matrices are replaced with the modified (Kähler-Dirac) gamma matrices defined as contractions of the canonical momentum currents with the imbedding space gamma matrices. In this manner one achieves super-conformal symmetry and conservation of fermionic currents among other things and consistent Dirac equation. The Kähler-Dirac gamma matrices define as anti-commutators effective metric, which might provide geometrization for some basic observables of condensed matter physics. One might also talk about bosonic emergence in accordance with the prediction that the gauge bosons and graviton are expressible in terms of bound states of fermion and anti-fermion.

6. An important result relates to the notion of induced spinor connection. If one requires that spinor modes have well-defined em charge, one must assume that the modes in the generic situation are localized at 2-D surfaces - string world sheets or perhaps also partonic 2-surfaces - at which classical W boson fields vanish. Covariantly constant right handed neutrino generating super-symmetries forms an exception. The vanishing of also Z^0 field is possible for Kähler-Dirac action and should hold true at least above weak length scales. This implies that string model in 4-D space-time becomes part of TGD. Without these conditions classical weak fields can vanish above weak scale only for the GRT limit of TGD for which gauge potentials are sums over those for space-time sheets.

   The localization simplifies enormously the mathematics and one can solve exactly the Kähler-Dirac equation for the modes of the induced spinor field just like in super string models.

At the light-like 3-surfaces at which the signature of the induced metric changes from Euclidian to Minkowskian so that $\sqrt{g_4}$ vanishes one can pose the condition that the algebraic analog of massless Dirac equation is satisfied by the nodes so that Kähler-Dirac action gives massless Dirac propagator localizable at the boundaries of the string world sheets.

The evolution of these basic ideas has been rather slow but has gradually led to a rather beautiful vision. One of the key problems has been the definition of Kähler function. Kähler function is Kähler action for a preferred extremal assignable to a given 3-surface but what this preferred extremal is? The obvious first guess was as absolute minimum of Kähler action but could not be proven to be right or wrong. One big step in the progress was boosted by the idea that TGD should reduce to almost topological QFT in which braids would replace 3-surfaces in finite measurement resolution, which could be inherent property of the theory itself and imply discretization at partonic 2-surfaces with discrete points carrying fermion number.

It took long time to realize that there is no discretization in 4-D sense - this would lead to difficulties with basic symmetries. Rather, the discretization occurs for the parameters characterizing co-dimension 2 objects representing the information about space-time surface so that they belong to some algebraic extension of rationals. These 2-surfaces - string world sheets and partonic 2-surfaces - are genuine physical objects rather than a computational approximation. Physics itself approximates itself, one might say! This is of course nothing but strong form of holography.

1. TGD as almost topological QFT vision suggests that Kähler action for preferred extremals reduces to Chern-Simons term assigned with space-like 3-surfaces at the ends of space-time (recall the notion of causal diamond (CD)) and with the light-like 3-surfaces at which the signature of the induced metric changes from Minkowskian to Euclidian. Minkowskian and Euclidian regions would give at wormhole throats the same contribution apart from coefficients and in Minkowskian regions the $\sqrt{g_4}$ factorc coming from metric would be imaginary so that one would obtain sum of real term identifiable as Kähler function and imaginary term identifiable as the ordinary Minkowskian action giving rise to interference effects and stationary phase approximation central in both classical and quantum field theory.

   Imaginary contribution - the presence of which I realized only after 33 years of TGD - could also have topological interpretation as a Morse function. On physical side the emergence of Euclidian space-time regions is something completely new and leads to a dramatic modification of the ideas about black hole interior.

2. The manner to achieve the reduction to Chern-Simons terms is simple. The vanishing of Coulomb contribution to Kähler action is required and is true for all known extremals if one makes a general ansatz about the form of classical conserved currents. The so called weak form of electric-magnetic duality defines a boundary condition reducing the resulting 3-D terms to Chern-Simons terms. In this manner almost topological QFT results. But only "almost" since the Lagrange multiplier term forcing electric-magnetic duality implies that Chern-Simons action for preferred extremals depends on metric.

TGD as a generalized number theory

Quantum T(opological)D(ynamics) as a classical spinor geometry for infinite-dimensional configuration space ("world of classical worlds", WCW), p-adic numbers and quantum TGD, and TGD inspired theory of consciousness, have been for last ten years the basic three strongly interacting threads in the tapestry of quantum TGD. The fourth thread deserves the name "TGD as a generalized number theory". It involves three separate threads: the fusion of real and various p-adic physics to a single coherent whole by requiring number theoretic universality discussed already, the formulation of quantum TGD in terms of hyper-counterparts of classical number fields identified as sub-spaces of complexified classical number fields with Minkowskian signature of the metric defined by the complexified inner product, and the notion of infinite prime.

1. p-Adic TGD and fusion of real and p-adic physics to single coherent whole

The p-adic thread emerged for roughly ten years ago as a dim hunch that p-adic numbers might be important for TGD. Experimentation with p-adic numbers led to the notion of canonical identification mapping reals to p-adics and vice versa. The breakthrough came with the successful

p-adic mass calculations using p-adic thermodynamics for Super-Virasoro representations with the super-Kac-Moody algebra associated with a Lie-group containing standard model gauge group. Although the details of the calculations have varied from year to year, it was clear that p-adic physics reduces not only the ratio of proton and Planck mass, the great mystery number of physics, but all elementary particle mass scales, to number theory if one assumes that primes near prime powers of two are in a physically favored position. Why this is the case, became one of the key puzzles and led to a number of arguments with a common gist: evolution is present already at the elementary particle level and the primes allowed by the p-adic length scale hypothesis are the fittest ones.

It became very soon clear that p-adic topology is not something emerging in Planck length scale as often believed, but that there is an infinite hierarchy of p-adic physics characterized by p-adic length scales varying to even cosmological length scales. The idea about the connection of p-adics with cognition motivated already the first attempts to understand the role of the p-adics and inspired "Universe as Computer" vision but time was not ripe to develop this idea to anything concrete (p-adic numbers are however in a central role in TGD inspired theory of consciousness). It became however obvious that the p-adic length scale hierarchy somehow corresponds to a hierarchy of intelligences and that p-adic prime serves as a kind of intelligence quotient. Ironically, the almost obvious idea about p-adic regions as cognitive regions of space-time providing cognitive representations for real regions had to wait for almost a decade for the access into my consciousness.

In string model context one tries to reduces the physics to Planck scale. The price is the inability to say anything about physics in long length scales. In TGD p-adic physics takes care of this shortcoming by predicting the physics also in long length scales.

There were many interpretational and technical questions crying for a definite answer.

1. What is the relationship of p-adic non-determinism to the classical non-determinism of the basic field equations of TGD? Are the p-adic space-time region genuinely p-adic or does p-adic topology only serve as an effective topology? If p-adic physics is direct image of real physics, how the mapping relating them is constructed so that it respects various symmetries? Is the basic physics p-adic or real (also real TGD seems to be free of divergences) or both? If it is both, how should one glue the physics in different number field together to get *the* Physics? Should one perform p-adicization also at the level of the WCW? Certainly the p-adicization at the level of super-conformal representation is necessary for the p-adic mass calculations.

2. Perhaps the most basic and most irritating technical problem was how to precisely define p-adic definite integral which is a crucial element of any variational principle based formulation of the field equations. Here the frustration was not due to the lack of solution but due to the too large number of solutions to the problem, a clear symptom for the sad fact that clever inventions rather than real discoveries might be in question. Quite recently I however learned that the problem of making sense about p-adic integration has been for decades central problem in the frontier of mathematics and a lot of profound work has been done along same intuitive lines as I have proceeded in TGD framework. The basic idea is certainly the notion of algebraic continuation from the world of rationals belonging to the intersection of real world and various p-adic worlds.

Despite various uncertainties, the number of the applications of the poorly defined p-adic physics has grown steadily and the applications turned out to be relatively stable so that it was clear that the solution to these problems must exist. It became only gradually clear that the solution of the problems might require going down to a deeper level than that represented by reals and p-adics.

The key challenge is to fuse various p-adic physics and real physics to single larger structures. This has inspired a proposal for a generalization of the notion of number field by fusing real numbers and various p-adic number fields and their extensions along rationals and possible common algebraic numbers. This leads to a generalization of the notions of imbedding space and space-time concept and one can speak about real and p-adic space-time sheets. One can talk about adelic space-time, imbedding space, and WCW.

The notion of p-adic manifold [K73] identified as p-adic space-time surface solving p-adic analogs of field equations and having real space-time sheet as chart map provided a possible solution of the basic challenge of relating real and p-adic classical physics. One can also speak of

real space-time surfaces having p-adic space-time surfaces as chart maps (cognitive maps, "thought bubbles"). Discretization required having interpretation in terms of finite measurement resolution is unavoidable in this approach and this leads to problems with symmetries: canonical identification does not commute with symmetries.

It is now clear that much more elegant approach based on abstraction exists [K77]. The map of real preferred extremals to p-adic ones is not induced from a local correspondence between points but is global. Discretization occurs only for the parameters characterizing string world sheets and partonic 2-surfaces so that they belong to some algebraic extension of rationals. Restriction to these 2-surfaces is possible by strong form of holography. Adelization providing number theoretical universality reduces to algebraic continuation for the amplitudes from this intersection of reality and various p-adicities - analogous to a back of a book - to various number fields. There are no problems with symmetries but canonical identification is needed: various group invariant of the amplitude are mapped by canonical identification to various p-adic number fields. This is nothing but a generalization of the mapping of the p-adic mass squared to its real counterpart in p-adic mass calculations.

This leads to surprisingly detailed predictions and far reaching conjectures. For instance, the number theoretic generalization of entropy concept allows negentropic entanglement central for the applications to living matter (see **Fig.** `http://tgdtheory.fi/appfigures/cat.jpg` or **Fig. ??** in the appendix of this book). One can also understand how preferred p-adic primes could emerge as so called ramified primes of algebraic extension of rationals in question and characterizing string world sheets and partonic 2-surfaces. Preferred p-adic primes would be ramified primes for extensions for which the number of p-adic continuations of two-surfaces to space-time surfaces (imaginations) allowing also real continuation (realization of imagination) would be especially large. These ramifications would be winners in the fight for number theoretical survival. Also a generalization of p-adic length scale hypothesis emerges from NMP [K32].

The characteristic non-determinism of the p-adic differential equations suggests strongly that p-adic regions correspond to "mind stuff", the regions of space-time where cognitive representations reside. This interpretation implies that p-adic physics is physics of cognition. Since Nature is probably a brilliant simulator of Nature, the natural idea is to study the p-adic physics of the cognitive representations to derive information about the real physics. This view encouraged by TGD inspired theory of consciousness clarifies difficult interpretational issues and provides a clear interpretation for the predictions of p-adic physics.

2. The role of classical number fields

The vision about the physical role of the classical number fields relies on certain speculative questions inspired by the idea that space-time dynamics could be reduced to associativity or co-associativity condition. Associativity means here associativity of tangent spaces of space-time region and co-associativity associativity of normal spaces of space-time region.

1. Could space-time surfaces X^4 be regarded as associative or co-associative ("quaternionic" is equivalent with "associative") surfaces of H endowed with octonionic structure in the sense that tangent space of space-time surface would be associative (co-associative with normal space associative) sub-space of octonions at each point of X^4 [**?**]. This is certainly possible and an interesting conjecture is that the preferred extremals of Kähler action include associative and co-associative space-time regions.

2. Could the notion of compactification generalize to that of number theoretic compactification in the sense that one can map associative (co-associative) surfaces of M^8 regarded as octonionic linear space to surfaces in $M^4 \times CP_2$ [**?**] ? This conjecture - $M^8 - H$ duality - would give for $M^4 \times CP_2$ deep number theoretic meaning. CP_2 would parametrize associative planes of octonion space containing fixed complex plane $M^2 \subset M^8$ and CP_2 point would thus characterize the tangent space of $X^4 \subset M^8$. The point of M^4 would be obtained by projecting the point of $X^4 \subset M^8$ to a point of M^4 identified as tangent space of X^4. This would guarantee that the dimension of space-time surface in H would be four. The conjecture is that the preferred extremals of Kähler action include these surfaces.

3. $M^8 - H$ duality can be generalized to a duality $H \to H$ if the images of the associative surface in M^8 is associative surface in H. One can start from associative surface of H and assume

that it contains the preferred M^2 tangent plane in 8-D tangent space of H or integrable distribution $M^2(x)$ of them, and its points to H by mapping M^4 projection of H point to itself and associative tangent space to CP_2 point. This point need not be the original one! If the resulting surface is also associative, one can iterate the process indefinitely. WCW would be a category with one object.

4. G_2 defines the automorphism group of octonions, and one might hope that the maps of octonions to octonions such that the action of Jacobian in the tangent space of associative or co-associative surface reduces to that of G_2 could produce new associative/co-associative surfaces. The action of G_2 would be analogous to that of gauge group.

5. One can also ask whether the notions of commutativity and co-commutativity could have physical meaning. The well-definedness of em charge as quantum number for the modes of the induced spinor field requires their localization to 2-D surfaces (right-handed neutrino is an exception) - string world sheets and partonic 2-surfaces. This can be possible only for Kähler action and could have commutativity and co-commutativity as a number theoretic counterpart. The basic vision would be that the dynamics of Kähler action realizes number theoretical geometrical notions like associativity and commutativity and their co-notions.

The notion of number theoretic compactification stating that space-time surfaces can be regarded as surfaces of either M^8 or $M^4 \times CP_2$. As surfaces of M^8 identifiable as a sub-space of complexified octonions (addition of commuting imaginary unit i) their tangent space or normal space is quaternionic- and thus maximally associative or co-associative. These surfaces can be mapped in natural manner to surfaces in $M^4 \times CP_2$ [**?**] provided one can assign to each point of tangent space a hyper-complex plane $M^2(x) \subset M^4 \subset M^8$. One can also speak about $M^8 - H$ duality.

This vision has very strong predictive power. It predicts that the preferred extremals of Kähler action correspond to either quaternionic or co-quaternionic surfaces such that one can assign to tangent space at each point of space-time surface a hyper-complex plane $M^2(x) \subset M^4$. As a consequence, the M^4 projection of space-time surface at each point contains $M^2(x)$ and its orthogonal complement. These distributions are integrable implying that space-time surface allows dual slicings defined by string world sheets Y^2 and partonic 2-surfaces X^2. The existence of this kind of slicing was earlier deduced from the study of extremals of Kähler action and christened as Hamilton-Jacobi structure. The physical interpretation of $M^2(x)$ is as the space of non-physical polarizations and the plane of local 4-momentum.

Number theoretical compactification has inspired large number of conjectures. This includes dual formulations of TGD as Minkowskian and Euclidian string model type theories, the precise identification of preferred extremals of Kähler action as extremals for which second variation vanishes (at least for deformations representing dynamical symmetries) and thus providing space-time correlate for quantum criticality, the notion of number theoretic braid implied by the basic dynamics of Kähler action and crucial for precise construction of quantum TGD as almost-topological QFT, the construction of WCW metric and spinor structure in terms of second quantized induced spinor fields with modified Dirac action defined by Kähler action realizing the notion of finite measurement resolution and a connection with inclusions of hyper-finite factors of type II_1 about which Clifford algebra of WCW represents an example.

The two most important number theoretic conjectures relate to the preferred extremals of Kähler action. The general idea is that classical dynamics for the preferred extremals of Kähler action should reduce to number theory: space-time surfaces should be either associative or co-associative in some sense.

Associativity (co-associativity) would be that tangent (normal) spaces of space-time surfaces associative (co-associative) in some sense and thus quaternionic (co-quaternionic). This can be formulated in two manners.

1. One can introduce octonionic tangent space basis by assigning to the "free" gamma matrices octonion basis or in terms of octonionic representation of the imbedding space gamma matrices possible in dimension $D = 8$.

2. Associativity (quaternionicity) would state that the projections of octonionic basic vectors or induced gamma matrices basis to the space-time surface generates associative (quaternionic)

sub-algebra at each space-time point. Co-associativity is defined in analogous manner and can be expressed in terms of the components of second fundamental form.

3. For gamma matrix option induced rather than Kähler-Dirac gamma matrices must be in question since Kähler-Dirac gamma matrices can span lower than 4-dimensional space and are not parallel to the space-time surfaces as imbedding space vectors.

3. Infinite primes

The discovery of the hierarchy of infinite primes and their correspondence with a hierarchy defined by a repeatedly second quantized arithmetic quantum field theory gave a further boost for the speculations about TGD as a generalized number theory.

After the realization that infinite primes can be mapped to polynomials possibly representable as surfaces geometrically, it was clear how TGD might be formulated as a generalized number theory with infinite primes forming the bridge between classical and quantum such that real numbers, p-adic numbers, and various generalizations of p-adics emerge dynamically from algebraic physics as various completions of the algebraic extensions of rational (hyper-)quaternions and (hyper-)octonions. Complete algebraic, topological and dimensional democracy would characterize the theory.

The infinite primes at the first level of hierarchy, which represent analogs of bound states, can be mapped to irreducible polynomials, which in turn characterize the algebraic extensions of rationals defining a hierarchy of algebraic physics continuable to real and p-adic number fields. The products of infinite primes in turn define more general algebraic extensions of rationals. The interesting question concerns the physical interpretation of the higher levels in the hierarchy of infinite primes and integers mappable to polynomials of $n > 1$ variables.

1.1.6 Hierarchy Of Planck Constants And Dark Matter Hierarchy

By quantum classical correspondence space-time sheets can be identified as quantum coherence regions. Hence the fact that they have all possible size scales more or less unavoidably implies that Planck constant must be quantized and have arbitrarily large values. If one accepts this then also the idea about dark matter as a macroscopic quantum phase characterized by an arbitrarily large value of Planck constant emerges naturally as does also the interpretation for the long ranged classical electro-weak and color fields predicted by TGD. Rather seldom the evolution of ideas follows simple linear logic, and this was the case also now. In any case, this vision represents the fifth, relatively new thread in the evolution of TGD and the ideas involved are still evolving.

Dark matter as large $\hbar$ phases

D. Da Rocha and Laurent Nottale [E5] have proposed that Schrödinger equation with Planck constant $\hbar$ replaced with what might be called gravitational Planck constant $\hbar_{gr} = \frac{GmM}{v_0}$ ($\hbar = c = 1$). v_0 is a velocity parameter having the value $v_0 = 144.7 \pm .7$ km/s giving $v_0/c = 4.6 \times 10^{-4}$. This is rather near to the peak orbital velocity of stars in galactic halos. Also subharmonics and harmonics of v_0 seem to appear. The support for the hypothesis coming from empirical data is impressive.

Nottale and Da Rocha believe that their Schrödinger equation results from a fractal hydrodynamics. Many-sheeted space-time however suggests that astrophysical systems are at some levels of the hierarchy of space-time sheets macroscopic quantum systems. The space-time sheets in question would carry dark matter.

Nottale's hypothesis would predict a gigantic value of h_{gr}. Equivalence Principle and the independence of gravitational Compton length on mass m implies however that one can restrict the values of mass m to masses of microscopic objects so that h_{gr} would be much smaller. Large h_{gr} could provide a solution of the black hole collapse (IR catastrophe) problem encountered at the classical level. The resolution of the problem inspired by TGD inspired theory of living matter is that it is the dark matter at larger space-time sheets which is quantum coherent in the required time scale [K45].

It is natural to assign the values of Planck constants postulated by Nottale to the space-time sheets mediating gravitational interaction and identifiable as magnetic flux tubes (quanta) possibly

carrying monopole flux and identifiable as remnants of cosmic string phase of primordial cosmology. The magnetic energy of these flux quanta would correspond to dark energy and magnetic tension would give rise to negative "pressure" forcing accelerate cosmological expansion. This leads to a rather detailed vision about the evolution of stars and galaxies identified as bubbles of ordinary and dark matter inside magnetic flux tubes identifiable as dark energy.

Certain experimental findings suggest the identification $h_{eff} = n\times = h_{gr}$. The large value of h_{gr} can be seen as a manner to reduce the string tension of fermionic strings so that gravitational (in fact all!) bound states can be described in terms of strings connecting the partonic 2-surfaces defining particles (analogous to AdS/CFT description). The values $h_{eff}/h = n$ can be interpreted in terms of a hierarchy of breakings of super-conformal symmetry in which the super-conformal generators act as gauge symmetries only for a sub-algebras with conformal weights coming as multiples of n. Macroscopic quantum coherence in astrophysical scales is implied. If also Kähler-Dirac action is present, part of the interior degrees of freedom associated with the Kähler-Dirac part of conformal algebra become physical. A possible is that tfermionic oscillator operators generate super-symmetries and sparticles correspond almost by definition to dark matter with $h_{eff}/h = n > 1$. One implication would be that at least part if not all gravitons would be dark and be observed only through their decays to ordinary high frequency graviton ($E = hf_{high} = h_{eff}f_{low}$) of bunch of n low energy gravitons.

Hierarchy of Planck constants from the anomalies of neuroscience and biology

The quantal ELF effects of ELF em fields on vertebrate brain have been known since seventies. ELF em fields at frequencies identifiable as cyclotron frequencies in magnetic field whose intensity is about 2/5 times that of Earth for biologically important ions have physiological effects and affect also behavior. What is intriguing that the effects are found only in vertebrates (to my best knowledge). The energies for the photons of ELF em fields are extremely low - about 10^{-10} times lower than thermal energy at physiological temperatures- so that quantal effects are impossible in the framework of standard quantum theory. The values of Planck constant would be in these situations large but not gigantic.

This inspired the hypothesis that these photons correspond to so large a value of Planck constant that the energy of photons is above the thermal energy. The proposed interpretation was as dark photons and the general hypothesis was that dark matter corresponds to ordinary matter with non-standard value of Planck constant. If only particles with the same value of Planck constant can appear in the same vertex of Feynman diagram, the phases with different value of Planck constant are dark relative to each other. The phase transitions changing Planck constant can however make possible interactions between phases with different Planck constant but these interactions do not manifest themselves in particle physics. Also the interactions mediated by classical fields should be possible. Dark matter would not be so dark as we have used to believe.

The hypothesis $h_{eff} = h_{gr}$ - at least for microscopic particles - implies that cyclotron energies of charged particles do not depend on the mass of the particle and their spectrum is thus universal although corresponding frequencies depend on mass. In bio-applications this spectrum would correspond to the energy spectrum of bio-photons assumed to result from dark photons by h_{eff} reducing phase transition and the energies of bio-photons would be in visible and UV range associated with the excitations of bio-molecules.

Also the anomalies of biology (see for instance [K41, K42, **?**]) support the view that dark matter might be a key player in living matter.

Does the hierarchy of Planck constants reduce to the vacuum degeneracy of Kähler action?

This starting point led gradually to the recent picture in which the hierarchy of Planck constants is postulated to come as integer multiples of the standard value of Planck constant. Given integer multiple $\hbar = n\hbar_0$ of the ordinary Planck constant $\hbar_0$ is assigned with a multiple singular covering of the imbedding space [K18]. One ends up to an identification of dark matter as phases with non-standard value of Planck constant having geometric interpretation in terms of these coverings providing generalized imbedding space with a book like structure with pages labelled by Planck constants or integers characterizing Planck constant. The phase transitions changing the value of

Planck constant would correspond to leakage between different sectors of the extended imbedding space. The question is whether these coverings must be postulated separately or whether they are only a convenient auxiliary tool.

The simplest option is that the hierarchy of coverings of imbedding space is only effective. Many-sheeted coverings of the imbedding space indeed emerge naturally in TGD framework. The huge vacuum degeneracy of Kähler action implies that the relationship between gradients of the imbedding space coordinates and canonical momentum currents is many-to-one: this was the very fact forcing to give up all the standard quantization recipes and leading to the idea about physics as geometry of the "world of classical worlds". If one allows space-time surfaces for which all sheets corresponding to the same values of the canonical momentum currents are present, one obtains effectively many-sheeted covering of the imbedding space and the contributions from sheets to the Kähler action are identical. If all sheets are treated effectively as one and the same sheet, the value of Planck constant is an integer multiple of the ordinary one. A natural boundary condition would be that at the ends of space-time at future and past boundaries of causal diamond containing the space-time surface, various branches co-incide. This would raise the ends of space-time surface in special physical role.

A more precise formulation is in terms of presence of large number of space-time sheets connecting given space-like 3-surfaces at the opposite boundaries of causal diamond. Quantum criticality presence of vanishing second variations of Kähler action and identified in terms of conformal invariance broken down to to sub-algebras of super-conformal algebras with conformal weights divisible by integer n is highly suggestive notion and would imply that n sheets of the effective covering are actually conformal equivalence classes of space-time sheets with same Kähler action and same values of conserved classical charges (see **Fig.** `http://tgdtheory.fi/appfigures/planckhierarchy.jpg` or **Fig. ??** the appendix of this book). n would naturally correspond the value of h_{eff} and its factors negentropic entanglement with unit density matrix would be between the n sheets of two coverings of this kind. p-Adic prime would be largest prime power factor of n.

Dark matter as a source of long ranged weak and color fields

Long ranged classical electro-weak and color gauge fields are unavoidable in TGD framework. The smallness of the parity breaking effects in hadronic, nuclear, and atomic length scales does not however seem to allow long ranged electro-weak gauge fields. The problem disappears if long range classical electro-weak gauge fields are identified as space-time correlates for massless gauge fields created by dark matter. Also scaled up variants of ordinary electro-weak particle spectra are possible. The identification explains chiral selection in living matter and unbroken $U(2)_{ew}$ invariance and free color in bio length scales become characteristics of living matter and of biochemistry and bio-nuclear physics.

The recent view about the solutions of Kähler- Dirac action assumes that the modes have a well-defined em charge and this implies that localization of the modes to 2-D surfaces (right-handed neutrino is an exception). Classical W boson fields vanish at these surfaces and also classical Z^0 field can vanish. The latter would guarantee the absence of large parity breaking effects above intermediate boson scale scaling like h_{eff}.

1.1.7 Twistors in TGD and connection with Veneziano duality

The twistorialization of TGD has two aspects. The attempt to generalize twistor Grassmannian approach emerged first. It was however followed by the realization that also the twistor lift of TGD at classical space-time level is needed. It turned out that that the progress in the understanding of the classical twistor lift has been much faster - probably this is due to my rather limited technical QFT skills.

Twistor lift at space-time level

8-dimensional generalization of ordinary twistors is highly attractive approach to TGD [**?**]. The reason is that M^4 and CP_2 are completely exceptional in the sense that they are the only 4-D manifolds allowing twistor space with Kähler structure [A26]. The twistor space of $M^4 \times CP_2$ is Cartesian product of those of M^4 and CP_2. The obvious idea is that space-time surfaces allowing

twistor structure if they are orientable are representable as surfaces in H such that the properly induced twistor structure co-incides with the twistor structure defined by the induced metric.

In fact, it is enough to generalize the induction of spinor structure to that of twistor structure so that the induced twistor structure need not be identical with the ordinary twistor structure possibly assignable to the space-time surface. The induction procedure reduces to a dimensional reduction of 6-D Kähler action giving rise to 6-D surfaces having bundle structure with twistor sphere as fiber and space-time as base. The twistor sphere of this bundle is imbedded as sphere in the product of twistor spheres of twistor spaces of M^4 and CP_2.

This condition would define the dynamics, and the original conjecture was that this dynamics is equivalent with the identification of space-time surfaces as preferred extremals of Kähler action. The dynamics of space-time surfaces would be lifted to the dynamics of twistor spaces, which are sphere bundles over space-time surfaces. What is remarkable that the powerful machinery of complex analysis becomes available.

It however turned out that twistor lift of TGD is much more than a mere technical tool. First of all, the dimensionally reduction of 6-D Kähler action contained besides 4-D Kähler action also a volume term having interpretation in terms of cosmological constant. This need not bring anything new, since all known extremals of Kähler action with non-vanishing induced Kähler form are minimal surfaces. There is however a large number of imbeddings of twistor sphere of space-time surface to the product of twistor spheres. Cosmological constant has spectrum and depends on length scale, and the proposal is that coupling constant evolution reduces to that for cosmological constant playing the role of cutoff length. That cosmological constant could transform from a mere nuisance to a key element of fundamental physics was something totally new and unexpected.

1. The twistor lift of TGD at space-time level forces to replace 4-D Kähler action with 6-D dimensionally reduced Kähler action for 6-D surface in the 12-D Cartesian product of 6-D twistor spaces of M^4 and CP_2. The 6-D surface has bundle structure with twistor sphere as fiber and space-time surface as base.

   Twistor structure is obtained by inducing the twistor structure of 12-D twistor space using dimensional reduction. The dimensionally reduced 6-D Kähler action is sum of 4-D Kähler action and volume term having interpretation in terms of a dynamical cosmological constant depending on the size scale of space-time surface (or of causal diamond CD in zero energy ontology (ZEO)) and determined by the representation of twistor sphere of space-time surface in the Cartesian product of the twistor spheres of M^4 and CP_2.

2. The preferred extremal property as a representation of quantum criticality would naturally correspond to minimal surface property meaning that the space-time surface is separately an extremal of both Kähler action and volume term almost everywhere so that there is no coupling between them. This is the case for all known extremals of Kähler action with non-vanishing induced Kähler form.

   Minimal surface property could however fail at 2-D string world sheets, their boundaries and perhaps also at partonic 2-surfaces. The failure is realized in minimal sense if the 3-surface has 1-D edges/folds (strings) and 4-surface 2-D edges/folds (string world sheets) at which some partial derivatives of the imbedding space coordinates are discontinuous but canonical momentum densities for the entire action are continuous.

   There would be no flow of canonical momentum between interior and string world sheet and minimal surface equations would be satisfied for the string world sheet, whose 4-D counterpart in twistor bundle is determined by the analog of 4-D Kähler action. These conditions allow the transfer of canonical momenta between Kähler- and volume degrees of freedom at string world sheets. These no-flow conditions could hold true at least asymptotically (near the boundaries of CD).

   $M^8 - H$ duality suggests that string world sheets (partonic 2-surfaces) correspond to images of complex 2-sub-manifolds of M^8 (having tangent (normal) space which is complex 2-plane of octonionic M^8).

3. Cosmological constant would depend on p-adic length scales and one ends up to a concrete model for the evolution of cosmological constant as a function of p-adic length scale and

other number theoretic parameters (such as Planck constant as the order of Galois group): this conforms with the earlier picture.

Inflation is replaced with its TGD counterpart in which the thickening of cosmic strings to flux tubes leads to a transformation of Kähler magnetic energy to ordinary and dark matter. Since the increase of volume increases volume energy, this leads rapidly to energy minimum at some flux tube thickness. The reduction of cosmological constant by a phase transition however leads to a new expansion phase. These jerks would replace smooth cosmic expansion of GRT. The discrete coupling constant evolution predicted by the number theoretical vision could be understood as being induced by that of cosmological constant taking the role of cutoff parameter in QFT picture [L52].

Twistor lift at the level of scattering amplitudes and connection with Veneziano duality

The classical part of twistor lift of TGD is rather well-understood. Concerning the twistorialization at the level of scattering amplitudes the situation is much more difficult conceptually - I already mentioned my limited QFT skills.

1. From the classical picture described above it is clear that one should construct the 8-D twistorial counterpart of theory involving space-time surfaces, string world sheets and their boundaries, plus partonic 2-surfaces and that this should lead to concrete expressions for the scattering amplitudes.

   The light-like boundaries of string world sheets as carriers of fermion numbers would correspond to twistors as they appear in twistor Grassmann approach and define the analog for the massless sector of string theories. The attempts to understand twistorialization have been restricted to this sector.

2. The beautiful basic prediction would be that particles massless in 8-D sense can be massive in 4-D sense. Also the infrared cutoff problematic in twistor approach emerges naturally and reduces basically to the dynamical cosmological constant provided by classical twistor lift.

   One can assign 4-momentum both to the spinor harmonics of the imbedding space representing ground states of super-conformal representations and to light-like boundaries of string world sheets at the orbits of partonic 2-surfaces. The two four-momenta should be identical by quantum classical correspondence: this could be seen as a concretization of Equivalence Principle. Also a connection with string model emerges.

3. As far as symmetries are considered, the picture looks rather clear. Ordinary twistor Grassmannian approach boils down to the construction of scattering amplitudes in terms of Yangian invariants for conformal group of M^4. Therefore a generalization of super-symplectic symmetries to their Yangian counterpart seems necessary. These symmetries would be gigantic but how to deduce their implications?

4. The notion of positive Grassmannian is central in the twistor approach to the scattering amplitudes in $calN = 4$ SUSYs. TGD provides a possible generalization and number theoretic interpretation of this notion. TGD generalizes the observation that scattering amplitudes in twistor Grassmann approach correspond to representations for permutations. Since 2-vertex is the only fermionic vertex in TGD, OZI rules for fermions generalizes, and scattering amplitudes are representations for braidings.

   Braid interpretation encourages the conjecture that non-planar diagrams can be reduced to ordinary ones by a procedure analogous to the construction of braid (knot) invariants by gradual un-braiding (un-knotting).

This is however not the only vision about a solution of non-planarity. Quantum criticality provides different view leading to a totally unexpected connection with string models, actually with the Veneziano duality, which was the starting point of dual resonance model in turn leading via dual resonance models to super string models.

1. Quantum criticality in TGD framework means that coupling constant evolution is discrete in the sense that coupling constants are piecewise constant functions of length scale replaced by dynamical cosmological constant. Loop corrections would vanish identically and the recursion formulas for the scattering amplitudes (allowing only planar diagrams) deduced in twistor Grassmann would involve no loop corrections. In particular, cuts would be replaced by sequences of poles mimicking them like sequences of point charge mimic line charges. In momentum discretization this picture follows automatically.

2. This would make sense in finite measurement resolution realized in number theoretical vision by number-theoretic discretization of the space-time surface (cognitive representation) as points with coordinates in the extension of rationals defining the adele [L34]. Similar discretization would take place for momenta. Loops would vanish at the level of discretization but what would happen at the possibly existing continuum limit: does the sequence of poles integrate to cuts? Or is representation as sum of resonances something much deeper?

3. Maybe it is! The basic idea of behind the original Veneziano amplitudes (see `http://tinyurl.com/yyhwvbqb`) was Veneziano duality. This 4-particle amplitude was generalized by Yoshiro Nambu, Holber-Beck Nielsen, and Leonard Susskind to N-particle amplitude (see `http://tinyurl.com/yyvkx7as`) based on string picture, and the resulting model was called dual resonance model. The model was forgotten as QCD emerged. Later came superstring models and led to M-theory. Now it has become clear that something went wrong, and it seems that one must return to the roots. Could the return to the roots mean a careful reconsideration of the dual resonance model?

4. Recall that Veneziano duality (1968) was deduced by assuming that scattering amplitude can be described as sum over s-channel resonances or t-channel Regge exchanges and Veneziano duality stated that hadronic scattering amplitudes have representation as sums over s- or t-channel resonance poles identified as excitations of strings. The sum over exchanges defined by t-channel resonances indeed reduces at larger values of s to Regge form.

   The resonances had zero width, which was not consistent with unitarity. Further, there were no counterparts for the *sum* of s-, t-, and u-channel diagrams with continuous cuts in the kinematical regions encountered in QFT approach. What puts bells ringing is the u-channel diagrams would be non-planar and non-planarity is the problem of twistor Grassmann approach.

5. Veneziano duality is true only for s- and t- channels but not been s- and u-channel. Stringy description makes t-channel and s-channel pictures equivalent. Could it be that in fundamental description u-channels diagrams cannot be distinguished from s-channel diagrams or t-channel diagrams? Could the stringy representation of the scattering diagrams make u-channel twist somehow trivial if handles of string world sheet representing stringy loops in turn representing the analog of non-planarity of Feynman diagrams are absent? The permutation of external momenta for tree diagram in absence of loops in planar representation would be a twist of π in the representation of planar diagram as string world sheet and would not change the topology of the string world sheet and would not involve non-trivial world sheet topology.

   For string world sheets loops would correspond to handles. The presence of handle would give an edge with a loop at the level of 3-surface (self energy correction in QFT). Handles are not allowed if the induced metric for the string world sheet has Minkowskian signature. If the stringy counterparts of loops are absent, also the loops in scattering amplitudes should be absent.

   This argument applies only inside the Minkowskian space-time regions. If string world sheets are present also in Euclidian regions, they might have handles and loop corrections could emerge in this manner. In TGD framework strings (string world sheets) are identified to 1-D edges/folds of 3-surface at which minimal surface property and topological QFT property fails (minimal surfaces as calibrations). Could the interpretation of edge/fold as discontinuity of some partial derivatives exclude loopy edges: perhaps the branching points would be too singular?

A reduction to a sum over s-channel resonances is what the vanishing of loops would suggest. Could the presence of string world sheets make possible the vanishing of continuous cuts even at the continuum limit so that continuum cuts would emerge only in the approximation as the density of resonances is high enough?

The replacement of continuous cut with a sum of *infinitely* narrow resonances is certainly an approximation. Could it be that the stringy representation as a sum of resonances with *finite* width is an essential aspect of quantum physics allowing to get rid of infinities necessarily accompanying loops? Consider now the arguments against this idea.

1. How to get rid of the problems with unitarity caused by the zero width of resonances? Could *finite* resonance widths make unitarity possible? Ordinary twistor Grassmannian approach predicts that the virtual momenta are light-like but complex: obviously, the imaginary part of the energy in rest frame would have interpretation as resonance with.

   In TGD framework this generalizes for 8-D momenta. By quantum-classical correspondence (QCC) the classical Noether charges are equal to the eigenvalues of the fermionic charges in Cartan algebrable (maximal set of mutually commuting observables) and classical TGD indeed predicts complex momenta (Kähler coupling strength is naturally complex). QCC thus supports this proposal.

2. Sum over resonances/exchanges picture is in conflict with QFT picture about scattering of particles. Could *finite* resonance widths due to the complex momenta give rise to the QFT type scattering amplitudes as one develops the amplitudes in Taylor series with respect to the resonance width? Unitarity condition indeed gives the first estimate for the resonance width.

   QFT amplitudes should emerge in an approximation obtained by replacing the discrete set of finite width resonances with a cut as the distance between poles is shorter than the resolution for mass squared.

   In superstring models string tension has single very large value and one cannot obtain QFT type behavior at low energies (for instance, scattering amplitudes in hadronic string model are concentrated in forward direction). TGD however predicts an entire hierarchy of p-adic length scales with varying string tension. The hierarchy of mass scales corresponding roughly to the lengths and thickness of magnetic flux tubes as thickened cosmic strings and characterized by the value of cosmological constant predicted by twistor lift of TGD. Could this give rise to continuous QCT type cuts at the limit when measurement resolution cannot distinguish between resonances?

1.2 TGD As A Generalization Of Physics To A Theory Consciousness

General Coordinate Invariance forces the identification of quantum jump as quantum jump between entire deterministic quantum histories rather than time=constant snapshots of single history. The new view about quantum jump forces a generalization of quantum measurement theory such that observer becomes part of the physical system. The basic idea is that quantum jump can be identified as momentum of consciousness. Thus a general theory of consciousness is unavoidable outcome. This theory is developed in detail in the books [K50, K5, K40, K4, K22, K28, K31, K47, K63].

It is good to list first the basic challenges of TGD inspired theory of consciousness. The challenges can be formulated as questions. Reader can decide how satisfactory the answered proposed by TGD are.

1. What does one mean with quantum jump? Can one overcome the basic problem of the standard quantum measurement theory, that which forcing Bohr to give up totally the idea about objective reality?

2. How do the experienced time and geometric time relate in this framework? How the arrow of subjective time translates to that of geometric time?

3. How to define conscious information? Is it conserved or even increased during time evolution as biological evolution suggests? How does this increase relate to second law implied basically by the randomness of state function reduction?

4. Conscious entities/selves/observers seem to exist. If they are real how do they emerge?

1.2.1 Quantum Jump As A Moment Of Consciousness

The identification of quantum jump between deterministic quantum histories (WCW spinor fields) as a moment of consciousness defines microscopic theory of consciousness. Quantum jump involves the steps

$$\Psi_i \to U\Psi_i \to \Psi_f \quad ,$$

where U is informational "time development" operator, which is unitary like the S-matrix characterizing the unitary time evolution of quantum mechanics. U is formally analogous to Schrödinger time evolution of infinite duration. The time evolution can however interpreted as a sequence of discrete scalings and Lorentz boosts of causal diamond (CD) and the time corresponds to the change of the proper time distance between between the tips of CD.

In TGD framework S-matrix is generalized to a triplet of U-, M-, and S-matrices. M-matrix is a hermitian square root of density matrix between positive and negative energy states multiplied by universal S-matrix depending on the scale of CD only. The square roots of projection operators form an orthonormal basis. U-matrix and S-matrix are completely universal objects characterizing the dynamics of evolution by self-organization.

The M-matrices associated with CDs are obtained by a discrete scaling from the minimal CD and characterized by integer n are naturally proportional to S^n, where S is the S-matrix associated with the minimal CD. This conforms with the idea about unitary time evolution as exponent of Hamiltonian discretized to integer power of S.

U-matrix elements between M-matrices for various CDs are proportional to the inner products $Tr[S^{-n_1} \circ H^i H^j \circ S^{n_2}\lambda]$, where λ represents unitarily the discrete Lorentz boost relating the moduli of the active boundary of CD and H^i form an orthonormal basis of Hermitian square roots of density matrices. $\circ$ tells that S acts at the active boundary of CD only. I turns out possible to construct a general representation for the U-matrix reducing its construction to that of S-matrix.

The requirement that quantum jump corresponds to a measurement in the sense of quantum field theories implies that each quantum jump involves localization in zero modes which parameterize also the possible choices of the quantization axes. Thus the selection of the quantization axes performed by the Cartesian outsider becomes now a part of quantum theory. Together these requirements imply that the final states of quantum jump correspond to quantum superpositions of space-time surfaces which are macroscopically equivalent. Hence the world of conscious experience looks classical. At least formally quantum jump can be interpreted also as a quantum computation in which matrix U represents unitary quantum computation which is however not identifiable as unitary translation in time direction and cannot be "engineered".

In ZEO U-matrix should correspond relates zero energy states to each other and M matrices defining the rows of U matrix should be assignable to a fixed CD. Zero energy states should have wave function in the moduli space of CDs such that the second boundary of every CD would belong to a boundary of fixed light-cone but second boundary would be free with possible constraint that the distance between the tips of CD is multiple of CP_2 time.

Zero energy states of ZEO correspond in positive energy ontology to physical events and break time reversal invariance. This because either the positive or negative energy part of the state is reduced/equivalently preparated whereas the second end of CD corresponds to a superposition of (negative/positive energy) states with varying particle numbers and single particle quantum numbers just as in ordinary particle physics experiment.

The first state function reduction at given boundary of CD must change the roles of the ends of CDs. This reduction can be followed by a sequence of reductions to the same boundary of CD and not changing the boundary nor the parts of zero energy states associated with it but changing the states at the second end and also quantum distribution of the second boundary in the moduli space of CDs. In standard measurement theory the follow-up reductions would not affect the state at all.

The understanding of how the arrow of time and experience about its flow emerge have been the most difficult problem of TGD inspired theory of consciousness and I have considered several proposals during years having the geometry of future light-cone as the geometric core element.

1. The basic objection is that the arrow of geometric time alternates at imbedding space level but we know that arrow of time looks the same in the part of the Universe we live. Possible exceptions however exist, for instance phase conjugate laser beams seem to obey opposite arrow of time. Also biological phenomena might involve non-standard arrow of time at some levels. This led Fantappie [J22] to introduce the notion of syntropy. This suggests that the arrow of time depends on the size scale of CD and of space-time sheet.

2. It took some time to realize that the solution of the problem is trivial in ZEO. In the ordinary quantum measurement theory one must assume that state function reduction can occur repeatedly: the assumption is that nothing happens to the state during repeated reductions. The outcome is Zeno effect: the watched pot does not boil.

   In TGD framework situation is different. Repeated state function reduction leaves the already reduce parts of zero energy state invariant but can change the part of states at the opposite boundary. One must allow a delocalization of the second boundary of CDs and one assumes that the second tip has quantized distance to the fixed one coming as multiple of CP_2 time. Also Lorentz boosts leaving the second CD boundary invariant must be allowed. One must therefore introduce a wave function in the moduli space of CDs with second boundary forming part of fixed light-cone boundary ($\delta M^4_{\pm} \times CP_2$).

3. The sequence of state function reductions on a fixed boundary of CD leads to the increase of the average temporal distance between the tips of CDs and this gives rise to the experience about flow of time as shifting of contents of perception towards future if the change is what contributes to conscious experience and gives rise to a fixed arrow of time.

4. Contrary to original working hypothesis, state function reduction in the usual sense does not solely determine the ordinary conscious experience. It can however contribute to conscious experience and the act of free will is a good candidate in this respect. TGD view about realization of intentional action assumes that intentional actions involve negative energy signals propagating backwards in geometric time. This would mean that at some level of CD hierarchy the arrow of geometric time indeed changes and the reduction start to occur at opposite boundary of CD at some level of length scale hierarchy.

1.2.2 Negentropy Maximization Principle (NMP)

Information is the basic aspect of consciousness and this motivates the introduction of Negentropy Maximization Principle (NMP) [K32] as the fundamental variational principle of consciousness theory. The amount of negentropy of zero energy state should increase in each quantum jump. The ordinary entanglement entropy is also non-negative so that negentropy could be at best zero. Since p-adic physics is assumed to be a correlate of cognition, it is natural to generalizes Shannon entropy to its number theoretic variant by replacing the probabilities appearing as arguments of logarithms of probabilities with their p-adic norms. This gives negentropy which can be positive so that NMP can generates entanglement.

Consistency with quantum measurement theory allows only negentropic density matrices proportional to unit matrix and negentropy has the largest positive value for the largest power of prime factor of the dimension of density matrix. Entanglement matrix proportional to unitary matrix familiar from quantum computation corresponds to unit density matrix and large $h_{eff} = n \times h$ states are excellent candidates for forming negentropic entanglement (see **Fig.** `http://tgdtheory.fi/appfigures/cat.jpg` or **Fig. ??** in the appendix of this book).

The interpretation of negentropic entanglement is as a rule. The instances of the rule correspond to the pairs appearing in the superposition and the large the number of pairs is, the higher the abstraction level of the rule is. NMP is not in conflict with the second law since negentropy in the sense of NMP is not single particle property. Ordinary quantum jumps indeed generate entropy at the level of ensemble as also quantum jumps for states for which the density matrix is direct sum of unit matrices with various dimensions.

NMP forces the negentropic entanglement resources of the Universe to grow and thus implies evolution. I have coined the name "Akashic records" for these resources forming something analogous to library. It has turned out that the only viable option is that negentropic entanglement is experienced directly.

1.2.3 The Notion Of Self

The concept of self seems to be absolutely essential for the understanding of the macroscopic and macro-temporal aspects of consciousness and would be counterpart for observer in quantum measurement theory.

1. The original view was that self corresponds to a subsystem able to remain un-entangled under the sequential informational "time evolutions" U. It is however unclear how it could be possible to avoid generation of entanglement.

2. In ZEO the situation changes. Self corresponds to a sequence of quantum jumps for which the parts of zero energy states at either boundary of CD remaim unchanged. Therefore one can say that self defined in terms of parts of states assignable to this boundary remains unaffected as sub-system and does not generate entanglement. At the other boundary changes occur and give rise to the experience of time flow and arrow of time since the average temporal distance between the tips of CD tends to increase.

   When the reductions begin to occur at the opposite boundary of CD, self "falls asleep": symmetry suggests that new self living in opposite direction of geometric time is generated. Also in biological the change of time direction at some level of hierarchy might take place.

3. It looks natural to assume that the experiences of the self after the last "wake-up" sum up to single average experience. This means that subjective memory is identifiable as conscious, immediate short term memory. Selves form an infinite hierarchy with the entire Universe at the top. Self can be also interpreted as mental images: our mental images are selves having mental images and also we represent mental images of a higher level self. A natural hypothesis is that self S experiences the experiences of its sub-selves as kind of abstracted experience: the experiences of sub-selves S_i are not experienced as such but represent kind of averages $\langle S_{ij} \rangle$ of sub-sub-selves S_{ij}. Entanglement between selves, most naturally realized by the formation of flux tube bonds between cognitive or material space-time sheets, provides a possible a mechanism for the fusion of selves to larger selves (for instance, the fusion of the mental images representing separate right and left visual fields to single visual field) and forms wholes from parts at the level of mental images.

4. Self corresponds in neuro science to self model defining a model for organism and for the external world. Information or negentropy seems to be necessary for understanding self. Negentropically entangled states - Akashic records - are excellent candidates for selves and would thus correspond to dark matter in TGD sense since the number of states in superposition corresponds to the integer n defining h_{eff}. It is enough that self is potentially conscious: this could mean that it conscious experience about self is generated only in interaction free measurement. Repeated state function reductions to given boundary of CD is second possibility. This would assign irreversibility and definite arrow of time and experience of time flow with self.

5. CDs would serve as imbedding space correlates of selves and quantum jumps would be followed by cascades of state function reductions beginning from given CD and proceeding downwards to the smaller scales (smaller CDs). At space-time level space-time sheets in given p-adic length scale would be the natural correlates of selves. One ends also ends up with concrete ideas about how the localization of the contents of sensory experience and cognition to the "upper" (changing) boundary of CD could take place. One cannot exclude the possibility that state function reduction cascades could also take place in parallel branches of the quantum state.

1.2.4 Relationship To Quantum Measurement Theory

TGD based quantum measurement has several new elements. Negentropic entanglement and hierarchy of Planck constants, NMP, the prediction that state function reduction can take place to both boundaries of CD implying that the arrow of geometric time can change (this is expected to occur in microscopic scales whether the arrow of time is not established), and the possibility to understand the flow and arrow of geometric time.

1. The standard quantum measurement theory a la von Neumann involves the interaction of brain with the measurement apparatus. If this interaction corresponds to entanglement between microscopic degrees of freedom m with the macroscopic effectively classical degrees of freedom M characterizing the reading of the measurement apparatus coded to brain state, then the reduction of this entanglement in quantum jump reproduces standard quantum measurement theory provide the unitary time evolution operator U acts as flow in zero mode degrees of freedom and correlates completely some orthonormal basis of WCW spinor fields in non-zero modes with the values of the zero modes. The flow property guarantees that the localization is consistent with unitarity: it also means 1-1 mapping of quantum state basis to classical variables (say, spin direction of the electron to its orbit in the external magnetic field).

2. The assumption that localization occurs in zero modes in each quantum jump implies that the world of conscious experience looks classical. It is also consistent with the state function reduction of the standard quantum measurement theory as the following arguments demonstrate (it took incredibly long time to realize this almost obvious fact!).

3. Since zero modes represent classical information about the geometry of space-time surface (shape, size, classical Kähler field, ...), they have interpretation as effectively classical degrees of freedom and are the TGD counterpart of the degrees of freedom M representing the reading of the measurement apparatus. The entanglement between quantum fluctuating non-zero modes and zero modes is the TGD counterpart for the $m - M$ entanglement. Therefore the localization in zero modes is equivalent with a quantum jump leading to a final state where the measurement apparatus gives a definite reading.

   This simple prediction is of utmost theoretical importance since the black box of the quantum measurement theory is reduced to a fundamental quantum theory. This reduction is implied by the replacement of the notion of a point like particle with particle as a 3-surface. Also the infinite-dimensionality of the zero mode sector of the WCW of 3-surfaces is absolutely essential. Therefore the reduction is a triumph for quantum TGD and favors TGD against string models.

Standard quantum measurement theory involves also the notion of state preparation which reduces to the notion of self measurement. In ZEO state preparation corresponds at some level of the self hierarchy to the a state function reduction to boundary opposite than before. In biology sensory perception and motor action would correspond to state function reduction sequences at opposite boundaries of CDs at some levels of the hierarchy.

Self measurement is governed by Negentropy Maximization Principle (NMP) stating that the information content of conscious experience is maximized. In the self measurement the density matrix of some subsystem of a given self localized in zero modes (after ordinary quantum measurement) is measured. The self measurement takes place for that subsystem of self for which the reduction of the entanglement entropy is maximal in the measurement. In p-adic context NMP can be regarded as the variational principle defining the dynamics of cognition. In real context self measurement could be seen as a repair mechanism allowing the system to fight against quantum thermalization by reducing the entanglement for the subsystem for which it is largest (fill the largest hole first in a leaking boat).

1.2.5 Selves Self-Organize

The fourth basic element is quantum theory of self-organization based on the identification of quantum jump as the basic step of self-organization [**?**]. Quantum entanglement gives rise to the

generation of long range order and the emergence of longer p-adic length scales corresponds to the emergence of larger and larger coherent dynamical units and generation of a slaving hierarchy. Energy (and quantum entanglement) feed implying entropy feed is a necessary prerequisite for quantum self-organization. Zero modes represent fundamental order parameters and localization in zero modes implies that the sequence of quantum jumps can be regarded as hopping in the zero modes so that Haken's classical theory of self organization applies almost as such. Spin glass analogy is a further important element: self-organization of self leads to some characteristic pattern selected by dissipation as some valley of the "energy" landscape.

Dissipation can be regarded as the ultimate Darwinian selector of both memes and genes. The mathematically ugly irreversible dissipative dynamics obtained by adding phenomenological dissipation terms to the reversible fundamental dynamical equations derivable from an action principle can be understood as a phenomenological description replacing in a well defined sense the series of reversible quantum histories with its envelope.

ZEO brings in important additional element to the theory of self-organization. The maxima of Kähler function corresponds to the most probable 3-surfaces. Kähler function receives contributions only from the Euclidian regions ("lines" of generalized Feynman diagrams) whereas the contribution to vacuum functional from Minkowskian regions is exponent of imaginary action so that saddle points with stationary phase are in question in these regions. In ZEO 3-surfaces are replaced by pairs of 3-surfaces at opposite boundaries of CD. The maxima actually correspond to temporal patterns of classical fields connecting these 3-surfaces: this means that self-organization is four spatiotemporal rather than spatial patterns - a crucial distinction from the usual view allowing to understand the evolution of behavioral patterns quantally. In biology this allows to understand temporal evolutions of organisms as the most probable self-organization patterns having as correlates the evolutions of the magnetic body of the system.

1.2.6 Classical Non-Determinism Of Kähler Action

A further basic element is non-determinism of Kähler action. This led to the concepts of association sequence and cognitive space-time sheet, which are not wrong notions but replaced by new ones.

1. The huge vacuum degeneracy of the Kähler action suggests strongly that the preferred is not always unique. For instance, a sequence of bifurcations can occur so that a given space-time branch can be fixed only by selecting a finite number of 3-surfaces with time like(!) separations on the orbit of 3-surface. Quantum classical correspondence suggest an alternative formulation. Space-time surface decomposes into maximal deterministic regions and their temporal sequences have interpretation a space-time correlate for a sequence of quantum states defined by the initial (or final) states of quantum jumps. This is consistent with the fact that the variational principle selects preferred extremals of Kähler action as generalized Bohr orbits.

2. In the case that non-determinism is located to a finite time interval and is microscopic, this sequence of 3-surfaces has interpretation as a simulation of a classical history, a geometric correlate for contents of consciousness. When non-determinism has long lasting and macroscopic effect one can identify it as volitional non-determinism associated with our choices. Association sequences relate closely with the cognitive space-time sheets defined as space-time sheets having finite time duration.

Later a more detailed view about non-determinism in the framework of ZEO has emerged and quantum criticality is here the basic notion. The space-time surface connecting two 3-surfaces at the ends of CD is not unique. Conformal transformations which act trivially at the ends of space-time surface generate a continuum of new extremals with the same value of Kähler action and classical conserved quantities. The number n of conformal equivalence classes is finite and defines the value of h_{eff} (see **Fig.** `http://tgdtheory.fi/appfigures/planckhierarchy.jpg` or **Fig. ??** in the appendix of this book). There exists a hierarchy of breakdowns of conformal symmetry labelled by n. The fractal hierarchy of CDs gives rise to fractal hierarchy of non-determinisms of this kind.

1.2.7 P-Adic Physics As Physics Of Cognition

A further basic element adds a physical theory of cognition to this vision. TGD space-time decomposes into regions obeying real and p-adic topologies labelled by primes $p = 2, 3, 5, ...$ p-Adic regions obey the same field equations as the real regions but are characterized by p-adic non-determinism since the functions having vanishing p-adic derivative are pseudo constants which are piecewise constant functions. Pseudo constants depend on a finite number of positive pinary digits of arguments just like numerical predictions of any theory always involve decimal cutoff. This means that p-adic space-time regions are obtained by gluing together regions for which integration constants are genuine constants. The natural interpretation of the p-adic regions is as cognitive representations of real physics. The freedom of imagination is due to the p-adic non-determinism. p-Adic regions perform mimicry and make possible for the Universe to form cognitive representations about itself. p-Adic physics space-time sheets serve also as correlates for intentional action.

A more precise formulation of this vision requires a generalization of the number concept obtained by fusing reals and p-adic number fields along common rationals (in the case of algebraic extensions among common algebraic numbers). This picture is discussed in [**?**] . The application this notion at the level of the imbedding space implies that imbedding space has a book like structure with various variants of the imbedding space glued together along common rationals (algebraics, see **Fig.** `http://tgdtheory.fi/appfigures/book.jpg` or **Fig. ??** in the appendix of this book). The implication is that genuinely p-adic numbers (non-rationals) are strictly infinite as real numbers so that most points of p-adic space-time sheets are at real infinity, outside the cosmos, and that the projection to the real imbedding space is discrete set of rationals (algebraics). Hence cognition and intentionality are almost completely outside the real cosmos and touch it at a discrete set of points only.

This view implies also that purely local p-adic physics codes for the p-adic fractality characterizing long range real physics and provides an explanation for p-adic length scale hypothesis stating that the primes $p \simeq 2^k$, k integer are especially interesting. It also explains the long range correlations and short term chaos characterizing intentional behavior and explains why the physical realizations of cognition are always discrete (say in the case of numerical computations). Furthermore, a concrete quantum model for how intentions are transformed to actions emerges.

The discrete real projections of p-adic space-time sheets serve also space-time correlate for a logical thought. It is very natural to assign to p-adic pinary digits a p-valued logic but as such this kind of logic does not have any reasonable identification. p-Adic length scale hypothesis suggest that the $p = 2^k - n$ pinary digits represent a Boolean logic B^k with k elementary statements (the points of the k-element set in the set theoretic realization) with n taboos which are constrained to be identically true.

1.2.8 P-Adic And Dark Matter Hierarchies And Hierarchy Of Selves

Dark matter hierarchy assigned to a spectrum of Planck constant having arbitrarily large values brings additional elements to the TGD inspired theory of consciousness.

1. Macroscopic quantum coherence can be understood since a particle with a given mass can in principle appear as arbitrarily large scaled up copies (Compton length scales as $\hbar$). The phase transition to this kind of phase implies that space-time sheets of particles overlap and this makes possible macroscopic quantum coherence.

2. The space-time sheets with large Planck constant can be in thermal equilibrium with ordinary ones without the loss of quantum coherence. For instance, the cyclotron energy scale associated with EEG turns out to be above thermal energy at room temperature for the level of dark matter hierarchy corresponding to magnetic flux quanta of the Earth's magnetic field with the size scale of Earth and a successful quantitative model for EEG results [K15].

Dark matter hierarchy leads to detailed quantitative view about quantum biology with several testable predictions [K15]. The general prediction is that Universe is a kind of inverted Mandelbrot fractal for which each bird's eye of view reveals new structures in long length and time scales representing scaled down copies of standard physics and their dark variants. These structures would correspond to higher levels in self hierarchy. This prediction is consistent with the belief that 75 per cent of matter in the universe is dark.

1. Living matter and dark matter

Living matter as ordinary matter quantum controlled by the dark matter hierarchy has turned out to be a particularly successful idea. The hypothesis has led to models for EEG predicting correctly the band structure and even individual resonance bands and also generalizing the notion of EEG [K15]. Also a generalization of the notion of genetic code emerges resolving the paradoxes related to the standard dogma [**?**, K15]. A particularly fascinating implication is the possibility to identify great leaps in evolution as phase transitions in which new higher level of dark matter emerges [K15].

It seems safe to conclude that the dark matter hierarchy with levels labelled by the values of Planck constants explains the macroscopic and macro-temporal quantum coherence naturally. That this explanation is consistent with the explanation based on spin glass degeneracy is suggested by following observations. First, the argument supporting spin glass degeneracy as an explanation of the macro-temporal quantum coherence does not involve the value of $\hbar$ at all. Secondly, the failure of the perturbation theory assumed to lead to the increase of Planck constant and formation of macroscopic quantum phases could be precisely due to the emergence of a large number of new degrees of freedom due to spin glass degeneracy. Thirdly, the phase transition increasing Planck constant has concrete topological interpretation in terms of many-sheeted space-time consistent with the spin glass degeneracy.

2. Dark matter hierarchy and the notion of self

The vision about dark matter hierarchy leads to a more refined view about self hierarchy and hierarchy of moments of consciousness [K14, K15]. The larger the value of Planck constant, the longer the life-time of self measured as the increase of the average distance between tips of CDs appearing in the quantum superposition during the period of repeated reductions not affecting the part of the zero energy state at the other boundary of CD- Quantum jumps form also a hierarchy with respect to p-adic and dark hierarchies and the geometric durations of quantum jumps scale like $\hbar$.

The fact that we can remember phone numbers with 5 to 9 digits supports the view that self experiencse subselves as separate mental images. Averaging over experiences of sub-selves of sub-self would however occur.

3. The time span of long term memories as signature for the level of dark matter hierarchy

The basic question is what time scale can one assign to the geometric duration of quantum jump measured naturally as the size scale of the space-time region about which quantum jump gives conscious information. This scale is naturally the size scale in which the non-determinism of quantum jump is localized. During years I have made several guesses about this time scales but zero energy ontology and the vision about fractal hierarchy of quantum jumps within quantum jumps leads to a unique identification.

CD as an imbedding space correlate of self defines the time scale τ for the space-time region about which the consciousness experience is about. The temporal distances between the tips of CD as come as integer multiples of CP_2 length scales and for prime multiples correspond to what I have christened as secondary p-adic time scales. A reasonable guess is that secondary p-adic time scales are selected during evolution and the primes near powers of two are especially favored. For electron, which corresponds to Mersenne prime $M_{127} = 2^{127} - 1$ this scale corresponds to.1 seconds defining the fundamental time scale of living matter via 10 Hz biorhythm (alpha rhythm). The unexpected prediction is that all elementary particles correspond to time scales possibly relevant to living matter.

Dark matter hierarchy brings additional finesse. For the higher levels of dark matter hierarchy τ is scaled up by $\hbar/\hbar_0$. One could understand evolutionary leaps as the emergence of higher levels at the level of individual organism making possible intentionality and memory in the time scale defined τ.

Higher levels of dark matter hierarchy provide a neat quantitative view about self hierarchy and its evolution. Various levels of dark matter hierarchy would naturally correspond to higher levels in the hierarchy of consciousness and the typical duration of life cycle would give an idea about the level in question. The level would determine also the time span of long term memories as discussed in [K15]. The emergence of these levels must have meant evolutionary leap since long

term memory is also accompanied by ability to anticipate future in the same time scale. This picture would suggest that the basic difference between us and our cousins is not at the level of genome as it is usually understood but at the level of the hierarchy of magnetic bodies [**?**, K15]. In fact, higher levels of dark matter hierarchy motivate the introduction of the notions of super-genome and hyper-genome. The genomes of entire organ can join to form super-genome expressing genes coherently. Hyper-genomes would result from the fusion of genomes of different organisms and collective levels of consciousness would express themselves via hyper-genome and make possible social rules and moral.

1.3 Quantum Biology And Quantum Neuroscience In TGD Universe

Quantum biology - rather than only quantum brain - is an essential element of Quantum Mind in TGD Universe. Cells, biomolecules, and even elementary particles are conscious entities and the biological evolution is evolution of consciousness so that it would be very artificial to restrict the discussion to brain, neurons, or microtubules.

1.3.1 Basic Physical Ideas

The following list gives the basic elements of TGD inspire quantum biology.

1. Many-sheeted space-time allows the interpretation of the structures of macroscopic world around us in terms of space-time topology. Magnetic/field body acts as intentional agent using biological body as a sensory receptor and motor instrument and controlling biological body and inheriting its hierarchical fractal structure. Fractal hierarchy of EEGs and its variants can be seen as communication and control tools of magnetic body. Also collective levels of consciousness have a natural interpretation in terms of magnetic body. Magnetic body makes also possible entanglement in macroscopic length scales. The braiding of magnetic flux tubes makes possible topological quantum computations and provides a universal mechanism of memory. One can also undersand the real function of various information molecules and corresponding receptors by interpreting the receptors as addresses in quantum computer memory and information molecules as ends of flux tubes which attach to these receptors to form a connection in quantum web.

2. Magnetic body carrying dark matter and forming an onion-like structure with layers characterized by large values of Planck constant is the key concept of TGD inspired view about Quantum Mind to biology. Magnetic body is identified as intentional agent using biological body as sensory receptor and motor instrument. EEG and its fractal variants are identified as a communication and control tool of the magnetic body and a fractal hierarchy of analogs of EEG is predicted. Living system is identified as a kind of Indra's net with biomolecules representing the nodes of the net and magnetic flux tubes connections between then.

   The reconnection of magnetic flux tubes and phase transitions changing Planck constant and therefore the lengths of the magnetic flux tubes are identified as basic mechanisms behind DNA replication and analogous processes and also behind the phase transitions associated with the gel phase in cell interior. The braiding of magnetic flux makes possible universal memory representation recording the motions of the basic units connected by flux tubes. Braiding also defines topological quantum computer programs updated continually by the flows of the basic units. The model of DNA as topological quantum computer is discussed as an application. In zero energy ontology the braiding actually generalize to 2-braiding for string world sheets in 4-D space-time and brings in new elements.

3. Zero energy ontology (ZEO) makes possible the proposed p-adic description of intentions and cognitions and their transformations to action. Time mirror mechanism (see **Fig.** `http://tgdtheory.fi/appfigures/timemirror.jpg` or **Fig. ??** in the appendix of the book) based on sending of negative energy signal to geometric past would apply to both long term memory recall, remote metabolism, and realization of intentional acting as an activity

beginning in the geometric past in accordance with the findings of Libet. ZEO gives a precise content to the notion of negative energy signal in terms of zero energy state for which the arrow of geometric time is opposite to the standard one.

The associated notion of causal diamond (CD) is essential element and assigns to elementary particles new fundamental time scales which are macroscopic: for electron the time scale is.1 seconds, the fundamental biorhythm. An essentially new element is time-like entanglement which allows to understand among other things the quantum counterparts of Boolean functions in terms of time-like entanglement in fermionic degrees of freedom.

4. The assignment of dark matter with a hierarchy of Planck constants gives rise to a hierarchy of macroscopic quantum phases making possible macroscopic and macrotemporal quantum coherence and allowing to understand evolution as a gradual increase of Planck constant. The model for dark nucleons leads to a surprising conclusion: the states of nucleons correspond to DNA, RNA, tRNA, and amino-acids in a natural manner and vertebrate genetic code as correspondence between DNA and amino-acids emerges naturally. This suggests that genetic code is realized at the level of dark hadron physics and living matter in the usual sense provides a secondary representation for it.

   The hierarchy of Planck constants emerges from basic TGD under rather general assumptions. The key element is the huge vacuum degeneracy which implies that preferred non-vacuum extremals of Kähler action form a 4-D spin glass phase. The basic implications following from the extreme non-linearity of Kähler action is that normal derivatives of imbedding space coordinates at 3-D light-like orbits of partonic 2-surfaces and at space-like 3-surfaces at ends of CDs are many-valued functions of canonical momentum densities: this is one of the reasons that forced to develop physics as an infinite-D Kähler geometry vision instead of trying to develop path integral formalism or canonical quantization. A convenient manner to treat the situation is to introduce local many-sheeted covering of imbedding space such that the sheets are completely degenerate at partonic 2-surfaces. This leads in natural manner to the hierarchy of Planck constants as effective hierarchy hierarchy and integer multiples of Planck constants emerge naturally.

5. p-Adic physics can be identified as physics of cognition and intentionality. The hierarchy of p-adic length scales predicts a hierarchy of universal metabolic quanta as increments of zero point kinetic energies. Negentropic entanglement (see **Fig.** `http://tgdtheory.fi/appfigures/cat.jpg` or **Fig. ??** in the appendix of this book) possible for number theoretic entanglement entropy makes sense for rational (and even algebraic) entanglement and leads to the identification of life as something residing in the intersection of real and p-adic worlds. NMP respects negentropic entanglement and the attractive idea is that the experience of understanding and positively colored emotions relate to negentropic entanglement.

6. Living matter as conscious hologram is one of the basic ideas of TGD inspired biology and consciousness theory. The basic objection against TGD is that the interference of classical fields is impossible in the standard sense for the reason that that classical fields are not primary dynamical variables in TGD Universe. The resolution is based on the observation that only the interference of the effects caused by these fields can be observed experimentally and that many-sheeted space-time allows to realized the summation of effects in terms of multiple topological condensations of particles to several parallel space-time sheets. One concrete implication is fractality of qualia. Qualia appear in very wide range of scales: our qualia could in fact be those of magnetic body. The proposed mechanism for the generation of qualia realizes the fractality idea.

1.3.2 Brain In TGD Universe

Brain cognizes and one should find physical correlates for cognition. Also the precise role of brain in information processing and its relationship to metabolism should be understood. Here magnetic body brings as a third player to the couple formed by environment and organism.

1. An attractive idea is that the negentropic entanglement can be assigned with magnetic flux tubes somehow and that ATP serves as a correlate for negentropic entanglement. This leads

to a rather detailed ideas about the role of phosphate bond and provides interpretation for the fact that the number of valence bonds tend to be maximized in living matter. In a loose sense one could even call ATP a consciousness molecule. The latest view encourages to consider the possibility that negentropic entanglement with what might be called Mother Gaia is what is transferred in metabolism.

2. The view about the function of brain differs from the standard view. The simplest option is that brain is a builder of symbolic representations building percepts and giving them names rather than the seat of primary qualia relevant to our conscious experience. Sensory organs would carry our primary qualia and brain would build sensory percepts as standardized mental images by using virtual sensory input to the sensory organs. The new view about time is absolutely essential for circumventing the objections against this vision. The prediction is that also neuronal and even cell membranes define sensory maps with primary qualia assignable to the lipids serving as pixels of the sensory screen. These qualia would not however represent our qualia but lower level qualia. At this moment it is not possible to choose between these two options.

3. The role of EEG and its various counterparts at fractally scaled frequency ranges is to make possible communications to the various onion-like layers of the magnetic body and the control by magnetic body. Dark matter at these layers could be seen as the intentional agent and sensory perceiver.

1.3.3 Anomalies

Various anomalies of living matter have been in vital role in the development of not only TGD view about living matter but also TGD itself.

1. TGD approach to living matter was strongly motivated by the findings about strange behavior of cell membrane and of cellular water, and gel behavior of cytoplasm. Also the findings about effects of ELF em fields on vertebrate brain were decisive and led to the proposal of the hierarchy of Planck constants found later to emerge naturally from the non-determinism of Kähler action. Rather satisfactorily, the other manner to introduce the hierarchy of Planck constants is in terms of gravitational Planck constant: at least in microscopic scales the equivalence of these approaches makes sense and leads to highly non-trivial predictions. The basic testable prediction is that dark photons have cyclotron frequencies inversely proportional to their massess but universal energy spectrum in visible and UV range which corresponds to the transition energies for biomolecules so that they are ideal for biocontrol at the level of both magnetic bodies and at the level of biochemistry.

2. Water is in key role in living matter and also in TGD inspired view about living matter. The anomalies of water lead to a model for dark nuclei as dark proton strings with the surprising prediction that DNA, RNA, anino-acids and even tRNA are in one-one correspondence with the resulting 3-quark states and that vertebrate genetic code emerges naturally. This leads to a vision about water as primordial life form still playing a vital role in living organisms. The model of water memory and homeopathy in turn generalizes to a vision about how immune system might have evolved.

3. Metabolic energy is necessary for conscious information processing in living matter. This suggests that metabolism should be basically transfer of negentropic entanglement from nutrients to the organism. ATP could be seen as a molecule of consciousness in this picture and high energy phosphate bond would make possible the transfer of negentropy.

1.4 Bird's Eye of View about the Topics of the Book

The topics of "*Genes and Memes*" relate to DNA and genome in several manners.

1. The oldest layers in the stratigraphy are the vision about DNA inspired by the notion of many-sheeted space-time and the model of genetic code inspired by the notion of Combinatorial

Hierarchy predicting also the existence of what I have called memetic code. Additional number theoretical models of genetic code based on p-adic thermodynamics for small p-adic primes and maximization of entropy or negentropy emerged much later. One must however admit that although these models reproduce the genetic code they fail to predict it. Models also fail also to make interesting predictions.

2. The almost exact symmetries of the code table with respect to the first letter lead to the proposal that the genetic code could has evolved from a simpler code involving only two letters and this leads to concrete suggestion about how the genetic code might have evolved as a fusion of two letter code and single letter code. These symmetries were also an essential element of number theoretical models.

3. The work with a model of topological quantum computation inspired by the vision about dark matter hierarchy and the idea that genome and cell membrane act as topological quantum computer generated several new chapters. The magnetic flux tubes as carriers of dark matter characterized by a large value of Planck constant would make living matter a macroscopic quantum system. DNA nucleotides and lipids of the cell membrane would be connected by magnetic flux tubes and the flow of the 2-D liquid formed by lipids induces braiding of flux tubes providing both temporal dynamics defining topological quantum computation and a storage of the program to memory by the braiding of flux tubes in the final state.

4. This model led to a cascade of ideas about quantum control in living matter. Quite generally, magnetic flux tubes would make living matter kind of Indra's net explaining the strange features of gel phase. For instance, the phase transitions changing Planck constant inducing a contraction or lengthening of the flux tubes would explain why bio-molecules are able to find each other extremely selectively in the dense soup of bio-molecules inside cell. The anomalies related to ionic currents find an explanation and a model of nerve pulse and EEG emerges along these lines.

5. The discoveries of Peter Gariaev about the interaction of ordinary and laser light with genome combined with the ideas about dark matter and water memory led to a concrete model for the interaction of photons with DNA. One prediction is that it is possible to "see" dark matter by allowing ordinary matter interaction with DNA and Peter Gariaev might have already done this. In this process ordinary photons would transform to dark ones, scatter from dark matter, transform back to ordinary photons and arrive at camera. A second discovery - certainly one of the greatest surprises of my professional life - was an end product of an attempt to understand the mechanism behind water memory for which rather strong support exists now. The idea was that dark nuclei which sizes zoomed up to atomic size scale could provide a representation of genes.

   It indeed turned out that the model for dark nucleon consisting of three quarks predicts counterparts of 64 DNAs and RNAs and 20 amino-acids and allows to identify genetic code as a natural mapping of DNA type states to amino-acid type states. The numbers of DNAs mapped to a given amino-acid are same as for the vertebrate genetic code. This would mean that genetic code would be realized at the level of elementary particle physics and chemical realization would be only one of the many. In fact, the quite recent experimental discoveries suggest that this kind of representation must exist besides the representation based on the temporal patterns of polarization direction discovered by Gariaev.

1.4.1 Organization of "Genes and Memes: Part II"

The topics of the first part of "Genes and Memes: Part II" are organized in 3 parts.

1. In the 1st part of "Genes and Memes: Part II" three chapters are devoted to TGD inspired models for prebiotic evolution. I will also consider TGD variant of expanding Earth model explaining several strange findings about Cambrian explosion and suggesting a direct link between biology and cosmic expansion as TGD describes it.

2. In the 2nd of the book mostly physics inspired ideas about genetic code are discussed. The basic vision looks natural to anyone living at computer age: it would be very natural for

the genetic code to have several representations. The first chapter describes 3 realizations of genetic code inspired by TGD based new physics. In dark nuclear code codons are represented as 3-proton states but one can imagine also a realization in terms of quark triplets. The first realization is supported by the findings of Gerald Pollack.

Second code is based on 3-chords formed by 3 dark photons (with large value of $h_{eff} = n \times h_0$) and leads to a model of bio-harmony leading also to the idea of that this music of light serves as correlate for emotions at molecular level. Second chapter considers the notion of homonymy of genetic code introduced by Peter Gariaev from TGD point of view. The third chapter discuss the correspondence between ordinary genetic code and dark nuclear code with codons represented as 3-proton states.

3. Im the 3rd part I have included two chapters about mathematical models of genetic code. The fact that these models have not developed as physics inspired models have done, suggests that they are unavoidable sidesteps in the development of ideas.

1.5 Sources

The eight online books about TGD [K54, ?, K70, K49, K35, K69, K68, K48] and nine online books about TGD inspired theory of consciousness and quantum biology [K50, K5, K40, K4, K22, K28, K31, K47, K63] are warmly recommended for the reader willing to get overall view about what is involved.

My homepage (`http://tinyurl.com/ybv8dt4n`) contains a lot of material about TGD. In particular, a TGD glossary at `http://tinyurl.com/yd6jf3o7`).

I have published articles about TGD and its applications to consciousness and living matter in *Journal of Non-Locality* (`http://tinyurl.com/ycyrxj4o` founded by Lian Sidorov and in *Prespacetime Journal* (`http://tinyurl.com/ycvktjhn`), *Journal of Consciousness Research and Exploration* (`http://tinyurl.com/yba4f672`), and *DNA Decipher Journal* (`http://tinyurl.com/y9z52khg`), all of them founded by Huping Hu. One can find the list about the articles published at `http://tinyurl.com/ybv8dt4n`. I am grateful for these far-sighted people for providing a communication channel, whose importance one cannot overestimate.

1.6 The contents of the book

1.6.1 PART I: TGD INSPIRED MODELS FOR EVOLUTION

Evolution in Many-Sheeted Space-Time

This chapter was originally about prebiotic evolution but gradually extended so that it became natural to drop the attribute "prebiotic". Of course, a collection of ideas rather than detailed history of life is in question. There are many rather speculative ideas such as the strong form of the hypothesis that plasmoid like life forms molecular life forms has evolved in "Mother Gaia's womb", maybe even in the hot environment defined by the boundary of mantle and core. The motivation for tolerating these "too crazy" ideas is that according to recent TGD inspired theory of consciousness life is a completely universal phenomenon appearing in all scales.

1. Basic facts about and TGD based model for pre-biotic evolution are discussed.

2. A model for the ATP-ADP process based on DNA as topological quantum computer vision, the identification of universal metabolic energy quanta in terms of zero point kinetic energies, and the notion of remote metabolism is discussed.

3. A model for the evolution of the recent genetic code (3-codons) as a fusion of codes for which codons are nucleotides (1-codons) and di-nucleotides (2-codons) is discussed. The symmetries of the genetic code, the observation that tRNA can be seen as a fusion of two hairpin like DNA molecules, and the finding that the first nucleotides of 3-codon code for the reaction path leading from a precursors of the amino-acid to amino-acids for hydrophobic/hydrophilic dichotomy, serve as motivations of the model. 1- and 2-codes corresponding to the two

forms of RNA (the exotic $2' - 5'$ RNA and the usual $3' - 5'$ RNA) would have prevailed in RNA world. Amino-acids would have served as catalysts for the copying of RNA on one hand, and RNA molecules would have catalyzed the formation of amino-acids from their precursors on one hand, meaning the presence of a positive feedback loop. In the transition to DNA-amino-acid era RNA began to be translated to amino-acid sequences.

4. Cambrian explosion represents a rather mysterious period in biology: new highly developed phylae emerged out of nowhere. A second strange finding is that continents would fit together to form single super-continent covering entire Earth's surface at time of Cambrian explosion if the radius of Earth would have been one half of its recent value. This finding has inspired Expanding Earth theories but it has not been possible to identify the mechanism causing the expansion. The success of the standard tectonic plate theory requires that possible expansion must have occurred in relatively short geological time scale. The hierarchy of Planck constants implies that cosmic expansion has occurred in quantum leaps increasing the value of h_{eff} and thus of quantum scales by factors which tend to be powers of 2. Cosmic expansion would have occurred as jerks even in the case of planets. In the proposed model Cambrian explosion would have accompanied the expansion of the Earth's radius by a factor of 2: during this period an outburst of highly developed life forms from underground seas to the surface of Earth would have taken place.

5. The last section of the chapter compares TGD based view about the evolution of genetic code to the views of McFadden. This section is a little bit out of date. For instance, the hypothesis that magnetic body of DNA could induce mutations purposefully is not discussed. This hypothesis is natural if one believes that magnetic flux tubes connecting bio-molecules play a key role in bio-catalysis. This idea is discussed in the chapter devoted to protein folding.

6. A vision about biological evolution and evolution of brain is discussed on basis of the wisdom gained from the construction of the models of sensory receptor and generalized EEG.

7. TGD inspired theory of consciousness in its recent form predicts that life is a universal phenomenon. The possibility that oil droplets could be seen as a primitive life form is discussed in the last section of the chapter.

Expanding Earth model and pre-Cambrian evolution of continents, climate, and life

TGD inspired quantum cosmology predicts that astrophysical objects do not follow cosmic expansion except in jerk-wise quantum leaps increasing the gigantic value of the gravitational Planck constant h_{gr} characterizing space-time mediating gravitational interactions between two masses or gravitational self interactions. This assumption provides explanation for the apparent cosmological constant. As a matter fact, gigantic value of h_{gr}. By Equivalence principle and independence of gravitational acceleration on mass it is enough to assume that only microscopic systems have the gravitational flux tube contacts with central mass. In this case the value range of h_{gr} is consistent with the identification as $h_{eff} = n \times h$ introduced with motivations coming from biology and in TGD framework following from the non-determinism of Kähler action.

Also planets are predicted to expand in a stepwise manner allowing to imagine a new version of Expanding Earth theory originally postulated to explain the intriguing findings suggesting that continents have once formed a connected continent covering almost the entire surface of Earth but with radius which was one half of the recent one.

This leads also to a rather fascinating vision about biology. The mysterious Cambrian Explosion in which a large number of new species emerged suddenly (realized already Darwin as the strongest objection against his theory) could be understood if the life would have gone to underground lakes and seas formed during the expansion period as fractures were formed and the underground cavities expanded and were filled with water. This would have allowed the life to escape cosmic radiation, meteoric bombardment, and the extremely cold climate during Proterozoic period preceding the Cambrian Explosion and migrate back as highly developed life forms as the period of glaciations ended.

Before the Proterozoic era the radius of Earth would have been one half of its recent value and started to grow with gradually accelerating rate. This forces to rewrite the entire geological and climate history of Earth during the Proterozoic period.

1. The postulated physically implausible cyclic appearance of single connected super-continent containing all land mass can be given up and replaced with a single continent containing large inland seas. There is no need to postulate the existence of series of super-oceans whose ocean floor would have subduced totally so that no direct information about them would exist nowadays.

2. The dominating model for pre-Cambrian climate is so called Snowball Earth model inspired by the finding that signatures of glaciations have been found at regions of Earth, which should have been near Equator during the Proterozoic. Snowball model has several difficulties: in particular, there is a lot of evidence that a series of ordinary glaciations was in question. For $R/2$ option the regions located to Equator would have actually been near North Pole so that the glaciations would have indeed been ordinary glaciations proceeding from the poles. A killer prediction is the existence of non-glaciated regions at apparent southern latitudes around about 45 degrees and there is evidence for these indeed exists! The model makes also testable paleomagnetic killer predictions. In particular, during periods when the magnetic dipole in the direction of rotation axis the directions of the magnetic fields for $R/2$ model are predicted to be same at South Pole and apparent Equator and opposite for the standard option.

Chapter 2

Dark Matter, Quantum Gravity, and Prebiotic Evolution Prebiotic Evolution

The ideas related to prebiotic evolution have developed rather rapidly after the discovery of the hierarchy of Planck constants around 2003 providing a general manner to understand living organisms as macroscopic quantum systems.

Magnetic body as carrier of dark matter realized as phases with non-standard value $h_{eff} = n \times h$ of Planck constant is the key concept in the developments and brings to the description of the living matter a third level besides organism and environment.This has led to developments in the model of EEG as communication tool between biological and magnetic body and led to the interpretation of bio-photons as decay products of dark EEG photons. Also bio-superconductivity is now reasonably well-understood and the model for cell membrane as Josephson junction is generalized to include cyclotron energy besides difference in Coulomb energy. Square root of thermodynamics inspired by Zero Energy Ontology suggests itself as a proper description of Josephson junctions defined by transmembrane proteins. The dark genetic code seems to have so strong explanatory power that it must be taken seriously. The model of water memory and homeopathy has led to an evolution of ideas relating to the development of immune system and bio-catalysis. The latest steps of progress were induced by the realization that the replication of magnetic body could be behind that of DNA and cell, the discovery of fourth phase of water and exclusion zones by Pollack et al, and by the observation that anomalously high gravimagnetic Thomson field implied by large value of gravitational Planck constant could explain the anomalously large mass measured for electronic Cooper pairs in rotating super-conductor.

In this chapter the model for water memory and homeopathy is discussed and shown to lead to a general model for how immune system and bio-catalysis could have developed from their dark primordial versions, how dark proteins might have emerged as concrete representations for invader molecules making it possible to make the invader non-dangerous by attaching to its magnetic body, how DNA and genetic code could have emerged as symbolic representations for the magnetic bodies of invader molecules and later as symbolic representation of the magnetic body of the system itself. ZEO implies that actually time evolution of the magnetic body can be coded by DNA and protein folding could provide a concrete representation for this time evolution.

Chapter 3

More Precise TGD Based View About Quantum Biology and Prebiotic Evolution

In this work I try to clarify the relation of the basic notions of TGD and of TGD inspired biology to the ordinary bio-chemistry. I also try to improve my understanding about work of Fröhlich, Del Giudice, and Pollack using the notions of TGD. The key idea is the notion of coherence induced by weak em fields with preferred frequencies, which in ordinary quantum theory correspond to energies much below the thermal energy in quantum theory - this creates what is called kT paradox.

In TGD framework one can do without coherence regions (one could perhaps identify them as special cases of Pollacks EZs), which can be much larger. The basic observation is that for a pair of hydrogen bonded water molecules the reaction $2H_2O \rightarrow H_3O_2^- +$ dark proton require UV photon with energy of O-H bond of about 5.15 eV. Water clathrates are good candidates for the precursors of EZs since they have size scale in the same range as EZs and contain hydrogen bonded water. Quantum criticality suggests that this process should occur spontaneously as a chain reaction. This is achieved in the same manner as in nuclear fusion if the dark protons at the flux tube fused to nuclear strings giving rise to dark nuclei.

If dark nuclear binding energy transforms as Coulomb energy, the nuclear energy scale of MeV scales down to 1-10 eV - depending on the value of h_{eff}. An attractive guess is that the energy range of bio-photons corresponds to that for dark nuclear binding and excitation energies. Their spontaneous transformation back to ordinary nuclei would liberate energy could at least partially explain the evidence for bio-transmutations. Also the relation to cold fusion is interesting.

Dark nuclear binding energy is liberated as dark photons decaying into bunches of ordinary photons inducing further reactions *hydrogen bonded* $2H_2O \rightarrow H_3O_2^- +$ *dark proton* also other kind of dark ionizations. If the size of EZs varies from about 1 micron to 100 microns and if the the size scale of EZ corresponds to the wavelength of dark gamma photon h_{eff}/h varies in the range $10^6 - 10^8$. This would be the total number of dark photons resulting in the decay to ordinary photons. Water clathrates have same size scale range as EZs and consist of hydrogen bonded water molecules and could serve as precursors of EZs: EZ would have different lattice structure than clathrates.

In this process ordinary protons transform dark protons at magnetic flux tubes outside EZ. Dark ionization differs from ordinary ionization only in that the proton is dark. The difference between dark and ordinary ionization would define the borderline between ordinary and bio-chemistry (or dark chemistry). Chemical quantum criticality is possible also for other cations and also anions and all biologically important ions can appear as dark ions.

The Urey-Miller experiment was very successful: it produced a large variety of amino-acids crucial for life from simple basic constituents. The variant of this experiment has even produced adenosine, DNA nucleotide fundamental for ATP. There is however a severe problem. The prebiotic atmosphere was not reducing as in the Urey-Miller experiment simulating it.

Clays are good candidates for the key structures in prebiotic evolution since they can replicate. One can even speculate with an analog of genetic code. Phyllosilicates containing -O-H

groups are especially interesting: they can adsorb basic biomolecules and induce their polymerization to oligomers. They also induce a formation of vesicles formed from lipid bilayer and serving as a candidate for a predecessor of cell. DNA is the problem and has led to a scenario known as RNA world. Phyllosilicates are also known to generate radiation with positive health effects. The natural and testable hypothesis is that the presence of EZs allows to circumvent the difficulties of the standard RNA world scenario and also generate DNA and biologically active phosphates containing the mysterious phosphate bond as ionized dark proton. The dark magnetic flux tubes and UV photon energy needed to generate EZs could be provided by gel in Pollacks's experiments and by electric discharges in Urey-Miller experiment. Also dark photons from the formation of dark nuclei decaying to bunches of bio-photons can be considered. Water chlathrates can contain atoms and even micrometer sized phyllosilicate crystals, which could catalyze the formation of biomolecules at their surfaces as dark nuclear fusion chain reaction. Chlathrate could also develop phospholipid bilayer around it - kind of primitive cell membrane.

TGD inspired proposal for prebiotic evolution was inspired by the TGD based realization of Expanding Earth hypothesis and assumes that life evolved in underground oceans and burst on the surface of Earth in Cambrian explosion. This view leads to a more precise view about prebiotic evolution.

Possible technological implications of this picture - if true - are quite impressive. Cold biofusion could make possible artificial generation of technologically important elements and the mechanism generating EZs could make possible creation of artificial intelligent life forms involving silicates and water.

3.0.2 PART II: TGD INSPIRED MODELS FOR GENETIC CODE

Three New Physics Realizations of the Genetic Code and the Role of Dark Matter in Bio-systems

TGD inspired quantum biology leads naturally to the idea that several realizations of genetic code exist. Besides the realizations based on temporal patterns of electromagnetic fields I have considered three different new physics realizations of the genetic code based the notions of many-sheeted space-time, magnetic body, and the hierarchy of Planck constants explaining dark matter in TGD framework.

1. The first realization - proposed in the model for DNA as topological quantum computer (tqc) - maps the nucleotides A,G and T,C to dark quarks u,d and their anti-quarks assignable to the ends of magnetic flux tubes representing braid strands and connecting nucleotides to lipids of cell membrane. This requires scaled up variant of QCD made possible the hierarchy of Planck cosntants.

2. Second realization was discovered in the model of dark nuclei as strings of dark baryons. Dark baryons realize codons in terms of quantum entanglement and without decomposition to letters. Dark baryons are strings of 3 quarks connected by two color flux tubes. The neutral states of the dark baryon predicted by the model are in 1-1 correspondence with DNA, RNA, aminoacids. Candidates for the counterparts of tRNA anticodons are also obtained if one accepts that genetic code actually decomposes to 2 steps $64 \to 40 \to 20$ such that there are 40 dark baryon counterparts for tRNA anticodons. The amazing finding is that vertebrate genetic code comes out correctly.

3. The third realization would be a physical realization for the divisor code proposed by Khrennikov and Nilsson. The realization relies on two integers labeling magnetic flux tubes containing dark matter. The dark magnetic flux tubes assignable to DNA codons and amino-acids could be labeled by these integers providing a representation of the genetic code consistent with the divisor code. Also a physical mechanism implying the physical equivalence of the dark baryon code and divisor code can be imagined.

4. Proposals for two further realizations are inspired by the observation that the number of vertices of icosahedron is 12 - the number of notes in 12-note scale - and that of vertices is 20 - the number of amino-acids. This suggests a connection between music and genetic code. The second model allows to "understand" the degeneracies of the genetic code in terms of

representations for discrete subgroups if icosahedral group and involves imbedding of 12-note scale as a Hamiltonian cycle to icosahedron.

The basic proposal is that dark baryon counterparts of basic bio-molecules and genetic code were present from beginning and gave rise to pre-biotic life at the magnetic flux tubes so that the evolution of biological life meant the development of translation and transcription mechanisms allowing to transform dark baryon variants of the codons to their chemical variants. These mechanisms would be still at work inside the living cell and allow the living matter to perform genetic engineering. This proposal is consistent with recent findings about large variations of genomes inside organism.

There is a strange experimental finding giving support for this picture. A water solution containing human cells infected by bacteria is sterilized by a filtering procedure and healthy cells are added to the filtrate. Within few weeks the infected cells re-appear. A possible explanation is that dark baryon variant of the bacterial genome realized as nano-sized particles remains in the solution despite the filtering. Another strong support comes from the exclusion zones and fourth phase of water discovered by Pollack.

The codes are discussed from the point of view of DNA as tqc hypothesis and the model for protein folding and bio-catalysis. The basic selection rules of bio-catalysis could be based on the two integers assignable to the dark magnetic flux tubes. Only bio-molecules whose dark magnetic bodies contain a layer characterized by same integers can be connected by dark magnetic flux tubes. The reconnection of the dark magnetic flux tubes selecting the bio-molecules participating the catalytic reaction and the contraction of these flux tubes induced by a phase transition reducing Planck constant and forcing the bio-molecules near to each other would represent basic mechanisms of bio-catalysis.

Homonymy of the genetic code from TGD point of view

Peter Gariaev and colleagues have applied the linguistic notions of synonymy and homonymy to genetic code. Also the notion of syhomy fusing these concepts is introduced. Homonymy is visible in mRNa-tRNA pairing and induced by the 1-to-many pairing of the third mRNA nucleotide with tRNA nucleotide. The homonymy in mRNA-AA (AA for amino-acid) pairing is also present albeit rare.

The codons for the standard code can be divided to two classes. For 32 codons the first two letters fix AA completely. For the remaining 32 codons this is not the case. There is however almost unbroken symmetry in that U and C *resp.* A and G code for the same AA. The breaking of this symmetry is minimal appearing only for 3 4-columns of the code table and present for A-G only. The deviations from the standard code as a rule break A-G or T-C symmetry or re-establish it.

The notion of homonymy is highly interesting from TGD point of view. TGD leads to two basic proposals for non-chemical realization of genetic code predicting the numbers of DNA codons coding for given AA rather successfully. The first proposal relies on TGD based view about dark matter as $h_{eff}/h = n$ phases of ordinary matter and identifies counterparts of DNA, RNA, tNRA, and AAs as entangled dark proton triplets.

Second proposal emerged from the model of music-harmony based on fusion of icosahedral and tetrahedral geometries. Codons are represented as photon triplets (dark or ordinary) defining the allowed 3-chords of given harmony defined by Hamilton cycle at icosahedron extended to Hamilton cycle to the fusion of icosahedron with tetrahedron along common face. Photon triplets give rise to resonant coupling giving rise to physical pairing of biomolecule and its dark counterpart. Remarkably, there are 3 different realizations of tRNA in terms of 3-chords. There is large number of bio-harmonies corresponding to Hamiltonian cycles. Since music expresses and creates emotions, the proposal is that a realization of emotions at molecular level adding additional degrees of freedom not visible at the level of chemistry is in question. This might give rise to a context dependence of the code.

The proposal is that genetic code at dark level extends to a sequence DDNA $\rightarrow$ DmRNA $\rightarrow$ DtRNA $\rightarrow$ DAA of horizontal pairings analogous to projections is fundamental one. Codon-codon pairings are realized via dark photon triplet resonance and mRNA-AA pairing by resonant coupling to the sum $f_{XYZ} = f_1 + f_2 + f_3$ of 3-chord frequencies: the codons coding same AA would have

frequencies f_{XYZ} differing only by a multiple of octave. One might perhaps say that AA sequence defines melody and mRNA sequence the accompaniment.

There is context dependence and homonymies already in DmRNA-DtRNA pairing and due the fact that DtRNA corresponds to a 2-harmony which is sub-harmony of 3-harmony and can be chosen in 3 different manners. The vertical pairings DDNA $\rightarrow$ DNA, DmRNA $\rightarrow$ mRNA, etc. also mediated by frequency couplings induce ordinary genetic code and horizontal pairings in DNA $\rightarrow$ mRNA $\rightarrow$ tRNA $\rightarrow$ AA. DAA $\rightarrow$ AA pairing dictates mRNA $\rightarrow$ AA pairing and mRNA $\rightarrow$ tRNA homonymy does not matter and actually makes the translation safer by increasing the number of tRNAs performing the same task.

The rather rare homonymies in DNA-AA pairing can be understood as accidental degeneracies. AA couples resonantly to the sum $f_{XYZ} = f_1 + f_2 + f_2$ of frequencies associated with codon XYZ and it can occur that the sum frequencies can be identical for two codons.

Chapter 4

About the Correspondence of Dark Nuclear Genetic Code and Ordinary Genetic Code

4.1 Introduction

The idea about the realization of genetic code in terms of dark proton sequences giving rise to dark nuclei is one of the key ideas of TGD inspired quantum biology [L21]. This vision was inspired by the totally unexpected observation that the states of three dark protons (or quarks) can be classified to 4 classes in which the number of states are same as those of DNA, RNA, tRNA, and amino-acids. Even more, it is possible to identify genetic code as a natural correspondence between the dark counterparts of DNA/RNA codons and dark amino-acids and the numbers of DNAs/RNAs coding given amino-acid are same as in the vertebrate code [L21]. What is new is that the dark codons do not reduce to ordered products of letters.

During years I have considered several alternatives for the representations of genetic code. For instance, one can consider the possibility that the letters of the genetic code correspond to the four spin-isospin states of nucleon or quark or for spin states of electron pair. Ordering of the letters as states is required and this is problematic from the point of view of tensor product unless the ordering reflects spatial ordering for the positions of particles representing the letters. One representation in terms of 3-chords formed by 3-photon states formed from dark photons emerges from the model of music harmony [L12]. By octave equivalence the ordering of the notes is not needed.

4.1.1 Insights

The above observations inspire several speculative insights.

1. The emergence of dark nuclei identified as dark proton sequences would relate to Pollack's effect in which irradiation of water generates in presence of gel phase bounding the water what Pollack calls exclusion zones (EZs). EZs are negatively charged and water has effective stoichiometry $H_{1.5}O$. EZs deserve their name: somehow they manage to get rid of various impurities: this might be very important if EZs serve as regions carrying biologically important information. The protons of water molecules must go somewhere and the proposal is that they go to the magnetic body of some system consisting of flux tubes. The flux tubes contain the dark protons as sequences identifiable as dark nuclei.

2. Since nuclear physics precedes chemistry, one can argue that prebiotic life is based on these dark biomolecules serving as a template for ordinary biomolecules. To some degree biochemistry would be shadow dynamics and dark dynamics would be extremely simple as compared to the biochemistry induced by it. In particular, DNA replication, transcription, and translation would be induced by their dark variants. One can even extend this vision: perhaps

also ordinary nuclear physics and its scaled up counterpart explaining "cold fusion" are parts of evolutionary hierarchy of nuclear physics in various scales.

3. Nature could have a kind of R&D lab allowing to test various new candidates for genes by using transcription and translation at the level of dark counterparts of the ordinary basic biomolecules.

4.1.2 Conditions on the model

The model must satisfy stringent conditions.

1. Both the basis A, T, C, G and A, U, C, G as basic chemical building bricks of RNA and DNA must have emerged without the help of enzymes and ribozymes. It is known that the biochemical pathway known as pentose-phosphate pathway (see `http://tinyurl.com/y9akkwok`) generates both ribose and ribose-5-phosphate defining the basic building brick of RNA. In DNA ribose is replaced with de-oxiribose obtained by removing one oxygen.

   Pyrimidines U, T, and C with single aromatic ring are are reported by NASA to be generated under outer space conditions (see `http://tinyurl.com/y7sh9zk4`). Carell et al [I73] (see `http://tinyurl.com/z65kpyo`) have identified a mechanism leading to the generation of purines A and G, which besides pyrimidines A,T (U) are the basic building bricks of DNA and RNA. The crucial step is to make the solution involved slightly acidic by adding protons. TGD inspired model for the mechanism involves dark protons [L24] [K19].

   Basic amino-acids are generated in the Miller-Urey type experiments (see `http://tinyurl.com/4q2arv`). Also nucleobases have been genererated in Miller-Urey type experiments [I79].

   Therefore the basic building bricks can emerge without help of enzymes and ribozymes so that the presence of dark nuclei could lead to the emergence of the basic biopolymers and tRNA.

2. Genetic code as a correspondence between RNA and corresponding dark proton sequences must emerge. Same true for DNA and also amino-acids and their dark counterparts. The basic idea is that metabolic energy transfer between biomolecules and their dark variants must be possible. This requires transitions with same transition energies so that resonance becomes possible. This is also essential for the pairing of DNA and dark DNA and also for the pairing of say dark DNA and dark RNA. The resonance condition could explain why just the known basic biomolecules are selected from a huge variety of candidates possible in ordinary biochemistry and there would be no need to assume that life as we know it emerges as a random accident.

3. Metabolic energy transfer between molecules and their dark variants must be possible by resonance condition. The dark nuclear energy scale associated with biomolecule could correspond to the metabolic energy scale of .5 eV. This condition fixes the model to a high extent but also other dark nuclear scales with their own metabolic energy quanta are possible. In fact, the dark nuclear binding energy for $k = 151$ scaled up from the typical value of the ordinary nuclear binding energy about 1 MeV is .5 eV.

4.1.3 Vision

The basic problem in the understanding of the prebiotic evolution is how DNA, RNA, amino-acids and tRNA and perhaps even cell membrane and microtubules . The individual nucleotides and amino-acids emerge without the help of enzymes or ribozymes but the mystery is how their polymers emerged. If the dark variants of these molecules served as templates for their generation one avoids this hen-and-egg problem. The problem how just the biomolecules were picked up from a huge variety of candidates allowed by chemistry could be solved by the resonance condition making possible metabolic energy transfer between biomolecules and dark nuclei.

The basic question is to what p-adic length scales $L(k)$ DNA, RNA and amino-acids correspond. The original hypothesis was that the p-adic length scale assignable to dark DNA is consistent with the radius of ordinary DNA. It however turned out that this implies that the

binding energy scale of corresponding dark nuclear physics is too high for the recent biology. Also the assumption that the dark variant of DNA double strand is horizontally scaled up variant of ordinary DNA strand excludes this identification since it requires that the horizontal size scale of dark DNA strand is larger than that of ordinary DNA strand.

DNA coil has radius $L(151) = 10$ nm and this suggests that dark DNA radius does not correspond to the radius of ordinary DNA (as assumed in the original version of this text) but to the p-adic length scale $L(151)$, where $k = 151$ corresponds to first Gaussian Mersenne prime belonging to the group $k = 151, 157, 163, 167$. The primes $k > 151$ would correspond to higher level coilings of DNA. From this hypothesis one ends up to the proposal that RNA, tRNA, and amino-acids correspond to $k = 149$. This picture follows essentially from the contraints posed by various biological anomalies.

Also the smaller primes $k = 127, 131, 137, 139$ can be present in pre-biotic evolutions. This hierarchy of dark nuclear physics leads to a vision about how prebiotic evolution led via RNA era to the recent biology. Unidentified infrared bands (UIBs) from interstellar space identified in terms of transition energies of dark nuclear physics support this vision and one can compare it to PAH world hypothesis.

The vision about dark matter as a controller of biomatter leads to ask whether cell membrane and microtubules could correspond to 2-D analogs of RNA strands associated with dark RNA codons forming lattice like structures related to by radial scaling to their counterparts at the level of ordinary biomatter. This is supported by p-adic length scale hypothesis and thermodynamical considerations. These 2-D structures could represent 2-D variants of 1-D structures represented by DNA, RNA, and amino-acids with each node of lattice representing code letter.

Thermal constraints allow cell membrane of thickness about 5 nm as am additional realization of $k = 149$ level with $n = 2^{22}$ in terms of lipids as analogs of RNA codons. For $k = 149$ metabolic energy quantum is predicted to be .5 eV. The thickness of neuronal membrane in the range 8-10 nm and could correspond to $k = 151$ and $n = 2^{23}$ in accordance with the idea that it corresponds to higher level in the cellular evolution reflecting that of dark nuclear physics. The energy quantum of ordinary Josephson radiation is just at the verge of thermal threshold. This could be understood in terms of minimization of metabolic resources. For bosonic singly charged ions the Josephson energy would be below the thermal threshold. The notion of generalized Josephson junction saves the situation. For massive particles associated with flux tubes the thermal energy $T/2$ is below the potential energy defined by action potential and that of metabolic energy quantum.

Also microtubules could correspond to $k = 151$ realization for which metabolic energy quantum is $E_{ex}(151) = .25eV$. Of course, the replacement of $E_{ex} = 1$ MeV for ordinary nuclei with $E_{ex} = 2$ MeV would give $E_{ex}(151) = .5$ eV so that one must take these estimates as order of magnitude estimates only. Also a proposal for how microtubules could realize genetic code with the 2 conformations of tubulin dimers and 32 charges associated with ATP and ADP accompanying the dimer thus realizing the analogs of 64 analogs of RNA codons is made.

The great vision would be that hierarchy of dark variants of DNA, RNA, amino-acids and their replication, transcription, and translation would be behind biological replication in various scales. Ordinary bio-chemistry would be shadow dynamics doing its best to mimic what happens at the level of dark matter. The reduction of bio-physics to that of dark matter level would mean a huge simplification of the vision about living matter.

4.2 About dark variants of DNA, RNA, and amino-acids

To make progress one must construct a concrete model for the dark nuclei. The recent picture relies strongly on various anomalies to which TGD provides a solution. The TGD inspired model for "cold fusion" leads to the notion of dark nuclear physics - actually hierarchy of them labelle by the values of $h_{eff}/h = n$ and corresponding p-adic length scales. Second basic idea [L15] is that cylindrical variants of EZs discovered by Pollack [L15] give rise to the dark counterparts of DNA, RNA, and amino-acids as dark proton sequences. tRNAs would be analogs of tritium and ^{3}He. Pollack effect serves as a strong constraint for the model. Also the effects of ELF em fields on vertebrate brain [J8] combined with the rather recent finding about clustering of RNA II polymerase molecules [I74] exhibiting Comorosan effect [I134] provide valuable constraints on

the model [L40]. The outcome of the arguments is that single strand of DNA, mRNA, tRNA and amino-acids most naturally correspond to $k = 149$ and double stranded DNA to $k = 151$.

Remark: The following argumentation is kind of Sherlock-Holmes-ing using all possible hints as constraints to select between imagined options rather than glorious march from axioms to theorems and thus not science in the usual sense.

4.2.1 Dark variant of DNA

Concerning the identification of the size scale of dark DNA one can consider several options. The first guess was that the scale is same as for ordinary DNA: L(141)=.34 nm obtained by scaling from the distance of protons in the $k = 127$ dark nucleus implicated by the findings of Holmlid et al [C1, L26] [L17]. It however turns out that the p-adic length scale assignable to dark DNA is most naturally $k = 151$ corresponding to the thickness 10 nm of DNA coil. The hypothesis that the integer k labelling p-adic length scale is prime is attractive working hypothesis leaving very few options under consideration. The options $k = 137$ and $k = 149$ are excluded since the pairing of dark DNA and ordinary DNA would not be possible without the coiling of ordinary RNA around dark DNA. This leaves only options for which $k \geq 149$ for prime values of k.

Remark: The p-adic length scale associated with a system is defined to be $L(k)$ if the size of the system is in the half open interval $[L(k), L(k+1))$. One can also consider the possibility that p-adic length scale corresponds to the upper end of $[L(k-1), L(k))$.

General considerations

Consider first some background.

1. The TGD based model leads to the proposal for a formation of this kind of dark nuclear strings such that the distance between protons is rather precisely electron Compton length $L_e \simeq .4 \times 10^{-12}$ meters explains "cold fusion" in terms of dark nucleosynthesis which should have preceded ordinary nucleosynthesis by heating the material to the temperature required by it [L29] [K74].

   Dark nucleosynthesis would have produced part of heavier nuclei outside stars. The binding energy scale for dark nuclear physics would be scaled down like 1/length and 2.6 MeV binding energy per nucleon for ^{3}He of the ordinary nuclei would be scaled down by a factor 2^{-11} to 1.3 keV. Note however that it is excitation energies of order 1 MeV what matters and would scale down to .5 keV. This level does not yet correspond to biology as we know it but could be one step in the evolutionary hierarchy leading from nuclear physics also based on nuclear strings to biology involving increase of Planck constant $h_{eff}/h = n$ identifiably as the dimension of algebraic extension of rationals characterizing the complexity of the dynamics.

2. These dark nuclei have $h_{eff}/h = n = 2^{11}$ (or near to it) and cannot be those responsible for the dark variants of biomolecules since the distances of dark protons given by electron Compton length are much shorter than the distance between DNA nucleotides about .34 nm, which is roughly 142 times the electron Compton length 2.4×10^{-3} nm.

3. The distance between the dark protons appearing as counterparts of DNA nucleotides should be larger than that between ordinary DNA nucleotides. The simplest assumption that dark DNA coil is a horizontally scaled variant of DNA coil with same twisting angle so that DNA nucleotides are projected horizontally to their dark counterparts at the surface of a cylinder. Once the p-adic length scale of this cylinder is given, the distance between dark protons is fixed by p-adic scaling from the distance between dark protons for $k = 127$ case - that is electron Compton length. In the case of uncoiled RNA/AA one could have also a coil rotating around the ordinary RNA/AA.

   The distance between dark nucleotides must be longer than the the distance $3 \times .34 \sim 1$ nm taken by single ordinary DNA codon. If k is prime this leaves only $k = 149$ or $k = 151$ into consideration.

4. The negative charge of DNA and RNA assignable to one oxygen of phosphate combining with ribose and DNA/RNA base could come from the tubular EZ formed in the formation

of DNA. The negative charge of phosphates and the positive charge of dark protons could guarantee the stability of pairs of dark proton sequences and ordinary RNA and DNA.

DNA strand has radius of $R = 1$ nm. The Debye length R_D of DNA gives rough idea about the scale above which the negative charge of DNA nucleotides associated with the phosphates screened. R_D should be longer than R: otherwise it is not possible to speak about charge of DNA only atomic length scales. One should have $R_D > R$: otherwise it does not make sense to assign negative DNA charge except in atomic length scales. The simplest option is that dark DNA has size scale $L(151)$.

Remark: The rough estimates depend on how one identifies p-adic length scale. For the identification as $L(k) = \sqrt{5}L_e(k)$ motivated by the mass formula for electron, one would have $L(k) = \sqrt{5}L_e(k)$ giving $L(141) = 0.67$ nm. With this interpretation the estimate for the screening radius would be still shorter than R.

Remark: Scaled up hadron physics would be associated with flux tubes of the magnetic body of the codon at which one would have nucleons as 3-quark color singlets. I have already earlier proposed that scaled variants of hadron physics [K21] appear in TGD inspired biology. One motivation comes from honeybee dance [A15]!

The pairing dark AAs with positive charge with ordinary AAs might lead to problems since 16 AAs are neutral. The only charged AA residues are Lys (+), Arg (+), Asp (-) and Glu (-).

1. The formation mechanism for dark proton sequences gives for dark AAs a large positive charge. AAs are however not accompanied by negatively charged phosphate ions. Does charge neutrality require that the dark bonds between dark proton has negative charge so that one has effectively neutron?

   Dark weak interactions correspond to large value of n [L29] so that in DNA length scale their proceed as fast as electromagnetic interactions (weak bosons would behave like massless particles below scaled up weak scale). This could make possible β decays changing the charges of the bonds between dark protons or dark neutrons [L29] and lead to a stability by β emission.

2. Proteins in water environment have a charge due to protons or electrons attaching to them. This charge depends on pH and becomes negative above certain critical pH. One might think that the limit of very large pH (no protons) corresponds to the situation in which the electrons of EZ attach to AAs.

Dark codons do not have decomposition to letters whereas ordinary codons have. In a well-defined sense one could say that dark code is "holistic" whereas the ordinary code is "reductionistic".

1. This brings in mind western written language in which words decompose to letters. In some eastern languages the symbols of written language correspond to entire words. Do these differences correspond at deeper level to ordinary and dark genes. Could the analytic and holistic aspects of cognition relate to the differences between ordinary and dark code.

2. One cannot exclude the entanglement between codons and evolution as emergence of entanglement even suggests this. Could this kind of entanglement give rise to basic units of DNA, in particular genes and introns. Could the decomposition of gene into coding regions and introns correspond to a decomposition to unentangled products of internally entangled pieces. This would increase exponentially the degrees of freedom involved and explain why organisms with practically the same code can be at so different evolutionary levels. In the splicing process when intronic portions are cut out from DNA sequence. Do the remaining pieces of RNA get entangled or does the decomposition of dark RNA to unentangled pieces have some meaning? Note that also ordinary RNA would be entangled or entangled. Could introns provide the means for decomposing the coding RNA to unentangled pieces.

3. The most natural possibility is that entanglement contains superposition of codon sequences in which each sequence codes for the same AA. The chemical codons appearing in the superposition have different masses and chemical properties but in zero energy ontology (ZEO)

this is possible. Situation would be like for a superconductor in which coherent state means superposition of states with different numbers of Cooper pairs and thus different fermion number in standard ontology but in ZEO this problem disappears.

Why one must have $k = 151$ for dark DNA

It was already found that for prime values of k the options $k < 149$ are not possible for dark DNA since ordinary DNA should coil around dark DNA. There is also second objection against prime $k < 149$ from energetics inspiring the hypothesis DNA corresponds to $k = 151$.

1. The scaling of the dark nuclear binding energy $E_b \sim 7$ MeV per nucleon as $L(107)/L(k)$ predicts very high binding energies for primes $k < 149$. For instance, $k = 139$ would correspond to the scaled binding energy $E_b(139) = E_b L(107)/L(139)$, $E_b \sim 7$ MeV, which is typical nuclear binding energy. This gives $E_b(139) = E_b/2^{(139-107)/2} = .14$ keV. For $k = 139$ the typical nuclear excitation energy $E_{ex} = 1$ MeV scales dow to 20 eV, which is still very high but could correspond to energies of atomic transitions. For $k = 151$ it E_b scales down to 3.5 eV. The typical dark excitation energy for $k = 151$ is $E_{ex}(151) = .5$ eV and the identification as a nominal value of metabolic energy quantum is attractive. Dark nuclear physics might therefore control biochemistry using dark nuclear transitions as a tool to provide desire energy currency.

2. The TGD based explanation of Pollack effect provides a consistency test for the idea [L15] [L15]. In Pollack effect IR light (besides either kinds of energy feeds) induces the formation of negative charged exclusion zones (EZs) in water bounded by gel phase. In TGD based model this would correspond to the formation of dark proton sequences at magnetic flux tubes. The scale of dark nuclear binding energy would be most naturally in eV scale. The binding energy scale of hydrogen atoms in water molecules is about 5 eV which suggests that the binding energy scale for dark protons sequences is smaller since otherwise energy would be liberated. This would suggest $k = 149$ as will be found.

3. One can imagine that an external perturbation induces

   (a) a transition in which the proton bound to water molecule transforms to its dark variant in higher energy state or

   (b) that the proton goes over a potential wall, whose height is measured in eV:s.

   If the dark nuclear binding energy is higher than the binding energy of proton in water molecule, the process should liberate energy and could occur spontaneously unless high potential wall prevents it. Hence the first option seems the only realistic one. Note that one could consider the cancellation of dark nuclear binding energy and repulsive Coulomb energy which scale in the same manner as function of p-adic length scale so that still the net energy would scale increase in shorter p-adic length scales.

Pollack effect suggests that if k is prime, one must have $k = 149$ for dark proton sequences formed in Pollack effect.

1. For $k = 149$ one has $E_b(151) \sim E_b/2^{(149-107)/2} = 3.5$ eV for $E_b = 7$ MeV, which is in UV range slightly above the visible range. The binding energy of hydrogen atom in water is about 5 eV which would require the incoming radiation to have energy 1.5 eV which is indeed in IR range. This option looks therefore realistic.

2. For $k = 151$ one would have $E_b(151) \sim 7MeV/2^{(151-107)/2} = 1.75$ eV, which just above the IR energy range. Now the energy needed to transform ordinary protons to dark protons in Pollack effect would be in UV range so that this options seems to be excluded.

This argument suggests that dark proton sequences generated in Pollack effect are analogs of single DNA strand, which would naturally correspond to $L(149) = L(151)/2$. Also RNA would naturally correspond to this scale.

1. $L(151) \simeq 10$ nm is the thickness of coiled DNA double strand. The size scale of dark nucleons would be $L(151)$ and the dark DNA strand should be horizontally scaled variant of ordinary DNA strand by a scaling factor $\lambda \sim L(151)/.33$ nm $= 30$. DNA double strand would be obtained by a transversal scaling from the ordinary DNA double strand.

2. The higher coilings of DNA could correspond to higher horizontally scaled variants of DNA corresponding to $k = 157, 163, 167$. $k = 167$ would correspond to nuclear membrane length scale of 2.5 μm. The emergence of nuclear membrane in $k = 151$ length scale would have been accompanied by the emergence of dark DNA in this scale. Cell membrane could correspond to $k = 173$ and p-adic length scale 17.6 μm. Neurons have size varying from 4-100 micrometers (the definition of size depends on whether one includes axons) and might correspond to $k = 179, 181$ and length scales of .16 mm and perhaps even .32 mm.

The only justification for this speculative picture is that it is consistent with the other basic ideas about TGD inspired quantum biology.

1. Cisse et al [I74] found that RNA II polymerase molecules cluster during transcription and their dynamics involves multiples of the time scale $\tau = 5$ seconds. Comorosan reported long time ago that just these time scales are universal bio-catalysis [I134]. The TGD inspired model [L40] for the findings of Cisse et al allows to sharpen the TGD based view about quantum biology considerably.

2. The basic parameter of the model is the value of gravitational Planck constant $\hbar_{gr} = GM_D m/v_0$ assigned to magnetic flux tubes mediating gravitational interactions. Already earlier work gives estimates for the value M_D of dark mass and velocity parameter v_0 and the model leads to the same estimates. The identification of the values of τ as Josephson periods assuming the potential difference V along flux tubes connecting reacting molecules is universal and same as over neuronal membrane fixed the value of h_{gr}. The value of V along flux tube serving as Josephson junction would be universal and equal to membrane potential. Josephson radiation would have energies coming as multiples ot ZeV just above the thermal energy at physiological temperatures fixed by the membrane potential.

3. The model forces the conclusion that the endogenous magnetic field B_{end} has at its upper bound $B_{end} = .2$ Gauss deduced from the findings of Blackman about effects of ELF em fields on vertebrate brain [J8]. The earlier ad hoc hypothesis was that $B_{end} = .2$ Gauss is minimum value of B_{end}. Furthermore, for the required value of h_{gr} $B_{end} = .2$ Gauss corresponds to dark cyclotron energy of .12 keV, which is surprisingly large energy at the upper end of UV band: the earlier intuitive guess was that energy scale is in visible range.

   Also harmonics of cyclotron frequencies were found to have effects so that really large energy scales are involved with the interaction of ELF radiation and one can ask whether this picture really makes sense. This raises a question about the mechanism of the interaction of ELF em radiation with living matter. One also wonder why the ELF radiation has effects on both behavior and physiology.

   Assume

   (a) that dark photons with energies coming as multiples of .12 keV are in question,

   (b) that these dark photons excite dark cyclotron states in the cellular length scale deduced from flux quantization and

   (c) that the dark cyclotron photons radiated as the excited cyclotron states return to the ground states perform some control action on ordinary DNA coil - this is in accordance with the basic vision about the role of magnetic body.

   X rays have energy range varying from 100 eV to 100 keV and wavelengths varying from 10 nm to .01 nm. The wavelength of an ordinary photon resulting from dark photon with energy of .12 keV would be of order 10 nm, the radius of DNA coil for $k = 151$!

   Could this energy induce an analog of standing em wave in transversal degrees of freedom of DNA perhaps transformable to many phonon state with very large number of photos and

thus classical acoustic wave? This would allow to understand how cyclotron harmonics can have non-trivial effects. The effects of ELF radiation on behavior and physiology could be understood as gene expression induced by the irradiation.

Both dark cyclotron radiation and radiation generated in dark nuclear transitions could have biological effects

1. Can one relate energy scale of .12 keV associated with dark cyclotron radiation to atomic physics? The ionization energies behave as Z_{eff}^2/n^2, where Z_{eff} is nuclear charge minus the charge of the closed shells. Z_{eff} is also reduced by electronic screening by other valence electrons. The binding energies of valence electrons decrease with the principal quantum number n so that only $n = 2$ row of the periodic table might allow so high ionization energies for valence electrons.

   Oxygen is certainly the first candidate to consider. The ionization energy for oxygen is .12 eV from an estimate assuming that the effective nuclear charge is 6 (with the contribution of 2 valence electrons subtracted). The actual value is 68.9 eV: the reduction is due to electron screening. This value is smaller than the estimate estimate for $E_b = .12$ keV and since harmonics of this energy are involved, the interpretation in terms of ionization does not make sense.

2. Not only oxygen but also heavier elements are ionized in living matter and at least to me this has remained more or less a mystery. Could dark photons emitted by dark nuclei of MB perform control by inducing the transitions and even ionization of oxygen and other biologically important atoms. The process could proceed also in opposite direction. The energy scale would correspond to that of nuclear excitations scaled down by the above ratio of p-adic length scales. If the energy scale of ordinary nuclear excitations is taken to be about 1 MeV, the dark energy scale for $k = 127$ assignable to the dark nuclei created in "cold fusion" is keV. For $k = 131$ the scale would be 250 eV and above the ionization energy scales for valence electrons. For $k = 137$ the scale would be 17 keV. These dark nuclear transitions could generate dark photons inducing transitions of atoms and even ionizations.

4.2.2 What about dark variants of RNA, tRNA, and AAs?

Also RNA and AAs should have dark variants and one should understand their role. Suppose that the integer k characterizing the p-adic length scale is prime. The vision about RNA era preceding DNA era suggests that RNA accompanying dark RNA is at lower level in the evolution, and hence the value of h_{eff} is smaller for dark RNA than for dark DNA. Also the p-adic length scale for RNA would be shorter.

1. The most natural option is that RNA corresponds to $k = 149$ as also single DNA strand. This would conform with the above suggestion that the Pollack effect generates $k = 149$ dark proton sequence (dark RNA?). DNA double strand would correspond to $k = 151$.

   The emergence of $k = 151$ level would mean the emergence of structures with scale characterized by $L(151)$. This includes DNA double strand forming a coil with thickness $L(151)$ and nuclear and cell membranes. During RNA era these structures would have been absent.Both DNA double strand and cell membrane have binary structures. Therefore single DNA strand and lipid layer could correspond to $k = 149$. In transcription DNA opens and double strand becomes pair of strands having naturally $k = 149$. Therefore mRNA should have also $k = 149$.

2. If AAs correspond to $k = 149$ then also tRNA should correspond to $k = 149$. On the other hand, tRNA does not form strands and should be more elementary structure than RNA. Could tRNA corresponds to $k = 139$ or $k = 137$? This would require that also the attached AA would correspond to $k = 139$ or $k = 137$, which does not look plausible.

   Remark: TGD vision assumes tRNA was present already at RNA era and the role of AA in tRNA was to catalyze RNA replication. In fact, RNA could have been just tRNA at very early stages.

What about AAs? The following arguments suggest that one has $k = 149$ for both AAs and RNA.

1. For dark AAs one can imagine p-adic evolutionary hierarchy analogous to that for DNA. In TGD inspired vision AA sequences emerged together with DNA. Proteins can appear also as coils. Since mRNA pairs with single DNA strand and AAs with mRNA, it seems that AAs should correspond to $k \geq 149$?

2. One could however argue that AAs are building bricks rather than information molecules and k could be rather small for dark AAs. Dark AAs should pair with proteins. Pairing without coiling is possible only if the length per letter is same as the length per AA and thus same as for DNA letter, which is longer than the length taken by $k = 139$ dark proton. Also this suggests $k = 149$ for dark AAs and their coiling around the ordinary AAs.

4.2.3 Clustering of RNA polymerase molecules and Comorosan effect

Once again I had good luck: I received a link (see `http://tinyurl.com/y7bego83`) to a highly interesting popular article telling about the work by Ibrahim Cisse at MIT and his colleagues [I74] (see `http://tinyurl.com/y9wzt5yl`) about the clustering of RNA polymerase proteins in the transcription of RNA. Similar clustering has been observed already earlier and interpreted as a phase separation giving rise to protein droplets [L47]. Now this interpretation is not proposed by experiments but they say that it is quite possible but they cannot prove it.

I have already earlier discussed the coalescence of proteins into droplets as this kind of process in TGD framework [K75] [L47]. The basic TGD based ideas is that proteins - and biomolecules in general - are connected by flux tubes characterized by the value of Planck constant $h_{eff} = n \times h_0$ for the dark particles at the flux tube. The higher the value of n is the larger the energy of given state. For instance, the binding energies of atoms decrease like $1/n^2$. Therefore the formation of the molecular cluster liberates energy usable as metabolic energy.

Remark: h_0 is the minimal value of h_{eff}. The best guess is that ordinary Planck constant equals to $h = 6h_0$ [L23, L42] (see `http://tinyurl.com/goruuzm` and `http://tinyurl.com/y9jxyjns`.

TGD view about the findings

Gene control switches - such as RNA II polymerases in DNA transcription to RNA - are found to form clusters called super-enhancers. Also so called Mediator proteins form clusters. In both cases the number of members is in the range 200-400. The clusters are stable but individual molecules spend very brief time in them. Clusters have average lifetime of $5.1 \pm .4$ seconds.

Why the clustering should take place? Why large number of these proteins are present although single one would be enough in the standard picture. In TGD framework one can imagine several explanations. One can imagine at least following reasons.

1. If the initiation of transcription is quantum process involving state function reduction, clustering could allow to make this process process deterministic at the level of single gene in spite of the non-determinism of state function reduction. Suppose that the initiation of transcription is one particular outcome of state function reduction. If there is only single RNA II polymerase able to make only single trial, the changes to initiate the transcription are low. This could be the case if the protein provides metabolic energy to initiate the process and becomes too "tired" to try again immediately. In nerve pulse transmission there is analogous situation: after the passing of the nerve pulse generation the neuron has dead time period. As a matter of fact, it turns out that the analogy could be much deeper.

   How to achieve the initiation with certainty in this kind of situation? Suppose that the other outcomes do not affect the situation appreciably. If one particular RNA polymerase fails to initiate it, the others can try. If the number of RNA transcriptase molecule is large enough, the transcription is bound to begin eventually! This is much like in fairy tales about princess and suitors trying to kill the dragon to get the hand of princess. Eventually comes the penniless swineherd.

2. If the initiation of transcription requires large amount of metabolic energy then only some minimal number of N of RNA II polymerase molecules might be able to provide it collectively. The collective formed by N molecules could correspond to a formation of magnetic body (MB) with a large value of $h_{eff} = n \times h_0$ and controlling the molecules and inducing its coherent behavior. The molecules would be connected by magnetic flux tubes.

3. If the rate for occurrence is determined by an amplitude which is superposition of amplitudes assignable to individual proteins the the rate is proportional to N^2, N the number of RNA II polymerase molecules. The process for the cluster is reported to to be surprisingly fast as compared to the expectations - something like 20 seconds. The earlier studies have suggests that single RNA polymerase stays at the DNA for minutes to hours.

   Clustering could allow to speed up bio-catalysis besides the mechanism allowing to find molecules to find by a reduction of $h_{eff}/h = n$ for the bonds connecting the reactants and the associated liberation of metabolic energy allowing to kick the reactants over the potential wall hindering the reaction.

Concerning the process of clustering there are two alternative options both relying on the model of liquid phase explaining Maxwell's rule assuming the presence of flux tube bonds in liquid and of water explaining its numerous anomalies in terms of flux tubes which can be also dark (see `http://tinyurl.com/ydhknc2c`).

1. **Option I**: Molecules could form in the initial situation a phase analogous to vapour phase and there would be very few flux tube bonds between them. The phase transition would create liquid phase as flux tube loops assignable to molecules would reconnect form flux tube pairs connecting the molecules to a tensor network giving rise to quantum liquid phase. The larger then value of n, the longer the bonds between molecules would be. This kind of model [L32] (see `http://tinyurl.com/yassnhzb`) is used to explain the strange findings that a system consisting of plastic balls seems to show primitive features of life such as metabolism.

2. **Option II**: The molecules are in the initial state connected by flux tubes and form a kind of liquid phase and the clustering reduces the value of $h_{eff}/h = n$ and therefore the lengths of flux tubes. This would liberate dark energy as metabolic energy going to the initiation of the transcription. One could indeed argue that connectedness in the initial state with large enough value of n is necessary since the protein cluster must have high enough "IQ" to perform intelligent intentional actions.

Protein blobs are said to be drawn together by the "floppy" bits (pieces) of intrinsically disordered proteins. What could this mean in the proposed picture? Disorder would mean absence of correlations between building bricks of floppy parts of the proteins in translational degrees of freedom.

1. Could floppiness correspond to low string tension assignable to long flux loops with large n assignable to the building bricks of "floppy" pieces of protein? Could reconnection for these loops give rise to pairs of flux tubes connecting the proteins in the transition to liquid phase (Option I)? Floppiness would also make possible to scan the environment by flux loops to get in touch with the flux loops of other molecules and in the case of hit (cyclotron resonance) induce reconnection.

2. In spite of floppiness in this sense, one could have quantum correlations between the internal quantum numbers of the building bricks of the floppy pieces. This would also increase the value of n serving as molecular IQ and provide molecule with higher metabolic energy liberated in the catalysis.

About Comorosan effect and clustering of RNA II polymerase proteins

What about the interpretation of the time scales τ equal 5, 10, and 20 seconds appearing in the clustering of RNA II polymerase proteins and Mediator proteins? What is intriguing that so called Comorosan effect [I134, I66] involves time scale of 5 seconds and its multiples claimed by Comorosan long time ago to be universal time scales in biology. The origin of these time

scales has remained more or less a mystery although I have considered several TGD inspired explanations for this time scale is based on the notion of gravitational Planck constant [K59] (see `http://tinyurl.com/yb8fw3kq`).

One can consider several starting point ideas, which need not be mutually exclusive.

1. The time scales τ associated with RNA II polymerase and perhaps more general bio-catalytic systems as Comorosan's claims suggest could correspond to the durations of processes ending with "big" state function reduction. In zero energy ontology (ZEO) there are two kinds of state function reductions [L36]. "Small" state function reductions - analogs of weak measurements - leave the passive boundary of causal diamond (CD) unaffected and thus give rise to self as generalized Zeno effect. The states at the active boundary change by a sequence of unitary time evolutions followed by measurements inducing also time localization of the active boundary of CD but not affecting passive boundary. The size of CD increases and gives rise to flow of time defined as the temporal distance between the tips of CD. Large reductions change the roles of the passive and active boundaries and mean death of self. The process with duration of τ could correspond to a life-time of self assignable to CD.

   Remark: It is not quite clear whether CD can disappear and generated from vacuum. In principle this is possible and the generation of mental images as sub-selves and sub-CDs could correspond to this kind of process.

2. In [K59] I proposed that Josephson junctions are formed between reacting molecules in bio-catalysis. These could correspond to the shortened flux tubes. The difference $E_J = ZeV$ of Coulomb energy of Cooper pair over flux tube defining Josephson junction between molecules would correspond to Josephson frequency $f_J = 2eV/h_{eff}$. If this frequency corresponds to $\tau_J = 5$ seconds, h_{eff} should be rather large since E_J is expected to be above thermal energy at physiological temperature.

   Could Josephson radiation serve as a kind of of synchronizing clock for the state function reductions so that its role would be analogous to that of EEG in case of brain? A more plausible option is that Josephson radiation is a reaction to the presence of cyclotron radiation generated at MB and performing control actions at the biological body (BB) defined in very general sense. In the case of brain dark cyclotron radiation would generate EEG rhythms responsible for control via genome and dark generalized Josephson radiation modulated by nerve pulse patterns would mediate sensory input to the MB at EEG frequencies.

   A good guess motivated by the proposed universality of the Comorosan periods is that the energy in question does not depend on the catalytic system and corresponds to Josephson energy for protein through cell membrane acting as Josephson junction and giving to ionic channel or pump. The flux tubes themselves have universal properties.

3. The hypothesis $\hbar_{eff} = \hbar_{gr} = GMm/\beta_0 c$ of Nottale [E5] for the value of gravitational Planck constant [K45, K37, K76, K75] gives large $\hbar$. Here $v_0 = \beta_0 c$ has dimensions of velocity. For dark cyclotron photons this gives large energy $E_c \propto \hbar_{gr}$ and for dark Josephson photons small frequency $f_J \propto 1/h_{gr}$. Josephson time scale τ_f would be proportional to the mass m of the charged particle and therefore to mass number A of ion involved: $f_J \propto A$ possibly explaining the appearance of multiples of 5 second time scale. Cyclotron time scale does not depend on the mass of the charged particle at all and now sub-harmonics of τ_c are natural.

The time scales assignable to CD or the lifetime-time of self in question could correspond to either cyclotron of Josephson time scale τ.

1. If one requires that the multiplies of the time scale 5 seconds are possible, Josephson radiation is favoured since the Josephson time scale proportional to $h_{gr} \propto m \propto A$, A mass number of ion.

   The problem is that the values $A = 2, 3, 4, 5$ are not plausible for ordinary nuclei in living matter. Dark nuclei at magnetic flux tubes consisting of dark proton sequences could however have arbitrary number of dark protons and if dark nuclei appear at flux tubes defining Josephson junctions, one would have the desired hierarchy.

2. Although cyclotron frequencies do not have sub-harmonics naturally, MB could adapt to the situation by changing the thickness of its flux tubes and by flux conservation the magnetic field strength to which f_c is proportional to. This would allow MB to produce cyclotron radiation with the same frequency as Josephson radiation and MB and BB would be in resonant coupling.

Consider now the model quantitatively.

1. For $\hbar_{eff} = \hbar_{gr}$ one has

$$r = \frac{\hbar_{gr}}{\hbar} = \frac{GM_D m}{c\beta_0} = 4.5 \times 10^{14} \times \frac{m}{m_p}\frac{y}{\beta_0} \quad .$$

Here $y = M_D/M_E$ gives the ratio of dark mass M_D to the Earth mass M_E. One can consider 2 favoured values for m corresponding to proton mass m_p and electron mass m_e.

2. $E = h_{eff} f$ gives the concrete relationship $f = (E/eV) \times 2.4 \times 10^{14} \times (h/h_{eff})$ Hz between frequencies and energies. This gives

$$x = \frac{E}{eV} = 0.4 \times r \times \frac{f}{10^{14} Hz} \quad .$$

3. If the cyclotron frequency $f_c = 300$ Hz of proton for $B_{end} = .2$ Gauss corresponds to bio-photon energy of x eV, one obtains the condition

$$r = \frac{GM_D m_p}{\hbar\beta_0} \simeq .83 \times 10^{12} x \quad .$$

Note that the cyclotron energy does not depend on the mass of the charged particle. One obtains for the relation between Josephson energy and Josephson frequency the condition

$$x = \frac{E_J}{eV} = 0.4 \times .83 \times 10^{-2} \times \frac{m}{m_p} \times x\frac{f_J}{Hz} \quad , \quad E_J = ZeV \quad .$$

One should not confuse eV in ZeV with unit of energy. Note also that the value of Josephson energy does not depend on h_{eff} so that there is no actual mass dependence involved.

For proton one would give a hierarchy of time scales as A-multiples of $\tau(p)$ and is therefore more natural so that it is natural to consider this case first.

1. For $f_J = .2$ Hz corresponding to the Comorosan time scale of $\tau = 5$ seconds this would give $ZeV = .66x$ meV. This is above thermal energy $E_{th} = T = 27.5$ meV at $T = 25$ Celsius for $x > 42$. For *ordinary* photon ($h_{eff} = h$) proton cyclotron frequency $f_c(p)$ would correspond for $x > 42$ to EUV energy $E > 42$ eV and to wavelength of $\lambda < 31$ nm.

The energy scale of Josephson junctions formed by proteins through cell membrane of thickness $L(151) = 10$ nm is slightly above thermal energy, which suggests $x \simeq 120$ allowing to identify $L(151) = 10$ nm as the length scale of the flux tube portion connecting the reactants. This would give $E \simeq 120$ eV - the upper bound of EUV range. For $x = 120$ one would have $GM_E m_p y/v_0 \simeq 10^{14}$ requiring $\beta_0/y \simeq 2.2$. The earlier estimates [K75] for the mass M_D give $y \sim 2 \times 10^{-4}$ giving $\beta_0 \sim 4.4 \times 10^{-4}$. This is rather near to $\beta_0 = 2^{-11} \sim m_e/m_p$ obtained also in the model for the orbits of inner planets as Bohr orbits.

For ion with mass number A this would predict $\tau_A = A \times \tau_p = A \times 5$ seconds so that also multiples of the 5 second time scale would appear. These multiples were indeed found by Comoran and appear also in the case of RNA II polymerase.

2. For proton one would thus have 2 biological extremes - EUV energy scale associated with cyclotron radiation and thermal energy scale assignable to Josephson radiation. Both would be assignable to dark photons with $h_{eff} = h_{gr}$ with very long wavelength. Dark and ordinary photons of both kind would be able to transform to each other meaning a coupling between very long lengths scales assignable to MB and short wavelengths/time scales assignable to BB.

   The energy scale of dark Josephson photons would be that assignable with Josephson junctions of length 10 nm with long wavelengths and energies slightly above E_{th} at physiological temperature. The EUV energy scale would be 120 eV for dark cyclotron photons of highest energy would be fixed by flux tube length of 10 nm.

   For lower cyclotron energies forced by the presence of bio-photons in the range containing visible [K65, K66] and UV and obtained for B_{end} below .2 Gauss, the Josephson photons would have energies below E_{th}. That the possible values of B_{end} are below the nominal value $B_{end} = .2$ Gauss deduced from the experiments of Blackman [J8] does not conform with the earlier ad hoc assumption that B_{end} represents lower bound. This does not change the earlier conclusions.

   Could the 120 eV energy scale have some physical meaning in TGD framework? The corresponding wavelength for ordinary photons corresponds to the scale $L(151) = 10$ nm which correspond to the thickness of DNA double strand. Dark DNA having dark proton triplets as codons could correspond to either $k = 149$ or $k = 151$. The energetics of Pollack effect suggests that $k = 149$ is realized in water even during prebiotic period [L38] (see `http://tinyurl.com/yalny39x`). In the effect discovered by Blackman the ELF photons would transform dark cyclotron photons having $h_{eff} = h_{gr}$ and energy about .12 keV. They would induce cyclotron transitions at flux tubes of B_{end} with thickness of order cell size scale. These states would decay back to previous states and the dark photons transformed to ordinary photons absorbed by ordinary DNA with coil structure with thickness of 10 nm. Kind of standing waves would be formed. These waves could transform to acoustic waves and induce the observed effects. Quite generally, dark cyclotron photons would control the dynamics of ordinary DNA by this mechanism.

   It is natural to assume that $B_{end} = .2$ Gauss corresponds to the upper bound for B_{end} since magnetic fields are expected to weaken farther from the Earth's surface: weakening could correspond to thickening of flux tubes reducing the field intensity by flux conservation. The model for hearing [K43] requires cyclotron frequencies considerably above proton's cyclotron frequency in $B_{end} = .2$ Gauss. This requires that audible frequencies are mapped to electron's cyclotron frequency having upper bound $f_c(e) = (m_p/m_e)f_c(p) \simeq 6 \times 10^5$ Hz. This frequency is indeed above the range of audible frequencies even for bats.

For electron one has $h_{gr}(e) = (m_e/mp) \times h_{gr}(p) \simeq 5.3 \times 10^{-4} h_{gr}(p)$, $\hbar_{gr}(p)/\hbar = 4.5 \times 10^{14}/\beta_0$. Since Josephson energy remains invariant, the Josephson time scales up from $\tau(p) = 5$ seconds to $\tau(e) = (m_e/m_p)\tau(p) \simeq 2.5$ milliseconds, which is the time scale assignable to nerve pulses [K44, K15].

To sum up, the model suggests that the idealization of flux tubes as kind of universal Josephson junctions. The model is consistent with bio-photon hypothesis. The constraints on $h_{gr} = GM_D m/v_0$ are consistent with the earlier views and allows to assign Comorosan time scale 5 seconds to proton and nerve pulse time scale to electron as Josephson time scales. This inspires the question whether the dynamics of bio-catalysis and nerve pulse generation be seen as scaled variants of each other at quantum level? This would not be surprising if MB controls the dynamics. The earlier assumption that $B_{end} = 0.2$ Gauss is minimal value for B_{end} must be replaced with the assumption that it is maximal value of B_{end}.

4.3 TGD view about the emergence of chemical life

Consider first the basic assumptions.

1. Dark DNA, RNA,... emerged before chemistry and serve as templates for ordinary DNA,

RNA,... The replication, transcription, and translation for ordinary DNA, RNA,... are induced by the corresponding processes for their dark counterparts.

2. Dark proton sequences are associated with tubular EZs in water generated by Pollack effect.

3. The amount of entanglement measured by entanglement negentropy (having a well-defined meaning in adelic physics [L34]) is expected to increase gradually during evolution. Hence one expects generation of more and more entangled sequences of dark nucleons. At the bottom - perhaps ordinary nuclear physics - one would have the product states of dark nucleons. Perhaps dark nuclear physics with $n = 2^{11}$ came next. After that came $n = 2^{18}$ dark nuclear physics. But which came first: dark variants amino-acids, tRNA, RNA, or DNA and their chemical counterparts? And could one see even genes as entangled codon sequences coding for the same protein?

4.3.1 The quantum vision about the prebiotic evolution

The following vision about quantal prebiotic evolution beginning from amino-acids suggests itself. The basic idea is that all processes took place at dark level and induced the processes for ordinary biomolecules in water environment. Even the enzyme and ribozyme actions essential in recent biology would be replaced with corresponding actions at dark level and biochemistry would reduce to shadow dynamics.

1. Amino-acids are easiest to produce (as Miller-Urey experiment demonstrated (see `http://tinyurl.com/4q2arv`)) requiring no enzymatic action and there is just single chemical amino-acid per dark RNAs coding for it. Therefore the pairs of amino-acids and their dark variants could have emerged first. Note that proteins were not yet present.

   Remark: Vivo-vitro difference could mean that dark partner of biomolecule is present in vivo and missing in vitro.

2. DNA requires cell membrane. This requires RNA emerged after amino-acids. This implies that dark variants of dark tRNA, their pairing with tRNA and the pairing of dark RNA with RNA emerged next?

   This picture supports that the old TGD inspired idea about the role of tRNA during RNA era. Dark tRNA would have made possible the replication of dark RNA sequences (rather than the translation of RNA to amino-acid sequence) during this era. The dark amino-acid of dark tRNA would have served as a catalyst inducing the addition of dark RNA codon to the growing RNA sequence. No chemical transcription machinery nor DNA was needed at this stage. This would solve one hen-or-egg problem.

3. After that a revolution would have occurred. For some reason dark amino-acids began to attach to the growing sequence of amino-acids and dark RNA codon was left alone. What prevented dark RNA codon to attach to the growing dark RNA sequence? Was it the emerging entanglement between dark codons giving rise to genes as entangled pieces of DNA that made this impossible.

   This means entanglement also between the ordinary codons, which makes sense only in ZEO. If possible at all this entanglement should respect genetic code so that entangled superposition would involve only codons coding for the same amino-acid so that the translation to a single amino-acid sequence rather than their quantum superposition is possible. If more general superpositions are allowed the translation process would be like state function reduction to amino-acid sequence.

4. At this step the replication of both dark and ordinary RNA was lost and it seems that dark DNA-DNA pairs replicating dark DNA and transcribing it to dark RNA and inducing corresponding process at the level of chemistry must have emerged at the same time.

   The emergence of DNA requires also the emergence of cell membrane. Could the emergence of cell membrane relate to the emergence of dark nuclei in the p-adic length scale $L(k)$, $k = 149$ and could the double layered structure of cell membrane serve as an analog for that of DNA double strand? Could lipid layers correspond to 2-D analogs of DNA strand with lipids taking the role of codons?

5. Could the full genetic code emerged in step-wise manner as proposed earlier [K17, K53]? Genetic code can be seen in a good approximation as a fusion of 16-letter code and 4-letter code. This might be understood if the entanglement of dark codons emerges first as entanglement of only two first letters.

What gave rise to the correspondences between dark DNA, RNA, tRNA, amino-acids and their dark variants? How the amino-acids and nucleotide bases were selected?

1. The basic principle would be the condition that metabolic energy can be transferred between chemical and dark levels. This is possible if there identical transition energies in the spectra of biomolecules and their dark variants making possible resonance.

2. Metabolic energy quantum in the range .4-.5 eV should correspond to the excitation energy scale of dark dark nuclear physics if $E_{ex} = 1$ MeV is taken as the estimate for a typical nuclear excitation energy. Hydrogen bonds also correspond to this energy scale but this might be just what is needed to give rise to coherent metabolic activity.

   The original proposal was that dark DNA associated with ordinary DNA corresponds to $k = 141$ assignable to the ordinary DNA but this proposal predicts $E_{ex}(141) = 16$ eV. This proposal turned out to be unrealistic also in other respects. $k = 149$ assignable to dark RNA predicts $E_{ex}(149) = .5$ eV and is a more plausible option in many other aspects. Also lower values of k than $k = 149, 151$ might be present - at least during the prebiotic stage. Pollack's findings however support the view that the irradiation of water with IR light generates dark proton sequences with $k = 149$. Does this mean that the evolutionary level of water is raised to $k = 151$ in presence of gel phase binding the water sample? Note that "cold fusion" [L17, L29] might be interpreted as creation of $k = 127$ dark proton sequences.

To sum up: for DNA,RNA, and tRNA the emergence of entanglement would have created the chemical counterparts of quantum superpositions: ZEO is necessary since in positive energy ontology superpositions are highly implausible.

There are some questions to ponder.

1. Why the decomposition into triplets? Does resonance condition for the metabolic energy transfer select triplets as basic units and also the RNA-amino-acid correspondence? Do also intronic regions have triplets as basic units?

   One ends up to a prediction of vertebrate genetic code also from a model of music harmony [L12]. In fact, the model explains also its slight variation and the 2 additional amino-acids. Could this help to understand why the triplet code is so unique.

2. Could one imagine that also quarks and antiquarks were involved? Could dark nucleon pair with dark quark with same spin and isospin and color confinement forces dark proton triplets? Dark quarks indeed define a representation for A,T,C, G. In the model of topological computation [K17, K53]. I have actually speculated with the possibility that dark quarks and antiquarks are paired with ordinary DNA codons.

3. Could dark conjugate protons or their triplets of parallel dark DNA strands form Cooper pairs or does pairing of dark protons triplets (their conjugates) with dark quarks (anti-quarks) give rise to bosonic states?

4.3.2 Unidentified Infrared Bands as a test for the proposal

Unidentified Infrared Bands (UIBs) are an ill-understood phenomenon associated with radiation coming from interstellar space. There are also other analogous phenomena having no explanation in terms of molecular transitions [**?**] and one can ask whether they could be seen as signatures of dark nuclear physics.

1. UIBs are observed around bands around IR energies $E \in \{.11, .20, .375\}$ eV.

2. Poly-aromatic hydrocarbons (PAHs) (see `http://tinyurl.com/atx4t9a`) are known to generate UIBs [**?**]. Therefore the UIBs from interstellar space could originate from PAHs.

TGD based models for UIBs

TGD suggests several explanations for UIBs involving new physics related to the p-adic length scale hypothesis and $h_{eff}/h = n$ hierarchy.

1. For years ago I discussed a model for UIBs based on p-adic length scale hypothesis [**?**]. The idea was that protons "drop" from atomic space-time sheet with $k = 137$ to a larger space-time sheet to $k_1 > 137$ space-time sheet and the difference of zero point kinetic energies is liberated as radiation [**?**]. The proposal was that the zero point kinetic energies give rise to a hierarchy of metabolic energy quanta.

   Second possibility is phase transition in which the size of the $k = 137$ space-time sheet increases to $k_1 > 137$ and liberates the difference of zero point kinetic energy. For the third option energy preserving phase transition increasing $h_{eff}/h = n$ by a factor $(k_1 - k)/2$ followed by a phase transition reducing the value of h_{eff} back to the initial one but without change of the size of the space-time sheet would liberate the difference of zero point kinetic energies.

2. Could dark nuclear transitions explain UIBs? For $k = 149$ as the p-adic length scale of DNA letters would give nuclear energy scale $E = .5$ eV equal to the metabolic energy quantum by scaling 1 MeV for the ordinary nuclei by factor $2^{149-107}/2 = 2^{21}$ (here the original version of text contained error: this claim was made for $k = 141$). This energy has correct order of magnitude but is too high an energy for UIBs but there are of course also smaller energies possible for the nuclear excitations possibly explaining the UIBs.

3. What about hydrogen bonds? The strength of hydrogen bond - essentially the bond energy - is in the range .4-.5 eV -, which as such does not correspond to the average UIB energy, which come approximately as three lowest powers of two. The range of bond energies is .1 eV is smaller than the smallest UIB energy .11 eV.

   UIBs can be associated with hydrogen bonds if there are states of bond with higher bond energy. They could correspond to higher values of $n = h_{eff}/h$ for the de-localized dark proton associated with the bond (analogous to de-localized valence electron). For instance, if the energy of the bond corresponds to the cyclotron energy of proton in a magnetic field associated with the bond, it is proportional to n.

   The photon energies come approximately as powers of 2. If the favored values of n are in bands around $n = 2^k$ favored by the p-adic length scale hypothesis, one has hopes of understanding the band structure in terms of transitions reducing the value of k.

Membrane potential (see `http://tinyurl.com/chylvs9`) plays a key role in metabolism and one can wonder whether UIBs might relate to the potential energies defining energies $E_J = ZeV$ of Josephson photons associated with membrane if it acts like Josephson junction like structures associated with the prebiotic lifeforms.

1. Membrane potential energy varies in the range (.04, .08) eV (cell interior is negatively charged). Excitable cells (able to generate action potentials) include neurons, muscle cells, endocrine cells, and some plant cells. The average value for them is around .06 eV and further depolarization makes these cell more excitable. This suggests that the instability is caused by thermal radiation with nearly the same energy. The threshold for the generation of the action potential E_{act} is in the range $(.050, .055)$ eV. Interestingly, during ageing neurons become more hyperpolarized and therefore less excitable. In photoreceptors the resting potential energy can be as low as .03 eV making them very sensitive to light.

2. In TGD inspired quantum biology axonal membrane can be seen as a generalized Josephson junction [K41, K42, K44] decomposing nanoscopically to Josephson junctions defined by cell membrane proteins. The protein as junction would correspond to a magnetic flux tube along which various charged particles with $h_{eff} = n \times h$ flow possibly as supra currents. As a special case cell membrane acts like an ordinary Josephson junction. In this case the increment of the electrostatic energy of the Cooper pair over membrane given by $E_J = 2eV$ defines the energy of the smallest quantum of Josephson radiation.

The intensity of thermal radiation at temperature T as function of photon energy Ehas a peak at $E \simeq 3T$, which for room temperature about $T = .03$ eV gives $E_{max} = .09$ eV. The energy ZeV of Cooper pair should be larger than E_{max}. For critical action potential one has $E_{act} = 0.1$ eV, which is slightly above $E_{max} = .09$ eV so that the action potential has minimal value and thus minimizes metabolic energy costs and implies quantum criticality with temperature as a critical parameter.

Note however that for energies below E_{max} the intensity of thermal radiation decreases so that also these energies might serve as Josephson energies: this and the fact that incoming photons have intensity higher than termal background at this energy could explain why some photoreceptors can have $eV = .03$ eV.

3. Could also Josephson radiation relate to UIBs? The Josephson energy of Cooper pair for the membrane potential is around $E_J = 0.1$ eV, which corresponds to the lowest UIB band, which could thus correspond to action potential .05 eV of excitable membrane. The higher bands would correspond roughly to two octaves suggesting that the action potentials in these case are roughly .1 eV and .2 eV. Quantum criticality would suggest that temperatures scale like the energies of the bands slightly higher than $E_{max} \simeq 3T$.

Metabolic energy transfer between magnetic body and biological body (defined in very general sense for any system) is possible if the spectra of transition energies share common transition energies. Therefore the spectrum of transition energies assignable to hydrogen bonds could have many transition energies common with that assignable to dark nuclear transitions and second and third explanation could be consistent with each other.

Model for hydrogen bond

The explanations of UIBs in terms of hydrogen bonds encourages to consider a concrete model for the hydrogen bond as flux tube. This suggests a connection with metabolism at cellular level involving transfer of protons through cell membrane against potential gradient assumed to take place as dark protons carrying the metabolic energy and providing it to ADP-ATP process after their return.

1. The simplest model for the proton inside flux tube is as particle in 1-D flux tube with magnetic field. Unless the magnetic field strength and/or n is very large, the kinetic energy in the direction of flux tube dominates and phase transition would change the scale of kinetic energy proportional to n^2 for fixed flux tube length. For $n = 2^k$ this would give too strong dependence of photon energies on k.

2. On the other hand, if the flux tubes are flux loops of the magnetic body of molecule their lengths naturally scale as n and the longitudinal kinetic energy is not affected in the transition. The cyclotron energy proportional to n would change and for $n \sim 2^k$ one obtains qualitatively correct behavior.

   For proton in magnetic field of $B_{end} = .2$ Gauss the cyclotron frequency is 300 Hz and corresponds to $E_c(B_{end}) = 1.2 \times 10^{-12}$ eV. The identification of $E_c(B) = .5$ eVs would give $E_c(B) = n(B/B_{end}) \times E_c(B_{end}) = E_c(B) = .5$ eV. An estimate for B for the flux tube of hydrogen bond comes from flux quantization: $eBS = 1$ holds true for unit quantum of flux and for flux tube radius of one Angstrom this would give $B/B_{end} \sim 5 \times 10^8$. This gives the estimate $n \sim 10^8 \sim 2^{27}$. The rather large value conforms with the general vision for the values of n for dark protons whereas dark electrons of valence bonds would have much smaller values. The emergence of dark protons could be seen as the transition from chemistry already involving n as characterizer of valence bonds [L31] to bio-chemistry.

3. The identification of the metabolic energy quantum in terms of cyclotron energy could apply also in the case of cellular metabolism. The model for the generation of ATP from ADP assumes that protons are pumped by the energy coming from nutrient molecules against the membrane potential.

   The membrane potential correspond to energy of .05 eV but metabolic energy quantum is 10 times larger. This looks like an inconsistency, which in thermodynamical approach is resolved

by introducing of chemical potentials. In genuine quantum approach the introduction of thermodynamics quantities is not allowed.

The general vision about metabolic energy as a tool to increase $h_{eff}/h = n$ defining kind of molecular IQ suggests that the transformation to dark proton at magnetic flux tube along which proton can travel through the membrane is responsible for the most of the energy needed for pumping. After the dark proton has returned through cell membrane it transforms to ordinary proton and liberates the metabolic energy and makes possible ADP-APT transformation.

The above model assumes that the lengths of hydrogen bonds as flux loops scale like n. This makes possible the reconnection of flux loops coming from opposite sides of the membrane to pair of flux tubes along which dark protons can flow. Similar picture applies also to other biologically important ions.

The general view about superconductivity in TGD Universe [K41, K42] suggests that reconnection can give rise to a Cooper pairs of protons with members at separate flux tubes. Also Cooper pairs of electrons and biologically important ions could form by the same mechanism.

4.3.3 PAH world hypothesis from TGD point of view

The so called PAH world hypothesis (see `http://tinyurl.com/ycxm9zes`) has been proposed as a prebiotic era preceding RNA world. As a matter of fact, PAH world hypothesis inspired more a detailed development of TGD based model for dark nuclei.

Let us first list some properties of poly-aromatic hydrocarbons (PAHs) (see `http://tinyurl.com/atx4t9a`).

1. PAHS consist of aromatic rings glued together along sides. By definition aromatic rings have delocalized electrons. In benzene, which is the classical and simplest example of PAH, the electronic state is quantum superposition of states in which bonds and double bonds alternate along the ring but are shifted by 60 degrees with respect to each other. Naphtalene has two aromatic rings and anthracene and pnenanthtrene have 3 rings.

2. PAHs are very stable non-charged non-polar molecules and are very common in Earth. They are found in coal and tar deposits and produced in an incomplete combustion of organic matter. PAHs are poisonous. For instance, tobacco smoke contains PAHs with carcinogenic effects. The stability of PAHs motivates the belief that a large fraction of carbon in the interstellar space consists of PAHs.

3. Benzene in difficult to detect in in the interstellar space since the rotational symmetry does not allow to detect rotational transitions. Recently however nitrobenzene was detected so that benzene and more complex PAHs presumably exist in interstellar space (see `http://tinyurl.com/yap9ksrg`).

Benzene and more complex PAHs can give rise to more complex aromatic by hydrogenation, oxidation, carboxylation, and nitrogenation and led also to the basic building bricks of DNA and amino-acids and PAHs are proposed to have played important role in prebiotic life.

1. PAH world hypothesis states that the polymer like sequences of PAHs serve as scaffoldings for the formation of RNA like polymers (see `http://tinyurl.com/ycxm9zes`). The key motivation is that the distances between PAHs are same as between RNA and DNA bases: 3.4 nm. The proposal is that during PAH era RNA nucleosides A, U, C, G were attached to PAHs by hydrogen bonds.

2. Second hypothesis is that formaldehyde molecules [(H_2C)=O] formed valence bonds with RNA bases and with each other giving rise to sequences analogous to the phosphate-ribose backbone of RNA. The sequence of disjoint CO=:s was replaced with the sequence ..(C-R)-O-(C-R)-O-.. with R denoting the RNA nucleoside. After this hydrogen bonds were split and the predecessor of RNA was detached from the PAH scaffolding. Later the pre-RNA strands were folded to form double pre-RNA strands similar to ribozymes. The problem is to understand how the formaldehyde backbone was replaces with more stable phosphate-ribose backbone.

In TGD framework dark nuclei would serve as scaffolding, which however does not detach from the corresponding biomolecules. The distances between dark variants of biomolecules would explain why the two distances are the same. Very many molecules, including PAHs, can attach around dark RNA/DNA and the periodic structure would be reflect the properties of dark nuclei. This could explain UIBs as emission bands of both dark nuclei and hydrogen bonds essential for the pairing and the transfer of metabolic energy between ordinary and dark biomolecules. Also in DNA double strand hydrogen bonds could serve similar function. If thermal radiation excites higher energy states of nuclei, the emission of UIBs depends on temperature. Perhaps this could be tested.

UIBs could therefore serve as a direct signature of dark nuclear physics. If dark nuclei are not associated with PAHs in vitro or in an environment not containing water, UIBs would be absent.

4.3.4 Did RNA replicate in codon-wise manner during RNA era?

4.3.5 Did RNA replicate in codon-wise manner during RNA era?

There was an interesting popular article in Spacedaily with title "*Scientists crack how primordial life on Earth might have replicated itself*" (see `http://tinyurl.com/y92ng5vd`). The research paper [I91] is titled "*Ribozyme-catalysed RNA synthesis using triplet building blocks*" and published in eLife (see `http://tinyurl.com/ya5qyjfn`).

It is possible to replicate unfolded RNA strands in Lab by using enzymes known as ribozymes, which are RNA counterparts of enzymes, which are amino-adic sequences. In the presence of folding the replication is however impossible. Since ribozymes are in general folded, they cannot thus catalyze their own replication in this manner. The researchers however discovered that the replication using RNA triplets - genetic codons - as basic unit can be carried out in laboratory even for the folded RNA strands and with rather low error rate. Also the ribozyme involved can thus replicate in codon-wise manner. For units longer than 3 nucleotides the replication becomes prone to errors.

These findings are highly interesting in TGD framework. In TGD the chemical realization of genetic code is not fundamental. Rather, dark matter level would provide the fundamental realizations of analogs of DNA, RNA, tRNA, and amino-acids as dark proton sequences giving rise to dark nuclei at magnetic flux tubes [L38] (see `http://tinyurl.com/yalny39x`). Also ordinary nuclei correspond in TGD Universe to sequences of protons and neutrons forming string like entities assignable to magnetic flux tubes.

The basic unit representing DNA, RNA and tRNA codon and amino-acid would consist of 3 entangled dark protons. The essential aspect is that by entanglement the dark codons do not decompose to products of letters. This is like words of some languages, which do not allow decomposition to letters. This representation is holistic. As we learn to read and write, we learn the more analytic western view about words as letter sequences. Could the same hold true in evolution so that RNA triplets would have come first as entities pairing with dark RNA codons from from dark proton triplets as a whole? Later DNA codons would have emerged and paired with dark DNA codons. Now the coupling would have have been letter by letter in DNA replication and transcription to mRNA.

It is intriguing that tRNA consists of RNA triplets combined from amino-acids and analogs of mRNA triplets! The translation of mRNA to amino-acids having no 3-letter decomposition alone forces the holistic view but one can ask whether something deeper is involved. This might be the case. I have been wondering whether during RNA era RNA replicated using a prebiotic form of translational machinery, which replicated mRNA rather than translated RNA to protein formed from amino-acids (AAs) with AA serving as a catalyst.

1. During RNA era amino-acids associated with pre-tRNA molecules would served as catalysts for replication of RNA codons. The linguistic mode would have been "holistic" during RNA era in accordance with the findings of the above experiments. RNA codon would have been the basic unit.

2. This would have led to a smaller number of RNAs since RNA and RNA like molecules in tRNA are not in 1-1 correspondence. A more realistic option could have been replication of

subset of RNA molecules appearing in tRNA in this manner.

3. Then a great evolutionary leap leading from RNA era to DNA era would have occurred. AA catalyzed replication of RNA would have transformed to a translation of RNA to proteins and the roles of RNA and AA in tRNA would have changed. [Perhaps the increase of h_{eff} in some relevant structure as quantum criticality was reached led to the revolution]

4. At this step also (subset of) DNA and its transcription to (a subset of) mRNA corresponding to tRNA had to emerge to produce mRNA in transcription. In the recent biology DNA replicates and is transcribed nucleotide by nucleotide rather than using codon as a unit so that helicases and DNA and RNA polymerases catalyzing replication and transcription should have emerged at this step. The ability of DNA to unwind with the help of helicase enzyme helping DNA to unwind is essential for the transcription and translation of DNA. Therefore helicase must have emerged together with the "analytic linguistic mode" as an analog of written language (DNA) decomposing codons to triplets of letters. This would been a crucial step in evolution comparable to the emergence of written language based on letters. Also the counterpart of RNA polymerase and separate RNA nucleotides for transcription should have emerged if not already present.

   An alternative option would involve "tDNA" as the analog of tRNA and the emergence of helicase and polymerases later as the transition from holistic to analytic mode took place.

   The minimal picture would be emergence of a subset of DNA codons corresponding to RNAs associated with pre-tRNA and the emergence of the analogs of helicase and DNA and RNA polymerases as the roles of amino-acid and RNA codon in tRNA were changed.

5. How DNA could have emerged from RNA? The chemical change would have been essentially the replacement of ribose with de-oxiribose to get DNA from RNA and U$\rightarrow$ T. Single O-H in ribose was replaced with H. O forms hydrogen bonds with water and this had to change the hydrogen bonding characteristics of RNA.

   If the change of $h_{eff} = n \times h_0$ was involved, could it have led to stabilization of DNA? Did cell membrane emerge and allow to achieve this? I have proposed [L38] (see `http://tinyurl.com/yalny39x`) that the emergence of cell membrane meant the emergence of new representation of dark genetic code based on dark nuclei with larger value of h_{eff}.

   Remark: One has $h = 6 \times h_0$ in the most plausible scenario [L23, L42] (see `http://tinyurl.com/goruuzm` and `http://tinyurl.com/y9jxyjns`).

The communication between dark and ordinary variants of biomolecules involves resonance mechanism and would also involve genetic code represented as 3-chords, music of light, and it is interesting to see whether this model provides additional insights.

1. The proposal is that 3-chords assignable to nucleotides as music of light with allowed 64 chords defining what I have called bio-harmony is essential for the resonance [L43, L46, L42](see `http://tinyurl.com/ydhxen4g`, `http://tinyurl.com/yd5t82gq`, and `http://tinyurl.com/y9jxyjns`). The 3 frequencies must be identical in the resonance: this is like turning 3 knobs in radio. This 3-fold resonance would correspond to the analytic mode. The second mode could be holistic in the sense that it would involve only the sum only the sum of the 3 frequencies modulo octave equivalence assigning a melody to a sequence of 3-chords.

2. The proposal is that amino-acids having no triplet decomposition are holistic and couple to the sum of 3 frequencies assignable to tRNA and mRNA in this manner. Also the RNAs in tRNA could couple to mRNA in this manner. One could perhaps say that tRNA, mRNA and amino-acids codons sing whereas DNA provides the accompaniment proceeding as 3-chords. The couplings of DNA nucleotides to RNA nucleotides would rely on the frequencies assignable to nucleotides.

3. If the sum of any 3 frequencies associated with mRNA codons is not the same except when the codons code for the same amino-acids, the representation of 3-chords with the sum of the notes is faithful. The frequencies to DNA and RNA nucleotides cannot be however independent of codons since the codons differing only by a permutation of letters would

correspond to the same frequency and therefore code for the same amino-acid. Hence the information about the entire codon would be needed also in transcription and translation and could be provided either by dark DNA strand associated with DNA strand or by the interactions between the nucleotides of the DNA codon.

4. The DNA codon itself would know that it is associated with dark codon and the frequencies assignable to nucleotides could be determined by the dark DNA codon. It would be enough that the frequency of the letter depends on its position in the codon so that there would be 3 frequencies for every letter: 12 frequencies altogether.

   What puts bells ringing is that this the number of notes in 12-note scale for which the model of bio-harmony [L12, L43] (see `http://tinyurl.com/yad4tqwl` and `http://tinyurl.com/ydhxen4g`) based on the fusion of icosahedral (12 vertices and 20 triangular faces) and tetrahedral geometries by gluing icosahedron and tetrahedron along one face, provides a model as Hamiltonian cycle and produces genetic code as a by-product. Different Hamiltonian cycles define different harmonies identified as correlates for molecular moods.

   Does each DNA nucleotide respond to 3 different frequencies coding for its position in the codon and do the 4 nucleotides give rise to the 12 notes of 12-note scale? There are many choices for the triplets but a good guess is that the intervals between the notes of triplet are same and that fourth note added to the triplet would be the first one to realize octave equivalence. This gives uniquely $CEG\sharp$, $C\sharp FA$,$DF\sharp B\flat$, and $DG\sharp B$ as the triplets assignable to the nucleotides. The emergence of 12-note scale in this manner would be a new element in the model of bio-harmony.

   There are 4!=24 options for the correspondence between $\{A,T,C,G\}$ as the first letter and $\{C,C\sharp,D,D\sharp\}$. One can reduce this number by a simple argument.

   (a) Letters and their conjugates form pyrimidine-purine pairs T,A and C,G. The square of conjugation is identity transformation. The replacement of note with note defining at distance of half-octave satisfies this condition (half-octave - tritonus - was a cursed interval in ancient music and the sound of ambulance realizes it). Conjugation could correspond to a transformation of 3-chords defined as

   $$CEG\sharp \leftrightarrow DF\sharp B\flat \ , \quad C\sharp FA \leftrightarrow D\sharp GB \ .$$

   (b) One could have

   $$\begin{aligned} &\{T,C\} \leftrightarrow \{CEG\sharp, C\sharp FA\} \ , \quad && \{A,G\} \leftrightarrow \{DF\sharp B\flat, D\sharp GB\} \ , \\ & && \text{or} \\ &\{T,C\} \leftrightarrow \{DF\sharp B\flat, D\sharp GB\} \ , \quad && \{A,G\} \leftrightarrow \{CEG\sharp, C\sharp FA\} \ . \end{aligned}$$

   .

   (c) One can permute T and C and A and G in these correspondences. This leaves 8 alternative options. Fixing the order of the image of (T,C) to say $(C,C\sharp)$ fixes the order of the image of (A,G) to $(D,D\sharp)$ by the half-octave conjugation. This leaves 4 choices. Given the bio-harmony and having chosen one of these 4 options one could therefore check what given DNA sequence sounds as a sequence of 3-chords [L12].

   That the position the frequency associated with the nucleotide depends on its position in the codon would also reflect the biochemistry of the codon and this kind of dependence would be natural. In particular, different frequencies associated with the first and third codon would reflect the parity breaking defining orientation for DNA.

4.4 Improved reckless speculation about higher level variants of dark genetic code

In an earlier article I represented what I called reckless speculations about higher level variants of genetic code (see [L38] for the updated version of the original article). The speculations turned out

to be not only reckless but to contain besides an unrealistic working hypothesis for p-adic length scale of dark DNA also a numerical error in the estimate of dark nuclear excitation energy scale leading to a wrong track.

The wrong working hypothesis was the assumption that ordinary DNA, RNA, etc correspond to same p-adic length scale as their dark variants. Simple argument shows that the dark scales must result via radial scaling of the typically linear structures such as DNA, RNA, etc and also 2-D structures such as membranes and microtubules giving rise to 2-D lattice like realizations of genetic code generalizing the ordinary 1-D realizations.

Also new improved picture conforms with the vision that dark realizations of genetic code at various p-adic length scales serve as controllers of the ordinary biochemistry, which is kind of shadow dynamics. Replication, certainly one of the most mysterious feats of living matter, would reduce to the replication at the level of dark DNA in various p-adic length scales involved. This would be a huge simplification.

A hierarchy of dark nuclear physics with hierarchy of $n = h_{eff}/h_0 = n$ coming as certain powers of two so that the corresponding length scales correspond to p-adic length scales is an attractive idea. I have speculated with this idea already earlier. A hierarchy of dark nuclear physics with hierarchy of $n = h_{eff}/h = n$ coming as certain powers of two so that the corresponding length scales correspond to p-adic length scales is an attractive idea. I have speculated with this idea already earlier [K27].

4.4.1 Ideas

Consider first the general ideas.

1. The assumption of prime values for k in $L(k)$ would pose extremely tight constraints on the allowed p-adic length scales and values of h_{eff}/h_0. One would have $k \in \{127, 131, 137, 139, 149\}$ and $k \in \{151, 157, 163, 167\}$ and $k \in \{173, ..\}$ at least at the level of dark matter. So predictive an idea deserves to be killed, if not anything else.

   A further motivation for these speculations is that the Gaussian Mersenne primes $M_{G,k=}(1+i)^k - 1$ for $k \in \{151, 157, 163, 167\}$ define p-adic length scale $L(k) \propto 2^{k/2}$ between 10 nm assignable to the neuronal membrane and 2.5 μm assignable to cell nucleus: so many Gaussian Mersenne in so short length scale range is a number theoretical miracle.

2. Cell membrane consisting of two lipid layers (see `http://tinyurl.com/h9a2hsq`) is a binary structure as also DNA double strand. DNAs replicate as would do also RNAs during RNA era. Also cells and therefore also cell membranes replicate so that the analogy might make sense. Since processes like translation and transcription do not occur, cell membrane might serve as 2-D as analog of RNA: the counterpart of RNA era might prevail at these levels. Neuronal membrane might correspond to 2-D analog of DNA.

   So: could various 2-D structures such as nuclear membrane, cell membrane, neuronal membrane, and microtubuli correspond to a new level in the hierarchy of dark codes for which genes and their dark variants would be 2-D rather than 1-D structures? One would have 2-D lattices of codons. Could there be entire hierarchy of them assignable to certain p-adic length scales? As 2-D realizations could be paired with their dark variants so that one could speak of dark variants of various membrane like structures. This applies also to microtubuli.

   The idea that dark variants of DNA, RNA, and AAs are their radially scaled up variants generalizes also. The processes like replication of cell could be induced by a much simpler replication of 2-D dark DNA. This kind of pairing hierarchy could be behind miraculous looking replication of entire organisms. p-Adic fractality and hierarchy of dark DNAs could lurk behind the curtains.

3. The structures of ordinary bio-matter and also their dark variants assumed to control them are characterized by p-adic length scales. How these p-adic length scales could relate? The natural idea inspired by scaling invariance is that the dark variants of 1-D linear structure and 2-D structures formed from ordinary bio-matter are obtained by radial scaling consistent with p-adic length scale hypothesis, and guaranteeing that the distances between building bricks are scaled to the size scales of dark variants of DNA and other basic molecules. This

rule makes sense also for the 2-D structures. For instance, it would scale up the p-adic length scale $L(143)$ characterizing lipid to $L(149)$ assignable to single dark RNA strand or $L(151)$ assignable to dark double DNA strand.

4. One can argue that cell membrane - in particular neuronal membrane - is highly dynamical unlike RNA. In ZEO however dynamical evolutions of space-time surfaces as preferred extremals - correlates for behaviors - replace 3-D static patterns as basic entities so that the emergence of cell membrane might mean dark genetic code for dynamical patterns analogous to deterministic computer programs defining predetermined dynamical patterns. In central nervous system nerve pulse patterns coded by dark RNA could provide similar coding of behavioral patterns.

5. I have claimed in earlier publications that the lipid double layer defining cell membrane has thickness $L_e(151) = 10$ nm: actually the thickness is $L_e(149) = 5$ nm for ordinary cells and 8-10 nm - roughly $L_e(151)$ - only for neuronal membranes. Therefore the emergence of neuronal membranes could be seen as an evolutionary step in p-adic and thus number theoretic sense. Needless to say, this little difference might be absolutely crucial for undestanding why neurons are at higher evolutionary level than ordinary cells. It would be nice if this difference could correspond to an increase of $h_{eff}/h_0 = n$ and p-adic length scale of ordinary and dark membrane like structure by a factor 2.

   There is double cell membrane associated with mitochondria. The thickness of the two double membranes is about 7 nm so that they might correspond to $k = 149$. The double membrane would have roughly the thickness 22 nm. If this structure is a functionally coherent structure it would corresponds to $L_e(153)$ and could be controlled by its dark counterpart.

6. I have proposed that the flux tubes connecting the dark DNA sequences above lipid layer to those associated with DNA could make possible to realize topological quantum computation [K17, K53] in terms of braiding induced by the 2-D liquid flow induced by nerve pulse patterns at nuclear membrane. Flux tubes might be associated with cytoskeleton and define an analog of central nervous system at the level of cell. A rough estimate for the numbers of codons for human DNA of length about 1 m and the number of codons allowed by the surface of the nuclear membrane are of order 10^9 so that the proposal might make sense.

   This proposal generalizes and has many alternative forms. For instance, microtubules inside axons could be connected by flux tubes to the surface of axons.

   One could also consider braidings between ordinary and dark levels, say braiding of flux tubes connecting lipid layers of neuronal membrane to 2-D analog of dark DNA. This braiding would code quantum computer programs and be part of coding of nerve pulse patterns inducing 2-D flow of lipids to memories represented as braidings. Quite generally, the braidings could be very naturally between ordinary and dark variants of structures considered.

4.4.2 Could cell membrane and neuronal membrane realize genetic codons as 2-D structures?

In the sequel I discuss in more quantitative level the idea that cell membrane and neuronal membrane realize analogs of genes as 2-D structures.

The p-adic length scales associated with the dark variants of 2-D structures?

Consider next the p-adic length scales associated with the structures considered.

1. The thickness of ordinary cell membrane corresponds roughly to $L_e(149) = 5$ nm whereas the coiling associated with the cell membrane corresponds to $L_e(151)$. Also neurons correspond to $L_e(151)$. Could $k = 149$ *resp.* $k = 151$ define levels of ordinary cell *resp.* neuron in the hierarchy of dark nuclear physics?

2. Cell membrane consists of lipid bilayer. The lipid layer has three parts (see `http://tinyurl.com/h9a2hsq`).

- The totally hydrated layer nearest to water is hydrophilic head group, which in the case of phospholipids contains negatively charged phosphate. This phosphate layer has thickness $.7 - 1.0$ nm.
- Below it is a partially hydrated layer of thickness .3 nm, which corresponds to $L(141)$: this of course puts bells ringing!
- Hydrophobic lipid tail layer below it is dehydrated. The thickness of single lipid layer is 1.25-1.75 nm and would correspond to the p-adic length scale $L_e(145) = 1.2$ nm. $k = 145$ is not prime.

3. The phosphate layer analogous to phosphate-ribose backbone and the thickness $L(141)$ of partially hydrated layer suggests that it corresponds to EZ created in Pollack effect so that there would be parallel dark RNA sequence along axon (possibly helical as for microtubules). In the case of cell membrane would have lattice like system formed from dark protons, and maybe even dark neutrons (as an analog for the neutron halo in some nuclei).

4. If the recent biology is the analog of RNA era for $k = 149$ codes, their manifestations could be seen as analogs of RNAs and the number of different lipids associated with the cell membrane could give some idea about their number. Cell membrane could perhaps be seen as a 2-D analog of RNA polymer. Cell division implying membrane replication would be induced by dark RNA replication. Even the analogs of tRNA and AAs but not proteins might be present if one takes the analogy very seriously. Could one identify pairs of lipids and some molecules analogous to proteins appearing in cell division?

What kind of general conditions can one pose on the dark variants of DNA, RNA, and AAs?

1. Dark variant of 2-D variants of DNA, RNA, or AAs realizing the hierarchy of dark codes should control their analogues or possibly some other molecules coded by them. The coupling would be by resonance. This suggest the hierarchy of codes uses as building bricks simpler structures by starting from 1-D structures and building from them more complex structures. Hence the natural hypothesis is that the 2-D variants of proteins consisting of a 2-D lattice like structure formed from proteins is in question.

2. The geometric aspect of membrane dynamics would be determined by basic dynamics of TGD determined by action, which is a generalization of charged point-like particle coupling to Maxwell field by replacing the particle orbit with 4-D surfaces. This allows as special case minimal surfaces such as deformations of cosmic strings giving magnetic flux tubes. Cell membranes should correspond to extremals for which coupling to Kähler force is non-trivial as it indeed is by membrane potential. This because static closed surfaces, in particular spherical layers, are not possible as minimal surfaces. Remarkably, these extremals are not analogs of external particles (geodesic lines) but correspond to interaction regions. This conforms with the fact that cell membrane is a self-organization pattern requiring a continual feed of metabolic energy.

   The 2-D dark variants of DNA, RNA, and AAs would be involved mostly with the control the electro-chemistry of membrane like structures. Of course their geometrodynamics would induce also morphogenesis of ordinary bio-matter.

   Also enzymes and ribozymes would have dark variants controlling their behavior. Folded protein represents an interesting example about possibly 3-dimensional graph like structure in which the protein forms an analog of Hamilton's cycle going through all points of the graph defined as a lattice with nearest neighbors connected by edges without self-intersections. This hypothesis is rather powerful since for Hamiltonian cycle do not necessarily exist for an arbitrary graph.

3. In the case of cell membrane membrane proteins are the natural candidate for the building bricks. They indeed have an active role and serve as both channels and pumps and in the case of the neural membrane this role is especially important. Membrane proteins are identified in TGD framework as generalized Josephson junctions. In the case of cell membranes mebrane proteins having length of about 5 nm (5 AAs) or 10 nm (10 AAs) going through the membrane

are an excellent candidate for the basic building brick. One could see the basic structure either as 2-D structure built from membrane proteins or 3-D structure build from AAs. Membrane proteins would form kind of generalized protein as a 2-D lattice of proteins and accompanied by their dark variants or of 2-D dark variants of RNA or DNA coding for them and identifiable as radial scalings of these proteins to $k = 149$ or $k = 151$.

The model for topological quantum computation [K17] suggesting that DNA codons of are connected to lipids of cell membrane could be modified so that that dark DNA, RNA, or AAs associated with membrane proteins are connected to them by flux tubes which can get braided. This would allow the quantum control of the 2-D protein like structure and make it effectively single quantum coherent Josephson junction as suggested in the quantum model for nerve pulse [K44].

The original proposal was that that there might exist an analog of genetic code for lipids. The number of different lipids is however too high to allow any simple correspondence. Lipids have also rather passive role in the dynamics of the cell membrane: their serve as signal pathways, provide metabolic energy, and serve as signal pathways (see `http://tinyurl.com/z7d7osm`). The proposal however deserves to be explained.

1. Both sides of the lipid bilayer of cell membrane could pair with 2-D lattice of dark RNA whose size scale would be obtained by radial scaling giving rise to what might be called dark cell membrane. In the case of neuronal membrane the dark lattice would consist of pairs of dark DNA codon and its conjugate. In the case of axon one could have the analog of dark DNA strand extended to a cylinder containing bundles of these strands at its surface. Lipid layers would be 2-D analogs of 1-D DNA strands in this case.

2. Lipids would be analogs of ordinary RNA codons and dark RNA codons would code for them: this would predict 64 different lipids in cell membrane. Single dark RNA would correspond to the size scale of single lipid given by $L(143) = 2L(141) = .625$ nm. The dark nuclear physics would correspond to $k = 149$. The number N of parallel dark RNA strands would be roughly the circumference of the axonal lipid layer divided by the size of single lipid about $L(143) = .625$ nm given by $N \sim 2\pi \times L_e(167)/L_e(143) = \pi \times 2^{24} \sim 5 \times 10^6$.

Thermodynamical constraints

Could this totally irresponsible speculation about p-adic hierarchy of dark nuclear physics and genetic codes survive thermodynamical constraints?

1. The condition that metabolic energy quantum is not below thermal energy at physiological temperatures poses constrains on the model. I have considered several identifications of the the metabolic energy quantum. These identification need not be mutually exlusive.

   - One interpretation is as 1-D zero point kinetic energy of proton at tubular space-time sheet of atomic size with transversal length scale $L(137)$. This energy is invariant under scalings induce by increase of h_{eff} since h_{eff}^2/L^2 is not changed.
   - Second identification of metabolic quanta would be as energies assignable to hydrogen bond and its dark variants.
   - Third identification of the metabolic energy quantum would be as scaled variant of $E_b(k) = 2^{(k-107)/2}E_b$ of typical dark nuclear binding energy $E_b =\sim 1$ MeV. The value would be about .5 eV for $k = 149$ and .25 eV for $k = 151$.

2. Note that the action potential assignable to $k = 151$ neuronal membrane is around .05 eV (the membrane potential for some photoreceptors is .03 eV). In TGD Universe the cell membrane can be seen as Josephson junction decomposing in an improved resolution to membrane proteins acting as Josephson junctions [K41, K42]. Josephson energy of Cooper pair is twice this - that is $E_J = 0.1$ eV slightly above the maximum $E_{max} = 3T = .09$ eV of the thermal distribution at physiological temperature.

3. As far Josephson radiation are considered, for $k = 151$ membrane would be a quantum critical system. Quantum criticality could give rise to instability making possible the generation of nerve pulses. During nerve pulse the dark protons at the dark space-time sheet would return to the neuronal membrane and destroy the ionic equilibrium. Also the temperature criticality of consciousness manifesting itself as the generation of hallucinations during fever could be understood. For $k = 151$ the situation would be overcritical and will be discussed separately.

The Josephson energy of Cooper pair is scaled down to $E_J = .1$ eV near to $E_{max} = .09$ eV. This is slightly above the thermal energy but one could still argue that Josephson radiation cannot carry information. Or could Nature have found the means to overcome this potential problem? The notion of generalized Josephson junction central in TGD inspired theory of EEG as communications from brain to MB [K44, K15] could save the situation.

1. For the generalized Josephson junction the energy of quantum of Josephson radiation is $E = E_J + \Delta E_c$, where ΔE_c is the difference of cyclotron energies at the two sides of the membrane. E_c is proportional to $h_{eff} = n \times h$ and large enough value of n guarantees that E_c is above $E_{max} \simeq 3T$ irrespective of the value of the membrane potential. The variations of the membrane potential modulate Josephson frequency, and are proposed to provide a coding of sensory data defined by nerve pulse patterns communicated to MB.

2. $h_{eff} = h_{gr} = GMm/v_0$ hypothesis [K76, K75] guarantees the spectrum of cyclotron energies is universal and does not depend on the mass m of the charged particle being in the range of visible and UV energies of photons (this allows to deduce information about the values of mass M and velocity parameter $v_0 < c$): bio-photons would be produced in energy conserving phase transitions transforming dark photons to ordinary ones [K65, K66].

3. If MB itself (a structure which has size scale of Earth at EEG frequencies around 10 Hz) has low enough temperature, this would allow to overcome the limitations caused by the thermal masking of the ordinary Josephson radiation so that the frequency modulations by nerve pulse patterns could code for the sensory data. $h_{eff} = h_{gr} = GMm/v_0$ hypothesis indeed allows very large values of h_{eff} for which ordinary cyclotron energies proportional to h_{eff} would be ridiculously small for the ordinary value of h.

What about the situation for massive particles like proton? Now Maxwell-Boltzmann (Gaussian) distribution is a good approximation and for effectively D-dimensional system the value of distribution is reduced by $1/e$ at thermal energy $E_{cr} = DT/2$. One could argue that above this energy thermal masking can be avoided. For $D = 1$ at magnetic flux tubes this would give $E_{cr} = T/2 = E_{max}/6$. At $T_{phys} = .03$ eV one would have $E_{cr} = 0.15$ eV. Metabolic energy quantum would be above E_{cr} for $k = 151$. Even $k = 153$ possibly assignable to mitochondrial double membrane can be considered but represents an upper bound at physiological temperatures.

Remark: In TGD view about information processing in brain [L28] active linear neuron groups relate to verbal cognition and 2-D neuronal groups relate to the geometric cognition associated with the decomposition of perceptive field to objects. At cellular level DNA and cell membrane could perhaps be seen as counterparts for these structures. In TGD framework neuronal membrane is proposed to be a constructor of sensory representations communicated to the magnetic body (MB) using generalized Josephson radiation whereas motor control by MB has been assumed to take place via DNA [K23].

4.4.3 DNA packing problem and p-adic length scales

DNA manages to pack huge amount of DNA to single cell nucleus. For instance, human DNA as length of about 1 meter. This is achieved by a hierarchical coiling structure involving 3 levels with highest level identifiable as chromatides and the lowest level defined by nucleosomes (see `http://tinyurl.com/yat5cm4y`) wound around histon isomers linked together by straight portions of DNA. One can find a detailed representation of the 4-levelled packing of DNA (see `http://tinyurl.com/ybxv6w4v`).

There are 4 levels involved. Could they relate to the Gaussian miracle primes $k = 151, 157, 163, 167$? The general proposal is that the products of powers of small primes define the scale hierarchy. There

is evidence that at least the powers of 2 and 3 define p-adic length scales, which would correspond also to dark scales. The simple guess is that the dark scales are identical to the ordinary p-adic scales.

- The diameter of the nucleosome is 11 nm $= 1.1L(151)$, which suggests $k = 151$. Chromatosome consists of histone H_1 plus nucleosome.
- Nucleosomes coil to form a fiber of diameter $d = 30$ nm. This scale is $3L(151)$.
- At the next level loops of average length 300 nm $= 30L(151) \sim 32L(151)$. This level is only intermediate level in packing.
- These loops compress and fold to 250 nm $=25L(151) \simeq 3 \times L(157)$, $L(157) = 8L(151)$ wide fiber. Thus third harmonic of also the miracle length scale $L(157)$ would be involved.
- This fiber compresses a tight coil of radius 700 nm $= 70L(151) \simeq 64L(151) = L(163) = 640$ nm giving rise to the chromatid fiber of chromosome. $k = 163$ is the third miracle length scale.
- Chromosomes have width 1400 nm which corresponds to the scale $L(165)$.

The 3 levels $k = 131, 157, 163$ seem to be realized although not in the simplest manner. Nuclear membrane would correspond to $L(k = 167) = 2.5$ μm. For $n = h_{eff}/h_0$ these levels would correspond to the values n of form $n = 2^r 3^s$.

Consider next nucleosome.

1. DNA wraps of around histone octamers forming a cubical structure consisting of 8 smaller cubes (octamers). There are 2×4 histones forming two identical layers. The 4 histones H_{2A}, H_{2B}, H_3, H_4 of given layer are not identical. There is also histone H_1 attached to the entire structure. The incoming DNA double strand enters to the upper end of H_1 and leaves from its lower end. H_1 is related to the secondary coiling. The wrapping gives rise nucleosomes as helices with two turns and containing about 146 base pairs making 48 codons plus 2 base pairs.
2. According to the standard model of nucleosome double DNA strand wraps around the analog of a spool formed from an octamer consisting of two identical units above each other consisting of 4 different histones. The incoming DNA strand enters the upper 4-histone unit and winds once around it and then does the same for the lower unit before leaving the nucleosome.

One can construct a rough TGD inspired model for this structure (not completely realistic) to get a concrete idea about what is involved.

1. The size scale of the cube like structure is $L(151) = 10$ nm so that single histone corresponds to a cube with side roughly about $L(149) = 5$ nm. One can estimate the total length L of the wire from the equation $z = xR\phi/\pi$, $R \sim L(149)$, $\phi \in [0, 4\pi]$, as $L = \sqrt{1 + \pi^{-2}} 4\pi R$. For $R \sim L(149)$ and $h = L(151)$ this gives $L \sim 66$ nm, There are roughly 146 DNA base pairs and 48 whole codons ($144 = 3 \times 48$ base pairs) and each codon has length about 1 nm. This gives total length of 48 nm. The reduction of radius R by factor $r = 48/66 = 3/4$ to $R = 3L(149)/4$ would give a correct value of L

   According to the representation for the hierarchy of packings (see `http://tinyurl.com/ybxv6w4v`), the diameter of the structure is $d = 1.1L(151)$ rather than small and the height of the structure is smaller in the illustration. This width is however not consistent with the helix structure for any value of the height.
2. If the double DNA strand is accompanied by a dark double strand of radius $L(149)$, the situation is like having a band of width $L(151)$ going around the spool. The dark double strand covers an area, which is 4/3 times the spool area. The horizontal thickness of the entire dark structure is about $d_D = (7/4)L(151)$. If the radius of DNA double strand is $r = L(151)$ the area covered by the double strand is roughly twice the area of the spool. This suggests that one should identify the p-adic length scale of DNA double strand as its diameter about $L(151)$ rather than its radius.

Remarks:

1. While trying to understand nucleosomes in TGD framework, I encountered an interesting side result related to Hamiltonian face paths and Hamiltonian cycles on octahedron, which to my best understanding must correspond to Hamiltonian paths and cycles on cube. The octahedral face paths can be identified as closed paths connecting the middle points of the centers of a cube. The 8 histones define a decomposition of the entire cube to 8 sub-cubes. The idea was that that Hamiltonian face cycles in these cubes could give up to tight packing of 6 codons. The number of the Hamiltonian paths for cube is 64 (see `http://tinyurl.com/ybqw6zpt`) and the number of cycles is 6! Single genetic codon would dictate the choice of the Hamiltonian path on cue! Although the idea did not work (the length of, it led to ask whether the Hamiltonian cycles on octahedron or their duals at cube might have some biological relevance.

2. A further interesting finding is that the sequence of 8 quints defines a piece of 12-note scale proceeding by quints as steps between nearest neighbor vertices (using octave equivalence) in the icosahedral model of harmony [L12, L50] based on 12-note scale could be interpreted as cubic Hamiltonian cycle giving rise to the notes $F, C, G, D, A, E, H, F\sharp$. This gives the notes of C major scale with 7 notes plus tritonus $F\sharp$ defining half-octave as 8:th note. One could also identify the cycles as consisting of the notes of 8-note scale along cycle in the usual order $C, D, E, F, G, A, H, F\sharp$ based on standard notion of nearness for which neighboring vertices correspond to neighboring notes of the scale. Allowed 3-chords would correspond to triplets containing no neighboring notes. The Hamiltonian cycle for cube is unique apart from isometries as also for tetrahedron and and dodecahedron.

4.4.4 Microtubules as quantum critical systems

Also microtubules (see `http://tinyurl.com/y8km9vve`) are 2-D structures having a strong resemblance with the lipid layers of cell membrane. Could a higher level representation of genetic code similar to the one proposed for cell membranes make sense for them. Also now one can imagine that the microtubular surface is accompanied by its dark variant realizing 2-D dark genes, dark RNA, or dark proteins with scaled up size. The p-adic prime should correspond to $k > 151$ so that higher level realization of genetic code would be in question. In the case of axons a possible identification for the dark scale would be as the radius of the axonal membrane.

1. Microtubules are hollow cylinders with outer *resp.* inner diameter equal to 24 *resp.* 12 nm (the scales differ by factor 2) so that their thickness is 12 nm is same as the inner radius and would correspond to $L(151) = 10$ nm. They decompose to 13 parallel helical filaments consisting of 13 tubulin proteins having size scale of order $L_e(151)$.

2. Tubulins are dimers of α and β tubulin and the pairs are oriented along the helical filament. One can estimate the size of α and β tubulin by diving the circumference of 24 nm of the microtubule with the number of filaments, which is 13. This gives for the size scale of tubulin the estimate $R_{tub} \sim 12$ nm not far from $L(151)$. This supports the view that p-adic length scale $L(151)$.

   The size scale of the transversal volume associated with lipid is roughly .62 nm that is $L(143) = 2L(141)$ so that they could correspond to $k \in \{141, 143\}$, presumably $k = 141$. Therefore one could see microtubules as scaled up variants of cell membrane with scaling factor $2^{(151-141)/2} = 2^5 = 32$. Similar scaling would take place for the value of $n = h_{eff}/h$ giving $n = 2^{23}$ so that microtubules would represent a higher level of evolution identified as increase of n. Microtubules have indeed emerged after cell membrane.

3. It has been proposed that the α and β conformations of tubulin give rise to bit or even qubit. If this were the case, single helical filament rotating one full turn would have 2^{13} states and carry 13 bits of information. 13 independent filaments would have $2^{26} \simeq 64 \times 10^6$ states and carry 26 bits of information. One could also think of codon as sequence of 13 filaments with the states of filaments representing 2^{13} letters of the code.

4. Microtubular surface has rather high charge density and is polarized: the almost stationary end has negative local charge density roughly equal to that of DNA whereas the growing end has lower surface charge density. One manner to control the charge of the tubulin dimer is in terms of the charge states of GDP and GTP by ionization of the phosphates. Maximal negative charge for tubulin dimer would be 5 units.

   Microtubules are highly dynamical objects with inherent instability and have varying length: one might say that microtubules are quantum critical objects. Quantum criticality and thus instability might relate to the fact that the metabolic energy quantum is very near to thermal energy at room temperature.

   The dynamics for the length of microtubule could be induced from the dynamics of EZ involving the flow of protons between microtubule and its magnetic body defined by dark DNA. The gradient in charge density would make possible positive net charge density at the growing end of the microtubule.

   In ZEO it looks reasonable to argue that the dynamical patters are coded by a generalization of genetic code just as computer programs code for deterministic dynamical patterns.

5. What could the dark code behind the dynamics be? The α- and β tubulins of tubulin dimer involve GTP (see `http://tinyurl.com/ybtjluaf`) *resp.* GDP (see `http://tinyurl.com/y8uok7kq`). In the case of DNA one has XMP, $X = A, T, C, G$. The analogs of dark RNA sequences would contain mere G and the information coded by the tubulin would be determined by the conformation of the tubulin dimer giving 1-bit code. This looks somewhat disappointing.

   If the charge states of the phosphates of GDP and GTP can vary and all charge combinations for phosphates are possible, one has 2^3 charge states for GTP and 2^2 charge states for GDP. Together with the bit associated with the tubulin conformation this would give 2^6 states and realize 6 bits of the ordinary genetic code! One would have 2-D realization of the genetic code analogous to that proposed for the lipid layer with the state of tubulin analogous to RNA codon.

   This coding together with thermal criticality would make microtubule a dynamical object since the deviation of the tubulin charge from -1 units would spoil charge local charge neutrality of tubulin-dark RNA pair.

I have proposed that flux tubes connecting tubulins to the lipids of the axonal lipid layer could give rise to topological quantum computation [K17, K17]. The size scale of lipid is about $L_e(141)$ and that of tubulin about $L_e(151) = 32L_e(141)$, and the the radius of axonal membrane is by two orders of magnitude larger than microtubular surface. Hence this proposal does not look realistic unless one assumes that sub-structures of cell membrane with size scale of order $L_e(167)/L_e(151) = 2^8$ larger than tubulin size represented as space-time sheets with cell nucleus size $L(167)$ have flux tube connections to tubulins.

This kind of map would give rise to a kind of abstraction about what happens at the level of axonal membrane integrating out un-necessary details. This abstraction is natural since microtubules would indeed correspond to a higher level of cognitive hierarchy. Roughly $N = 2^{16}$ lipids would contribute to the information received by single tubulin. Could nerve pulse patterns can induce braiding of the flux tubes in this scale?

4.4.5 PART III: NUMBER THEORETICAL MODELS FOR GENETIC CODE

Could Genetic Code Be Understood Number Theoretically?

The number of DNA triplets is 64. This inspires the idea that DNA sequence could be interpreted as an expansion of an integer using 64 as the base. Hence given DNA triplet would represent some integer in {0,1....,63} (sequences of I Ching symbols give a beautiful realization of these sequences).

The observation which puts bells ringing is that the number of primes smaller than 64 is 18. Together with 0, and 1 this makes 20: the number of amino-acids!

1. Questions

The finding just described stimulates a whole series of questions.

Do amino-acids correspond to integers in the set $S = \{primes < 64\} \cup \{0, 1\}$. Does amino-acid sequence have an interpretation as a representation as a sequence of integers consisting of 0, 1 and products of primes $p = 2, ..., 61$? Does the amino-acid representing 0 have an interpretation as kind of period separating from each other structural units analogous to genes representing integers in the sequence so that we would quite literally consists of sequences of integers? Do 0 and 1 have some special biological properties, say the property of being biologically inert both at the level of DNA and amino-acids?

Does genetic code mediate a map from integers 0,...,63 to set S such that 0 and 1 are mapped to 0 and 1? If so then three integers $2 \leq n \leq 63$ must correspond to stopping sign codons rather than primes. What stopping sign codon property means at the level of integers? How the map from integers 2,...,61 to the primes $p = 2, ..., 61$ is determined?

2. The chain of arguments leading to a number theoretical model for the genetic code

The following chain of arguments induced to large part by concrete numerical experimentation leads to a model providing a partial answer to many of these questions.

1. The partitions of any positive integer n can be interpreted in terms of number theoretical many boson states. The partitions for which a given integer appears at most once have interpretation in terms of fermion states. These states could be identified as bosonic and fermionic states of Super Virasoro representation with given conformal weight n.

2. The generalization of Shannon entropy by replacing logarithms of probabilities with the logarithms of p-adic norms of probabilities allows to have systems with negative entropy and thus positive negentropy. The natural requirement is that n corresponds to such prime $p \leq 61$ that the negentropy assigned to n is maximal in some number theoretic thermodynamics. The resulting correspondence $n \to p(n)$ naturally determined the genetic code.

3. One can assign to the bosonic and fermionic partitions a number theoretic thermodynamics defined by a Hamiltonian. Purely bosonic and fermionic thermodynamics are defined by corresponding partition functions Z_B and Z_F whereas supersymmetric option is defined by the product $Z_B \times Z_F$. Supersymmetric option turns out to be the most realistic one.

4. The simplest option is that Hamiltonian depends only on the number r of the integers in the partition. The dynamics would be in a well defined sense local and would not depend on the sizes of summands at all. The thermodynamical states would be degenerate with degeneracy factors given by total numbers $d_I(n, r)$ of partitions of type $I = B, F$. The invariants known as rank and crank define alternative candidates for the basic building blocks of Hamiltonian.

5. Ordinary exponential thermodynamics based on, say $e^{-H/T} = q_0^{r-1}$, q_0 a rational number, produces typically unrealistic genetic codes for which most integers are mapped to small primes $p \leq 11$ and many primes are not coded at all. The idea that realistic code could result at some critical temperature fails also.

6. Quantum criticality and fractality of TGD Universe inspire the idea that the criticality is an inherent property of Hamiltonian rather than only thermodynamical state. Hence Hamiltonian can depend only weakly on the character of the partition so that all partitions contribute with almost equal weights to the partition function. Fractality is achieved if Boltzmann factors are given by $e^{-H/T} = (r + r_0)^{n_0}$ so that $H(r) = log(r + r_0)$ serves as Hamiltonian and n_0 corresponds to the inverse temperature. The super-symmetric variant of this Hamiltonian yields the most realistic candidates for the genetic code and there are good hopes that a number theoretically small perturbation not changing the divisors $p \leq 61$ of partition function but affecting the probabilities could give correct degeneracies.

   Numerical experimentation suggests however that this might not be the case and that simple analytic form of Hamiltonian is too much to hope for. A simple argument however shows that $e^{-H/T} = f(r)$ could be in quantum critical case be deduced from the genetic code by fixing the 62 values of $f(r)$ so that the desired 62 correspondences $n \to p(n)$ result. The idea about almost universality of the genetic code would be replaced with the idea that quantum

criticality allows to engineer a genetic code maximizing the total negentropy associated with DNA triplet-amino-acid pair.

7. A natural guess is that the map of codons to integers is given as a small deformation of the map induced by the map of DNA codons to integers induced by the identification of nucleotides with 4-digits 0,1,2, 3 (this identification depends on whether first, second, or third nucleotide is in question). This map predicts approximate $p(n) = p(n+1)$ symmetry having also a number theoretical justification. One can deduce codon-integer and amino-acid-prime correspondences and at (at least) two Boltzmann weight distributions $f(n)$ consistent with the genetic code and Negentropy Maximization Principle (NMP) constrained by the degeneracies of the genetic code.

Unification of Four Approaches to the Genetic Code

A proposal unifying four approaches to genetic code is discussed.

The first approach is introduced by myself and is geometric: genetic code is interpreted as an imbedding of the aminoacid space to DNA space possessing a fiber bundle like structure with DNAs coding for a given aminoacid forming a discrete fiber with a varying number of points. Also Khrennikov has proposed an analogous approach based on the identification of DNAs coding for a given aminoacid as an orbit a discrete flow defined by iteration of a map of DNA space to itself.

Much later (2014) I have introduced a variant of this scenario in which the fiber space structure is by assigning aminoacids to the 20 vertices of icosahedron. This model allows to understand the degeneracies of genetic code group theoretically.

Second approach starts from the 5-adic approach of Dragovich and Dragovich. Codons are labelled by 5-adic integers n which have no non-vanishing 5-digits so that the n is in the range $[31, 124]$. The number of primes in the range $[31, 124]$ is 20. This suggests the labelling of aminoacids by these primes. This inspires an additional condition on the geometric code: if possible, one of the integers n projected to p equals to $p(n)$. This condition fails only for the primes 53,79,101,103 for which some of 5-digits vanishing in 5-ary expansion.

The third approach relies on the generalization of the basic idea of the so called divisor code proposed by Khrennikov and Nilsson. The requirement is that the number of factors for integer n labelling one of DNAs, call it n_d coding for a given aminoacid is the total number of codons coding for the aminoacid, its degeneracy. Therefore a given aminoacid labelled by prime p with no non-vanishing 5-digits is coded by DNAs labelled by p itself and by n_d. A group theoretic and physical interpretation for the origin of the divisor code is proposed.

The fourth approach is a modification of the earlier 4-adic number theoretic thermodynamics approach of Pitkänen.

1. 5-adic thermodynamics involving a maximization of number theoretic negentropy $N_p(n) = -S_p(n) > 0$(!) as a function of p-adic prime p labelling aminoacids assigns a unique prime to the codon. If no prime in the range divides S_p, the codon is identified as a stopping codon.

2. The number theoretic thermodynamics is assigned with the partitions P of the integer $n_{2)}$ determined by the first two letters of the codon (16 integers belonging to the range $[6, 24]$). The integer valued number theoretic Hamiltonian $h(P) \in Z_{25}$ appearing in the Boltzmann weight $5^{h(P)/T_5}$ is assumed to depend on the number r of summands for the partition only. $h(r)$ is assumed to be tailored by evolution so that it reproduces the code.

3. The effect of the third nucleotide is described in terms of 5-adic temperature $T_5 = 1/n$, $n \in [0, 24]$: the variation of T_5 explains the existence of variants of genetic code and its temporal variation the observed context sensitivity of the codon-aminoacid correspondence for some variants of the code.

A numerical calculation scanning over $N \sim 10^{30}$ candidates for $h(r)$ allows only 11 Hamiltonians and with single additional symmetry inspired condition there are 2 solutions which differ only for 5 largest values of r. Due to the limited computational resources available only 24 percent of the available candidates have been scanned and the naive expectation is that the total number of Hamiltonians is about about 45 unless one poses additional conditions.

The problem of the number theoretic models is that they do not predict but only reproduce. This is in sharp contrst to the model based on dark proton sequences, which leads to a radically new vision about the evolution of prebiotic life and to the vision about how immune system and genetic code evolved and what is the meaning of the genetic code.

Part I

TGD INSPIRED MODELS FOR THE EVOLUTION

Chapter 5

Evolution in Many-Sheeted Space-Time

5.1 Introduction

This chapter was originally about prebiotic evolution but gradually extended so that it became natural to drop the attribute "prebiotic" away. Of course, a collection of ideas rather than detailed history of life is in question.

If was already early that the notion of many-sheeted space-time could allow to understand many puzzles related to the pre-biotic evolution [I64, I122]. There are many constraints on the models for pre-biotic evolution. The models have also many difficulties [I67, I108].

TGD replaces materialistic view about universe with a continual re-creation in which classical universe in 4-dimensional sense is replaced by a new one in each quantum jump. p-Adic length scale hypothesis allows to formulate the notion of evolution more precisely as a generation of increasingly larger space-time sheets characterized by preferred p-adic primes. A second aspect is the emergence of new levels in dark matter hierarchy characterized by effective Planck constant $h_{eff} = n \times h$ making possible macroscopic quantum coherence and inducing great leaps in evolution. Also a hierarchy of dark weak bosons and gluons becomes an essential part of the physics of living matter. The notion of field/magnetic body carrying dark matter is a further key element in the model and has become increasingly important during years, and the vision about DNA-cell membrane system as a topological quantum computer utilizing braids defined by magnetic flux tubes connecting nucleotides to lipids meant a breakthrough in the understanding of the real function of DNA in information processing.

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5.1.1 Questions And Answers About Evolution

A good manner to introduce the essentials of the TGD inspired model for the prebiotic evolution is by a sequence of questions and answers relating to evolution. The progress occurred during last

years in the understanding of water as primitive lifeform has modified considerably the original answers and I have comments about this.

Q: Is life as we know it result of an accident?.

A: Quantum TGD predicts a genuine cosmic evolution occurring by quantum jumps for which dynamics is characterized by Negentropy Maximization Principle (NMP) [K32]. The generalization of the notion of space-time implies dark matter hierarchy with levels characterized by arbitrarily large values of effective Planck constant so that macroscopic quantum coherence is possible even in astrophysical length scales. Even astrophysical systems are analogous to atomic systems which implies a strong standardization of planetary system so that Earth like planets are abundant. There are also other good reasons for why the evolution of life would not have been accident in TGD Universe and life should appear everywhere in TGD Universe.

Even stronger conclusions follow from NMP in zero energy ontology (ZEO). The view about quantum jump in ZEO implies that the formation of what might be regarded as generalizations of sensory and other representations defining reflective level of consciousness appearing universally. These representations would be kind of Akashic records. The braiding of the magnetic flux tubes would serve as a geometric correlate of the negentropic entanglement, which together with Negentropy Maximization Principle (NMP) guarantees approximate invariance of representations under quantum jumps. Also the sensory-motor dichotomy characterizing living matter is a universal property of quantum jump sequence in ZEO [K67]. This would strongly suggest that consciousness and even life has not emerged but has been present already at elementary particle level. These ideas are however newcomers and do not yet appear in the formulations represented in the article series.

Q: What were the most primitive living systems?

A: The notion of magnetic body brings to biology several completely new elements. Magnetic flux quanta containing dark charged matter and quantum controlling ordinary matter in plasma phase is perhaps the simplest system which can develop characteristics of a living system. The braiding of magnetic flux tubes makes possible topological quantum computation and a fundamental representation of memories and its presence could be even taken as a definition for what it is to be living. Topological quantum computation (TQC) programs correspond to asymptotic self organization patterns for liquid flows inducing braidings and are non-trivial in presence of external energy feed.

The recent findings about water inspire the vision that primordial life corresponds to the exclusion zones discovered by Pollack and the model of dark protons suggests that vertebrate genetic code could be realized at the this level so that dark proton sequences could define primordial genes.

Q: How metabolic machinery emerged?

A: Many-sheeted space-time concept predicts a hierarchy of universal metabolic energy quanta as differences of zero point kinetic energies for space-time sheets characterized by different p-adic length scales. These energies define an attractive candidate for univeral metabolic quanta. What remains is to understand how chemical energy storage and utilization mechanisms developed. Also the deeper purpose of the metabolic energy must be understood and metabolic energy carrier as a storage of negentopic entanglement or as something making possible the generation of negentropic entanglement (braiding) is an attractive interpretation.

Q: What is behind biocatalytic machinery?

A: The magnetic flux tubes connecting bio-molecules imply long range correlations between molecules and also as correlates of attention meaning fusion of two systems to single quantum coherent unit. The reduction of Planck constant for magnetic flux tubes implying their shortening provides a mechanism making possible for bio-molecules to "find" each other in a very selective manner, and explains also why molecules end up to precisely defined conformations necessary for a selective bio-catalysis. Reconnections of flux tubes would change the topology of system formed from negentropically entangled flux quanta.

Q: How symbolic dynamics emerged?

A: There is a temptation to assign the origin of the symbolic dynamics with the magnetic body. The notion of fractional atom [K16] suggested by the fractionization of electron and nucleon quantum numbers for dark matter hierarchy brings in a candidate for a symbolic dynamics assigning to molecules "names" which need not correlate very strongly with the chemical properties of the molecule but would dictate to a high degree its biochemical behavior. Molecular "sex" emerges in

the sense that molecules labeled with "names" and "co-names" tend to pair. The model of DNA as TQC assumes a 4-coloring of braid strands realized by an assignment of DNA nucleotides to quarks and anti-quarks. Also this means symbolic dynamics since only molecules connected by colored braids have high probability to participate in same biochemical reaction and do it in a very specific manner. Since the quarks involved with braid strands can have fractional charges, molecular sex can be realized also in this manner.

The dark DNA coding for dark proteins (both consisting of dark proton sequences) at the magnetic body of the system mimicking the 2-braiding of the magnetic bodies of invader molecules might have defined the prebiotic symbolic representation and could still be a part of immune system.

Q: What selected the bio-molecules during chemical evolution?

A: The proposed symbolic dynamics based on the notions of colored braids and fractional atom poses very strong constraints on the subsets of bio-molecules that can react with considerable rates.

Q: How biochemical pathways emerged?

A: It is now possible to realize in practice sequences of arbitrarily complex self-catalyzing biochemical reactions utilizing DNA hairpins. The mechanism generalizes to more complex molecules. At a given step of the reaction sequence the structure formed during the previous steps acts as a key fitting to a lock represented by some hairpin in the solution, and opens it to a linear molecule and in this manner makes it a key. The braids between reactants make it possible for the key and lock to find each other.

The lock and key mechanism can be generalized with key being replaced with a password. In computer languages like LISP lock-key pair corresponds to a memory position represented as a pair formed by its own address and the address to which the memory position points and the program consisting of sequence of this kind of associations. These addresses can be represented also as collections of resonance frequencies.

Q: How genetic code evolved?

A: The symmetries of the third codon of the genetic code allow in DNA as TQC model an interpretation as isospin and matter antimatter symmetries for quarks and antiquarks assigned with DNA nucleotides and representing 4-color of braid strands. These symmetries together with the study of the detailed structure of tRNA lead to a model for the evolution of the genetic code as a fusion of a non-deterministic 1-code and one-to-one 2-code corresponding to the conjugation of mRNA molecules. During RNA era two kinds of RNAs, call them RNA_1 and RNA_2, were present and played the roles of mRNA and amino-acid sequences. 2-code *resp.* 1-code mediated the analog of replication *resp.* translation using hairpin like molecules $tRNA_1$ and $tRNA_2$ to bring in RNA nucleotides and RNA doublets to the growing RNA_i sequence. Amino-acids attached to the stem of $tRNA_2$ acted as catalysts. The transition to RNA-amino-acid era took place via a fusion of the $tRNA_1$ and $tRNA_2$ to the ordinary tRNA and instead of sequences of two kinds of RNAs were replaced by amino-acid sequences were formed. After a period of symbiosis involving all these three tRNAs a transition to DNA-RNA-amino-acid world took place as an amino-acid sequence acting like reverse transcriptase emerged.

More strongly TGD based approach is provided by the vision about water as a primitive life-form inspired by Pollack's findings about fourth phase of water and exclusion zones [L15]. In this framework the dark proton strings defining "dark amino-acid" sequences [L2, K24] could have coded the 2-braiding (braiding in space-time) patterns of invader molecules as their own 2-braidings, and dark DNA would have provided symbolic coding of "dark proteins". Therefore dark DNA would originally have coded dynamical patterns for magnetic bodies of invader molecules. This would make possible pre-biotic immune system, which would be a part of the recent immune system.

Q: Did RNA world precede the life as we know it?

A: The model for the evolution of the genetic code forces to conclude tha RNA world [I142] preceded the recent biology and allows also to deduce that the nucleotides involved with second form of RNA where A,T,U,I(nositol). The exotic RNA in question could have been $2', 5'$ form of RNA rather than $3', 5'$ RNA produced also in the classical experiments of Leslie Orgel [I24].

Another and more plausuible option in TGD framework is water as a primitive lifeform with dark counterparts of basic biomolecules realizes as dark protonic strings (dark nuclei). RNA world

could have followed this period but the fact that both DNA, RNA, tRNA and aminoacids can have dark counterparts does not suggest special role for RNA.

Q: Does the notion of protocell make sense?

A: The model of DNA as TQC involves essentially the magnetic flux tubes connecting DNA nucleotides and cell membrane. Since topological quantum computation should have taken place also during the RNA era, some kind of cell membrane consisting of exotic RNA should have been present. It has been found that DNA indeed forms membrane like structures which are liquid crystals consisting of sequences of DNA nucleotides with length up to 20 nucleotides [I96] and same might be true in the case of exotic RNA.

Another very attractive option is that the counterparts of exclusion zone carrying negative charge due to the transfer of protons to the flux tubes of the magnetic body of exclusion zone [L15] defines protocell.

Q: How life could evolve in the harsh primordial environment? Does the notion of primordial ocean make s

A: Evolving life had to cope with the grave difficulties due to the irradiation by UV light and meteoric bombardment. A simple solution of these problems is to evolve in the interior of Earth, say in underground lakes. This idea conforms nicely with the observation that continents would have formed a single super continent at time of Cambrian explosion provided the radius of Earth at that time was by a factor 1/2 smaller than now. TGD predicts that cosmic evolution does not occur continuously but by quantum jumps in which the Planck constant of appropriate space-time sheet increases. A phase transition of this kind increasing the radius of Earth during a relatively short time interval would have led to a burst of life from underground lakes to the surface of Earth. This would also explain the sudden emergence of a huge variety of highly developed life forms during Cambrian explosion.

Few words about the key ideas behind the chapter are in order.

1. The idea about hierarchy of Josephson junctions discussed in [K15] (cell membrane would provide the basic realization leading to a model of nerve pulse [K44]) is central and emerged already around 2000 as I learned by looking at old CASYS conference proceedings [L1].

2. The considerations rely also heavily on the notion of magnetic body and the identification of dark matter as a hierarchy of phases of ordinary matter (at least) labelled by an effective value of Planck constant $\hbar_{eff} = n\hbar$ coming as an integer multiple of the ordinary Planck constant (this idea [K18, K39] was introduced around 2005). These phases are assumed to reside at flux tubes and sheets appearing as parts of the magnetic body assignable to any physical system.

   The basic implication is that basic quantum scales proportional to $\hbar$ are scaled up so that nanoscopic and even macroscopic quantum phases become possible for sufficiently large values of Planck constant. Magnetic body is assumed to act as an intentional agent receiving sensory data from cell membranes and controlling biological body with the mediation of genome. Signals are realized as dark photons and cyclotron Bose-Einstein condensates at magnetic bodies are central in this picture. Photon with given energy can correspond to arbitrarily long wavelengths and one can understand the effects of ELF radiation on vertebrate brain in terms of dark photons. DNA as topological quantum computer is one of the implications [**?**].

3. In [K65] the identification of bio-photons as ordinary photons resulting in decays of (say) dark photons with same energy and frequency in EEG range is discussed. In this and subsequent articles neither bio-photons nor the notions of zero energy ontology [K32] having profound biological implications [K3, K67] are not discussed. The reason is that all the articles in this series are prepared from the chapters of online book "Genes and Memes" [K22] - most of them have been written for the first time for more than decade ago. A fascinating challenge is to find how the considerations are modified by bringing in these new ideas.

5.1.2 Topics Of The Chapter

The topics of the chapter has been restricted to those, which seem to represent the most well-established ideas. The topics of the article have been restricted to those, which seem to represent the most well-established ideas about evolution in TGD Universe. There are many other, more

speculative, ideas such as the notion of fractional atom [K16] based on fractalization of electron charge and strong form of the hypothesis that some life forms has evolved in "Mother Gaia's womb", maybe even in the hot environment defined by the boundary of mantle and core.

1. The basic facts believed to be known about pre-biotic evolution are discussed first. After that the TGD inspired vision about prebiotic evolution is introduced. The key ideas discussed are the notion of magnetic body and plasmoids as primitive life-forms, emergence of symbolic dynamics as dynamics of dark matter, universal metabolic currencies identified as increments of zero point kinetic energies in many-sheeted space-time, time mirror mechanism giving rise to models of intentional action, memory and remote metabolism and finding justification in zero energy ontology (ZEO) [K67], the idea that primitive life forms evolved in "Mother Gaia's womb" [L45] (to be discussed in the fourth part of the article in detail), and possible mechanisms making possible coherence of biochemical activities. Prebiotic chemistry is discussed from the point of new physics: the idea that dark matter makes possible symbolic dynamics justifying the idea that DNA can be seen as written text is the key notion. High energy phosphate bond as a carrier of negentropy is discussed in terms of negentropic entanglement and Negentropy Maximization Principle (NMP) [K32]. A weaker assumption is that ATP$\rightarrow$ ADP makes only possible to generate negentropic entanglement.

   Some important topics have been left out since they have been discussed in [K29] and in an earlier article [L6, L7]. In particular, the idea about DNA as topological quantum computer realized in terms of braids defined by flux tubes connecting DNA nucleotides or codons to the lipids of the nuclear and cell membranes is not discussed [L6, L7]. If topological quantum computation really takes place in living matter, the question is when topological quantum computation did emerge. The universality of the braiding defining topological quantum computer programs [K67] gives also rise to a universal representations (sensory -. memory -. etc...) suggests that topological quantum computation like processes must have been present from already during pre-biotic period.

2. A model for the evolution of the recent genetic code (3-codons) as a fusion of codes for which codons are nucleotides (1-codons) and di-nucleotides (2-codons) is discussed. The symmetries of the genetic code, the observation that tRNA can be seen as a fusion of two hairpin like DNA molecules, and the finding that the first nucleotides of 3-codon code for the reaction path leading from a precursors of the amino-acid to amino-acids for hydrophobic/hydrophilic dichotomy, serve as motivations of the model. 1- and 2-codes corresponding to the two forms of RNA (the exotic $2' - 5'$ RNA and the usual $3' - 5'$ RNA) would have prevailed in RNA world. Amino-acids would have served as catalysts for the copying of RNA on one hand, and RNA molecules would have catalyzed the formation of amino-acids from their precursors on one hand, meaning the presence of a positive feedback loop. In the transition to DNA-amino-acid era RNA began to be translated to amino-acid sequences.

   TGD based view about the evolution of genetic code is compared to the views of McFadden [I114]. This section is a little bit out of date. For instance, the hypothesis that magnetic body of DNA could induce mutations purposefully is not discussed. This hypothesis is natural if one believes that magnetic flux tubes connecting bio-molecules play a key role in bio-catalysis. This idea is discussed in the chapter devoted to protein folding [K2].

3. A vision about biological evolution and evolution of brain is discussed on basis of the wisdom gained from the construction of the models of sensory receptor and generalized EEG [K21, K15]. As I started to develop this vision. several obvious questions popped up. The preferred values of (effective) Planck constant are assumed to be integer multiples of ordinary Planck constant: does this integer have preferred values? For eight years later I take the original speculative answer to this question with a grain of salt. Can one distinguish between evolution of biological and magnetic body and identify cultural evolution as evolution of magnetic body? EEG and its variants (and the predicted scaled variants of these) are expected to characterize living organisms, even super organisms like ant nest, bee hive, and bacterial colony: is this really the case? Does bee hive possess a long term memory and what is the role of the queen? One can also ask questions about the evolution of nervous system in the same conceptual framework. Are the magnetic bodies of neurons and larger structures characterized by $\hbar_{eff}$? What about collective and transpersonal levels of consciousness?

Sheldrake's vision [I128, I129], [J10] about species memory is also highly interesting from TGD point of view but is not considered in the article series about prebiotic evolution. The interested reader can however consult the article at [L9]. The latest view about TGD inspired theory of consciousness justifying Sheldrake's vision in terms of negentropically entangled states defining representations invariant under quantum jump sequence and in this manner giving rise to "Akashic records" defining sensory -. memory -. etc. representations can be found at [K67].

Dark photons characterized by the value of $\hbar_{eff}$ and transforming to ordinary photons with the same energy identified as bio-photons are becoming a central element of TGD inspired quantum biology [K65]: in particular the non-destructive conscious reading of the memories represented in terms of negentropically entangled states by interaction free measurement is very attractive idea [K67]. The communications by dark photons might have been present already during the prebiotic era before the emergence of biochemical signalling and neural communications. The role of dark photons is not discussed in the vision as it was formulated for more than five years ago.

4. Cambrian explosion represents a rather mysterious period in biology: new highly developed phylae emerged out of nowhere. A second strange finding is that continents would fit together to form single super-continent covering entire Earth's surface at time of Cambrian explosion if the radius of Earth would have been one half of its recent value. This finding has inspired Expanding Earth theories but it has not been possible to identify the mechanism causing the expansion. The success of the standard tectonic plate theory requires that possible expansion must have occurred in relatively short geological time scale. The hierarchy of Planck constants implies that cosmic expansion has occurred in quantum leaps increasing the value of $\hbar_{eff}$ and thus of quantum scales by factors which tend to be powers of 2. Cosmic expansion would have occurred as jerks even in the case of planets. In the proposed model Cambrian explosion would have accompanied the expansion of the Earth's radius by a factor of 2: during this period an outburst of highly developed life forms from underground seas to the surface of Earth would have taken place. This topic is discussed in separate chapter [L45].

To sum up, TGD does not yet provide a unique view about prebiotic evolution. Life as primitive lifeform is very attractive proposal but it is not clear whether it is natural to assume RNA world could have been its follower since both DNA,RNA, aminoacids, and tRNA seem to have dark counterparts.

The appendix of the book gives a summary about basic concepts of TGD with illustrations. Pdf representation of same files serving as a kind of glossary can be found at `http://tgdtheory.fi/tgdglossary.pdf` [L11].

5.2 What Is Known About Pre-Biotic Evolution?

In the following the basic facts and ideas about pre-biotic are summarized.

5.2.1 Some Believed-To-Be Facts About The Early History Of Life

The following basic facts allow to get rough view about the time scales of the pre-biotic evolution.

1. The origin of Earth occurs roughly 4.5 Ga (Ga=billion years ago). Bombardment phase, that is the period of large scale impacts, ended roughly 4-3.8 Ga.

2. ^{12}C enrichment is seen as a signature of photosynthesis. By this criterion the oldest known micro-fossils date back to 3.5 Ga and are found in volcanoes. There is a hot debate going on about whether these micro-fossils are really genuine micro-fossils. For instance, they are accompanied by complex quartz structures and this does not conform with what one might expect.

3. Levels of atmospheric oxygen began to increase during second half of precambrian era (2 Ga) and reached 10 per cent level at the eon's end at 1 Ga.

4. There are not many fossils or fossil bearing rocks from the precambrian eon. The simplest explanation is that the precambrian fossils have been soft bodied. Abundant fossils appear at Cambrian period which started.55 Ga. Cambrian explosion meant emergence of extremely rich spectrum of various life-forms.

5. The time interval between bombardment phase and the emergence of the first micro-fossils is only.3 billion years. This means that the time window for the life to develop on the surface of Earth is surprisingly narrow, and one can ask whether the primordial life could really have developed spontaneously in the environment provide by the surface of young Earth.

5.2.2 Standard Approaches Are Mechanistic

Various hard science approaches to the pre-biotic evolution share a common philosophy dating to the beginning of the previous century. This philosophy is reductionistic materialism according to which life can be explained as a purely mechanistic phenomenon which just happened to occur by change ("change and necessity" using the phrase in the title of the classic of Monod). This view is highly questionable and certainly in dramatic conflict with more modern views relying on macroscopic and even astrophysical quantum coherence as basic elements.

At the experimental level the failure of mechanistic approach is easy to see. The components of cell inside test tube do not form a living system. The numerical simulations using computer models have demonstrated convincingly that spontaneous emergence of life is not possible. Empirical facts support completely different conclusion: the emergence of life is unavoidable and occurs everywhere in the universe, and there are good reasons that it has some universal characteristics. The challenge is to develop the conceptual framework so that it can explain this naturally.

5.2.3 The Notion Of Primordial Ocean

The following discussion uses basic facts which I have learned from articles of Chris King [I64] representing updated view about facts and theories about pre-biotic evolution as well as articles criticizing the existing theories [I67, I108].

The generation of biomonomers requires the presence of C, H and O. During 1920′s Oparin and Haldane independently proposed that life, or its chemical precursors including amino-acids, formed spontaneously under the conditions associated with primordial atmosphere. Genetic code was not yet known, and both Oparin and Haldane believed that life evolved from proteins, and that life's precursors including amino-acids were formed spontaneously in a reducing atmosphere whose principal components where CH_4 and/or CO_2, NH_3, and H_2O.

Oparin suggested that methane served as the source of carbon whereas Haldane believed that the source was CO_2. Oparin also suggested that what he called coacervatives were predecessors of the cell. Haldane thought that the gradual increase in the complexity of pre-biotic molecules in the presence of UV radiation led automatically to the generation of a protocell.

The assumption that the atmosphere is reducing is essential: the presence of oxygen would be fatal for the biomonomers. This assumption can be however questioned. The primordial atmosphere was due to the outgassign associated with volcanic eruptions but due to volcanic fumes the atmosphere is oxidizing which means that biomonomers would have been rapidly destroyed by oxidation. Interestingly, the photographs of Earth taken during the Apollo 16 mission allow to conclude that a gigantic cloud of hydrogen, extending 40, 000 miles into space surrounds the Earth. The only source of hydrogen can be water vapour, bombarded by high energy UV light rays above ozone layer [I139]. If this water has been there during the primordial period, the atmosphere must have contained oxygen so that the basic assumption would be wrong.

Even if the atmosphere was reducing, one encounters a problem. There would have been no shield against UV radiation which according to [I67] would have dissociated COOH whereas CH_4 and heavier hydrocarbons would have polymerized forming an oil slick 1-10 deep over the surface of the Earth. Ammonium would have photo-dissociated into nitrogen and hydrogen so that the conditions of the experiments of Miller [J23] and others to be discussed below would not been satisfied.

5.2.4 Urey-Miller Experiment

Urey-Miller experiment [J23] meant a dramatic step of progress on the experimental side, and for a along time it was believed to be conform the vision of Oparin and Haldane. The experiment involved a reducing atmosphere and electric sparks simulating the effect of lightnings. In the later experiments 19 of 20 amino-acids were identified. Also nucleosides A, G were produced. Cyanoacetaldehyde together with urea believed to be accumulated to primordial ponds, allowed to generate U and C as was discovered by Miller 40 years after his classical experiment. These impressive results were interpreted as a support for the view about primordial ocean as a "dilute soup" of organic molecules which precipitated out of the atmosphere.

For a long time it was believed that the synthesis of ribose necessary for the generation of RNA was impossible in these circumstances. It turn out that ribose was generated from glyseralhehyde phosphate in presence of COOH [I69]. Glyseraldehyde phosphate was generated also in Miller's experiments. In case of deoxiribose necessary for DNA no plausible synthesis mechanism has been identified.

Organic compounds (in particular A, U, C, G) and even membrane forming products are present in carbonaceous chondrites (meteorites). Chondrites are essentially what the Earth is made of. Galactic gas clouds contain sugars, amino-acids, nucleic acids. In an experiment of Dworkin and his colleagues [I77] thin ice at temperature of 10 K containing H_2O, ammonia, CO, CO_2 methanol was located in vacuum and bombarded by UV radiation to mimic the situation prevailing in the interstellar space. Contrary to expectations, hundreds of different complex organic molecules appearing also in meteorites were generated. Thus it seems that the molecules generated by pre-biotic evolution appear everywhere in cosmos but ironically, the environment provided by the surface of young Earth's does not seem to favor the pre-biotic evolution.

5.2.5 RNA World

One of the basic questions in theorizing about pre-biotic evolution is which came first: proteins, nucleic acids or both or possibly something else. The vision known as RNA world [I113, I142] is dominating the stage at this moment. It is assumed that RNA polymers serve all the basic functions associated with DNA, RNA and amino-acids. These functions are based on genetic and catalytic capacity of RNA. Later a genetic takeover occurred involving the emergence of DNA and genetic code in which amino-acids replaced RNA somehow.

One can represent good experimental justifications for the RNA world vision (for the summary and for references the article of Chris King [I64] is recommended warmly).

1. Ribose can be synthetized in the same circumstances as amino-acids and nucleosides. The presence of kaolinite clays and volcanic magmas stabilizes RNA polymerization. When montmorillonite, a positively charged clay believed to exist copiously in young Earth, was added to a solution of negatively charged amino-acids, a solution of RNA nucleotides gave rise to RNA 10-15 nucleotides long [I101]. These chains attached to the surface of the clay, and when more nucleotides were fed by washing them with the solution, they grew up to 55 nucleotides long. It seems that reversible dehydration in a medium containing phosphates, bases and sugars provides the routes to polynucleotide formations. Besides water, Mg_{++} plays a key role in stabilizing mono- and oligonucleotides by compensating the negative charges of the phosphates.

2. RNA can form double helices and has 3-dimensional tertiary structures analogous to that of proteins so that one might expect the ability to act as catalyst. The discovery of spontaneous splicing of RNAs in living systems is possible meant a breakthrough in this respect [I140]. Second crucial finding was that these RNAs could act as catalysts in trans-esterifications crucial for the protein synthesis [I113]. Even high fidelity complementary replication of arbitrary short RNA sequences has been demonstrated [I92]. Simple biological RNAs have shown to have autocatalytic self-assembling capacity. The catalytic activity hinges on various forms of proton transfer (perhaps the leakage of protons between space-time sheets is involved). RNA appears to be the agent of peptide-bond synthesis in the modern ribosome [I63] and modified ribozymes are able to act as amino-acyl esterases [I97]. Thus RNA seems able to

serve synthetizing, transfer, messenger and ribosomal functions so that it can guide both its own replication and ordered polymerization of proteins.

3. Support for the RNA world pictures comes also from the fact that the ancient fossil nucleotide coenzymes including ATP, NAD, coenzyme A and vitamin B12 are all ribonucleotides. Eucariote organisms continue to posses massive RNA processing within the nucleus. Reverse transcriptase, whose function contradicts the Central Dogma, and encountered in retroviruses (such as HIV), might have ancient origin. Reverse transcriptase is indeed crucial for the transition from RNA→RNA predecessor of genetic code to DNA→amino-acid genetic code in TGD framework.

5.2.6 How Biochemical Pathways And DNA-Amino-Acid Code Emerged?

The traditional viewpoint is that biochemical pathways have developed from some simple basic systems. This approach encounters difficulties when one tries to understand how integrated systems such as electron transport and metabolic machinery could have worked in primitive systems. TGD based solution to the problem is the universality of metabolism and other basic functions relying on super-conductivity and its breakdown by the leakage of various supra currents between space-time sheets.

Furthermore, one can also decompose the evolution to two parts corresponding to the development of genetically controlled structures and self-organizing structures not controlled genetically [**?**]. Chris King has formulated the same idea in a more concrete manner in his article [I64] from the point of view of complex systems. According to King, the basic mechanisms developed without genetic control and were finally taken under control as the genetic takeover occurred. These kind of generic structures include proteins and nuclei acids, nucleotide coenzymes, bilayered membrane structures, ion transport and membrane excitability, membrane bound electron transport, glycolysis and the citric acide cycle. In TGD framework one can add to this list topologically quantized classical fields as universal structures.

A second open question is how DNA and amino-acids took the command. Here many-sheeted space-time provides a possible answer. DNA nucleotides are stable only inside regions containing ordered or liquid crystal water forming a macroscopic quantum phase. The transformation of DNA to RNA nucleotide requires water molecule which is not available in this kind of environment. The transition from RNA-RNA predecessor of genetic code to DNA-amino-acid genetic code is also a deep problem and here the trick might be very simple: reverse RNA transcriptase used by retro-viruses (also HIV) could have transformed RNA genes to DNA genes.

The model for the evolution of genetic code as a fusion of singlet and doublet codes in turn allows to understand the emergence of amino-acids as being due to a change in tRNA structure implying that amino-acids acting as catalyzers of the attachment of RNA to tRNA molecule began to stick to tRNA, and were loosened only when tRNA was attached to RNA so that the used amino-acids began to form amino-acid sequences replacing RNA sequences as coded sequences.

5.2.7 Problems With The Polymerization In Primordial Ocean

Polymerization occurs universally by dehydration in case of polynucleotides, polypeptides, polysaccharides and lipids serving as basic building blocks of living structures. The basic difficulty is that polymers are not stable in an aqueous environment. Several cures to this problem have been proposed.

1. Various mineral interfaces could serve as templates for the formation of polymers and the evaporation of water from these structures could give rise to polymers. For instance, mud flats might have made possible polymerization.

2. Fox has proposed that the heat flow from geoactive sites like hot springs, volcanic rims and submarine vents could have caused the dehydration [I80]. Fox has indeed managed to show how to generate protenoids consisting of up to several hundred amino-acids possessing weak catalytic activities. The temperatures needed are typically above 100 C and somewhat too high. Archea as well as nanno-bacteria are indeed found in this kind of environments, and they utilize heat and sulphur compounds as a source of metabolic energy. The first objection

is that the high temperature destroys the biological molecules in this kind of environment. Furthermore, the atmosphere around volcanoes contains CO_2 and water and only minor amounts of nitrogen, hydrogen sulfide and sulfur dioxide so that this kind of atmosphere does not give rise to the biomonomers in analogs of Urey-Miller experiments.

3. The un-stability of polymers against hydration is so serious a shortcoming for the primordial soup approach that it has inspired quite radical alternative proposals. For instance, Crick has concluded that pre-biotic life might have extraterrestrial origin. The panspermia hypothesis however only shifts the problem to the outer space. The evolution of life in intra-terrestrial environement is much less radical variant of this approach if one is ready to accept the notion of many-sheeted space-time.

4. Dr. Cairns-Smith has proposed that so called clay genes appeared as predecessors of genes [I60]. For instance, Al atoms in the lattice containing Si and O can have three states at each site so that enormous information storage capacities become available. These structures would have acted as scaffolding for present day bio-molecules of RNA and DNA. This idea might create more problems than it solves. One could however turn the idea around and ask whether primitive life-forms such as nanno-bacteria could express their genetic code with the help of kaolinite clays.

To my personal opinion, an invention of a clever mechanism is probably not enough to solve the basic problem. Polymerization in modern cells is basically a process involving metabolic control, and it seems that the metabolic control must have been present from the beginning in some primitive form. TGD predicts that magnetosphere can perform quantum control in astrophysical length scales from the magnetic flux tubes of the Earth's magnetic field B_E or, rather, from the flux quanta of dark magnetic field accompanying it and having strength $B_E = 2B_E/5$. A further prediction is that metabolism is completely universal and existed in primitive form already during the primordial period. This in turn makes possible the option that the pre-biotic life need not have developed through stages differing dramatically from the recent life forms. One could even assume that a generalization of ontogeny recapitulates phylogeny principle holds true for the intracellular dynamics so that it would give precise information about pre-biotic evolution.

One must also clarify what one really means when one speaks of aqueous environment. Water allows an extremely rich variety of structures. Liquid crystal water/ordered water encountered inside cells might automatically stabilize polymers, and provide also a solution to how DNA and polymers were stabilized. Sol-gel transition giving rise to macroscopic quantum coherence would generate this liquid crystal phase.

5.2.8 The Notion Of Protocell

The emergence of membrane bounded structures has certainly been decisive for the evolution of life. Cell membrane made possible differentiation forced by the competition for metabolic resources. Cell membrane imports metabolics, exports waste products, and acts as a signalling system. In TGD universe the receptors at cell membrane also serve as cellular sensory receptors.

A variety of answers to the question about the predecessor of the cell has been proposed. The natural constraint is that the membrane in question results via self-organization. If one requires consistency with the generalization of ontogeny recapitulates phylogeny principle (ORP), the number of options is reduced dramatically.

1. Lipid bi-layers are certainly a natural guess since they formed spontaneously in solutions on biological conditions. There is thus a consistency with the generalized ontogeny recapitulates phylogeny principle requiring that all primordial structures appear also in modern cells.

2. An elegant an plausible candidate for protocell is the gel phase resulting in sol-gel transition inside cell [I104, I64] . Gel phase has indeed many properties of cell membrane bound region and is routinely generated also inside modern cells. A compact ordered liquid crystal type phase is in question. Negatively charged proteins are generated inside the gel phase and gel phase rejects Na_+ ions and attracts K_+ ions just as cell interior. Also negatively charged proteins are stable inside gel phase. In TGD framework gel phase is a macroscopic quantum

phase so that new physics is necessary involved. In particular, the evolution by quantum jumps is expected to lead to this kind of self-organized structures automatically. In TGD framework one expects that the liquid crystal/ordered water phase leads to the stabilization of RNA and that even DNA nucleotides become stable.

3. The proposal of Sidney Fox [I80] is that protocells could correspond to the called micro-spheres formed from protenoids in geolocically active sites like hots springs and volcanic rims. He also demonstrated that this really occurs. Protedoids are amino-acid sequences differing from ordinary peptides in that peptide bonds are different: hence this option is not consistent with the generalization of ORP. When proteneids are washed into a warm water allowed to cool, micro-spheres are formed. Micro-spheres are bilayered structures able to divide. A concentration roughly 10 million times higher than believed to appear in primordial soup is required so that either the idea of protenoid or of primordial soup is wrong. Further objections are that micro-spheres do not perform any functions of cell, and that the structure is like an inpermeable cell wall or spore coat rather than a cell membrane [I67, I108].

The common problem of all these options is that the required concentrations of biomonomers are much higher than those expected in the primordial soup. This forces to question the notion of primordial soup and even the assumption about the occurrence of the pre-biotic evolution at the surface of Earth.

5.3 TGD Based Scenario About Pre-Biotic Evolution

TGD framework leads to a radical view about life. Magnetosphere can be seen as a living system controlling the evolution of life and chicken-egg question can be seen in a totally new perspective. Super-conducting magnetosphere can be seen as a higher level life-form which controls and guides the biological evolution from the very beginning. Second key element is dark matter hierarchy.

5.3.1 Basic Prerequisites

A short summary of basic requirements and problems is in order.

1. A stable star and planet providing appropriate conditions such as temperature for liquid water is needed.

2. Atoms like C, N, and O and smaller amounts of P and S giving rise to bio-monomers, and metals like Al, Fe, and Zn are the basic building blocks. The formation of various chemical bonds like hydrogen bonds, covalent bonds, and peptide bonds is necessary.

3. The formation of biological monomers (amino acids, nucleotides, fatty acids, sugars) is an essential element of life. Except for DNA nucleotides, basic monomers evolve in the circumstances simulating to what have been believed to be the primordial atmosphere. These bio-monomers are found even in the interstellar space and in galactic clouds so that the question is not whether the pre-biotic life can develop but whether our recent day materialistic science allows to understand how it develops. The standard wisdom about primordial atmosphere as a reducing environment (containing no oxygen) indeed leads to grave difficulties. Also the concentrations in the primordial ocean seem to be quite too low for the bio-monomers to be synthesized [I108].

4. The formation of the biological polymers such as proteins, nucleic acids, lipids, and carbohydrates occurs universally by dehydration. The problem is that in water environment polymers are un-stable against decay by hydration: it would seem that a metabolic energy feed is required already at this stage to guarantee non-equilibrium situation. The assembly of these macro-molecules into organized aggregates like chromosomes, micro-tubules and cell organelles suggests the emergence of symbolic representations and only a weak independence of hard facts of chemistry which makes the problem even more difficult from the point of view of standard physics.

5. The emergence of catalysts and metabolism, should be understood. Here one encounters an egg-hen problem. Standardized metabolic currency seems to be necessary for effective catalysis but metabolism according to the standard view involves extremely complex web of reaction pathways needing refined catalytic actions.

6. Membrane bound structures are essential for life and one should understand how they emerge and even predict correctly basic facts about them.

7. The emergence of the genetic code has remained a mystery in various scenarios of pre-biotic evolution.

8. How the incredible ability of the components of bio-systems to co-operate pops up from primordial soup is not always included to the list of mysteries since everything smelling "holism" is regarded as pseudo science in reductionistic circles.

5.3.2 TGD Based Vision About Pre-Biotic Evolution

The prevailing mechanistic world view forces to conclude that life emerged accidentally in young Earth during a relatively short time period of about.3 billion years. On basis of extensive computer simulations, one can fairly say that a spontaneous generation of life in primordial ocean seems extremely implausible [I67] .

TGD replaces materialistic view with a continual re-creation in which classical universe in 4-dimensional sense is replaced by a new one in each quantum jump. p-Adic length scale hypothesis allows to formulate the notion of evolution precisely as a generation of increasingly larger space-time sheets characterized by preferred p-adic primes meaning also a sequence of symmetry breakings. A second aspect is the emergence of new levels in dark matter hierarchy meaning great leaps in evolution. A crucially new element is the predicted fractal hierarchy of copies of electro-weak and color physics. Dark weak bosons and gluons thus become an essential part of the physics of living matter.

Macroscopic and even astrophysical quantum coherence becomes a key feature of living matter. Theory is partially non-deterministic also in classical sense but the variational principle for Kähler action implying that space-time surfaces are analogous to Bohr orbits and self-organization lead to Darwinian selection of selected patterns.

Is life really a result of accident?

Life is often regarded as an extremely improbable accident. The estimates for the probability of the formation of amino-acids, DNA, and of emergence of genetic code from random soup of molecules are indeed found to be extremely small. In TGD Universe the situation is different.

1. Intentional action is basic aspect of TGD Universe. Negentropy Maximization Principle [K32] states that the dynamics of quantum jumps maximizes the information content of the conscious experience and implies evolution as a continual recreation of the Universe eventually leading unavoidably to the emergence of information rich systems and explaining also why the values of "fundamental constants" seem to be tailored for the emergence of life as we are used to identify it. p-Adic dynamics for cognitive space-time sheets implies local randomness but long range fractal correlations for the real dynamics.

2. The hierarchy of Planck constants implies macroscopic and macro-temporal quantum coherence in all length scales. Universe becomes single conscious organism in this framework. This has many implications. For instance, low frequency photon can have arbitrarily high energy. This makes it possible control of short length and time scales by the dynamics in long scales, say by EEG. The enormous values of gravitational Planck constant for dark matter and the assumption that visible matter condenses around dark matter imply that planetary orbits correspond to Bohr orbits [K45, K37]. Only very few orbital radii are possible and for a star with mass around solar mass planets at distance of Earth are possible and probable irrespective of the mass of the planet. Hence solar systems are standardized to high degree. Also the quantization of masses of stars is highly suggestive and the number of stars with mass not far from solar mass is large. Obviously this raises the probability for having Earth like environments dramatically.

3. TGD based nuclear physics [L2] , [L2] explains cold fusion [C4] , [D10] as well as biological nuclear transmutations for which there is considerable empirical support [C2] . The direct empirical evidence comes from the observation that the abundances of heavier elements in an astrophysical object at distance of order 10 billion light years are essentially the same as in solar system [E10]. If elements are created only in the stellar interiors, the abundances should be much smaller. This suggests that the heavier elements result by cold fusion in the interstellar space. The implication is that environments allowing life have existed much earlier than believed hitherto.

4. The hierarchy of Planck constants and the notion of magnetic body allow a mechanism of topological quantum computation [K17] based on the representation of braids represented as flux tubes of wormhole magnetic field whose presence might provide a definition for what it is to be living. The first implication is an explanation for the miraculous ability of biomolecules to find each other in terms of the reduction of Planck constant inducing a shortening of the flux tubes connecting reactants and catalysts. The structure of flux tube patterns connecting various molecules allows to program complex series of biochemical reactions to the structure of braids connecting the molecules since given spots of molecules can be forced to meet each other in reaction. Conserved braid color allowing to identify whether the braid strand comes from A, T, C or G implies even stronger selection rules. One can assign also to amino-acid a 3-braid corresponding to one of the DNA codons coding for it. These extremely selective interactions between living bio-molecules give good hopes of understanding why DNA and amino-acids were selected as molecules able to co-operate.

5. Many-sheeted space-time concept implies the existence of fundamental metabolic energy currencies [**?**] defined by the differences of zero point kinetic energies of particles for space-time sheets labeled by different value of p-adic prime p. The existence of standardized metabolic currencies simplifies the situation dramatically and living matter must face only the problem of storing metabolic energy. Plasmoid like life forms suggest themselves as predecessors of biological life. p-Adic length scale hypothesis $p \simeq 2^k$ is what implies standardization of zero point kinetic energies and follows from zero energy ontology which also assigns to a particle labeled by prime p a time scale $T_p = \sqrt{p}L_p/c = L_p(2)/c$ characterizing the temporal size of the space-time sheet having particle and its negative energy counterpart at its time-like boundaries. The fact that the fundamental 10 Hz biorhythm corresponds to the time scale assignable to electron suggests that fundamental biological time scales are hidden in the space-time structure of fundamental particles.

The notions of magnetic body and plasmoid

The model of high T_c super-conductivity and the general vision about dark matter hierarchy have led to a rather precise model for magnetic body as an intentional agent utilizing biological body or its part as motor instrument and sensory receptor [K15]. Dark matter plasmoids and plasma oscillation patterns as representations of control commands are one important aspect of the model. The prediction is that plasmoids should have been predecessors of ordinary life forms. There is laboratory evidence that plasmoids behave like life forms [I119]. Very high temperatures catastrophic for ordinary life forms could prevail at magnetic flux quanta associated with plasmoids. This forces a radical reconsideration of the question how pre-biotic life have evolved and forces to ask whether even the hot interior of Earth could have served or still serve as a seat of life.

Does the Earth's magnetic field have a dark counterpart?

The notion of dark matter as a hierarchy of phases characterized by arbitrarily large values of Planck constant has established itself as a part of TGD [K18, K15]. This raises several questions. For instance: does the magnetic body of Earth have a dark counterpart and its the dark magnetic body relevant for functioning of living matter?

A partial answer to this question came from a frustrating realization that I had for years erratically believed that the magnitude of the magnetic field assignable to the biological body is $B_E = .5$ Gauss, the nominal value of the Earth's magnetic field. Probably I had made the calculational error at very early stage when taking Ca^{++} cyclotron frequency as a standard. I

am grateful for Bulgarian physicist Rossen Kolarov for pointing to me that the precise magnitude of the magnetic field implying the observed 15 Hz cyclotron frequency for Ca^{++} is .2 Gauss and thus slightly smaller than the minimum value.3 Gauss of B_E. This value must be assigned to the magnetic body carrying dark matter rather than to the flux quanta of the Earth's magnetic field. This field value corresponds roughly to the magnitude of B_E at distance 1.4R, R the radius of Earth.

Dark matter hierarchy leads to a detailed quantitative view about quantum biology with several testable predictions [K15] . In principle all integer and even rational values of Planck constant are allowed. Number theoretical arguments suggest a general formula for the favored values of $r \equiv \hbar/\hbar_0$ [K18] as $r = n_1^{\pm 1} n_2^{\pm 1}$, where n_i characterizes the quantum phase $q = exp(i\pi/n_i)$ characterizing Jones inclusion [K57] . The values of n_i for which quantum phase is expressible in terms of squared roots are number theoretically preferred and correspond to integers n expressible as $n_i = 2^k \prod_n F_{s_n}$, where $F_s = 2^{2^s} + 1$ is Fermat prime and each of them can appear only once The lowest Fermat primes are $F_0 = 3, F_1 = 5, F_2 = 17$. The prediction is that also r-multiples of p-adic length scales are possible as preferred length scales.

TGD inspired quantum biology and number theoretical considerations suggest preferred values for $r = \hbar/\hbar_0$. For the most general option the values of $\hbar$ are products and ratios of two integers n_a and n_b. Ruler and compass integers defined by the products of distinct Fermat primes and power of two are number theoretically favored values for these integers because the phases $exp(i2\pi/n_i)$, $i \in \{a, b\}$, in this case are number theoretically very simple and should have emerged first in the number theoretical evolution via algebraic extensions of p-adics and of rationals. p-Adic length scale hypothesis favors powers of two as values of r.

The hypothesis that Mersenne primes $M_k = 2^k - 1$, $k \in \{89, 107, 127\}$, and Gaussian Mersennes $M_{G,k} = (1 + i)k - 1$, $k \in \{113, 151, 157, 163, 167, 239, 241..\}$ (the number theoretical miracle is that all the four scaled up electron Compton lengths $L_e(k) = \sqrt{5}L(k)$ with $k \in \{151, 157, 163, 167\}$ are in the biologically highly interesting range 10 nm-2.5 μm) define scaled up copies of electro-weak and QCD type physics with ordinary value of $\hbar$ and that these physics are induced by dark variants of corresponding lower level physics leads to a prediction for the preferred values of $r = 2^{k_d}$, $k_d = k_i - k_j$, and the resulting picture finds support from the ensuing models for biological evolution and for EEG [K15]. This hypothesis - to be referred to as Mersenne hypothesis - replaces the earlier rather ad hoc proposal $r = \hbar/\hbar_0 = 2^{11k}$ for the preferred values of Planck constant.

In the case of magnetic flux simplest quantization suggests the scaling $B \to B/r$ for the magnetic fields. This is assumed to hold true also in more general case when the quantization condition reads as $\oint (p - ZeA)dl = n\hbar$ and involves currents flowing at the boundaries of flux quanta so that magnetic flux need not be anymore quantized to a multiple of Planck constant. For axonal membranes the flux quantization with $n = 0$ is natural since the size of flux quantum does not depend on the value of Planck constant. Assuming flux quantization and standard value of Planck constant $B_{end} = .2$ Gauss would give flux tube radius $L = \sqrt{5/2} \times L(169) \simeq 1.58L(169)$, which does not correspond to any p-adic length scale as such.

Concerning the interpretation of B_{end} there are two options. It could correspond to a personal magnetic body or to a dark variant of the Earth's magnetic field. At this moment it is impossible to say which if any hypothesis is right. However the fact that the ELF fields have no direct effect on conscious experience mildly supports the identification as the dark variant of B_E.

Emergence of symbols at molecular level and new view about hydrogen bond, water, and bio-catalysts

The hierarchy of dark matter leads to novel ideas about what distinguishes living matter from ordinary matter. The emergence of symbols and symbolic dynamics and what might be called "molecular sex" could be a fundamental step in the process and I have considered two visions for how this would take place.

1. First vision

First vision is relies on the model of DNA as TQC based on braids and has quite close contact with empirical reality [**?**, K17]. In this case DNA nucleotides are analogous to colors of braid strands and base pairing corresponds to molecular sex for DNA molecules. The color of

braid strand implies long ranged highly selective interactions between DNA and distant molecules, such as lipids of the lipid layer of cell membrane or amino-acids. Free amino-acids inherit the colors of the first two nucleotides in the codon XYZ whereas the color of the third nucleotide corresponds to a quantum superposition of colors for codons coding for the amino-acid this defines the quantum counterpart of wobble base pairing. Amino-acids can be divided into amino-acids and their conjugates analogous to opposite sexes and generalized base pairing determines the interactions of the amino-acids to a high degree. Hydrogen bond can be identified as a special case of flux tube. There are also flux tubes connecting acceptors of hydrogen bonds acting as plugs in the connection lines formed by the magnetic flux tubes and Y corresponds to this kind of plug at the level of amino-acids.

2. Second vision

The mathematical realization for the hierarchy of Planck constants leads to a generalization of the notion of imbedding space and this leads to four kinds of phases resulting as combinations of phases with increased or reduced unit of spin and quantum numbers associated with CP_2 degrees of freedom. Each phase corresponds to its own Planck constant and is characterized by a discrete symmetry group.

Especially interesting are phases with large value of Planck constant involving charge fractionization and increase of spin unit. The electrons of free electron pairs of aromatic cycle are reasonable candidates for dark electrons of this kind. One can consider variants of hydrogen atom containing $n \leq N$ fractionally charged electrons with with lepton number and electronic charge equal to n/N. The values n/N and $(N-n)/N$ for the fractional charge would correspond "name" and "conjugate name" since their combination would give a maximal charge and a state analogous to a full electron shell. Thermal stability poses strong constraints since atomic and molecular energy scales are reduced as Planck constant increases.

The notion of fractional electron inspires the notion of "half" hydrogen bond for which electron has a fractionized fermion number. The full hydrogen bond would be formed in the fusion of half hydrogen bonds and give rise to a structure analogous to a full electron shell expected to be especially stable. Catalyst sites might correspond to half hydrogen bonds and the basic recognition mechanism could be the fusion of half bond and its conjugate to form a full hydrogen bond. One could speak about "molecular sex". The sequences of half bonds would represent words so that molecules would have names. Also interpretation as quantum computer codes might make sense. The problem of this vision is the lack of direct contact with experimental facts and for this reason it will not be discussed in the sequel.

Universal metabolic currencies

In TGD framework a primitive many-sheeted metabolism is present from the beginning and becomes only refined during evolution. Most importantly, metabolic currencies identified as zero point kinetic energies liberated as particles drop to larger space-time sheets are constants of nature by the p-adic length scale hypothesis.

Phosphate-sugar polymers form the backbone of nucleic acids and metabolism is based on ADP and ATP formed from adenine and phosphate ions. It has been already earlier found that the generation of ATP and its metabolic utilization involve the flow of protons between the atomic space-time sheets and some larger space-time sheets, say magnetic flux tube of Earth [K25]). It will be found that this mechanism is involved also with the dehydration leading to polymerization and phosphorylation. The reversal of this process also implies the in-stability of DNA in an ordinary aqueous environment.

The interpretation of the role of phosphate ions as metabolic energy batteries seems to be wrong in TGD framework: the main function of negatively charge phosphates would be to make biopolymers critical against local modifications making them thus ideal for catalytic manipulations. Even deeper function would be the role as standard plugs to which magnetic flux tube can attach and which second flux tube can begin. $ATP \rightarrow$ADP would in this framework mean reconnection process for a magnetic flux tubes modifying the hardware of TQC.

Time mirror mechanism, intentional action, memory, and remote metabolism

Time mirror mechanism having negative energy MEs as space-time correlate has phase conjugate laser waves as standard physics counterparts. Essentially negative energy signals propagating to the geometric past and reflecting back is in question. Intentional action realized in terms of negative energy signals to the geometric past and appearing already at the level of molecular magnetic bodies, is expected to become an increasingly important when the complexity of the structures increases. The charge entanglement by negative energy W MEs is especially interesting control mechanism and makes also possible sharing of mental images. Time mirror mechanism allows also remote metabolism by inducing the dropping of population inverted system to the ground state liberating in this manner positive energy photons received by the sender of negative energy signal. What makes this mechanism so elegant is its enormous flexibility (credit card is the counterpart in economy). Time mirror mechanism provides also a mechanism of memory as communications with the geometric past.

In many-sheeted space-time particles topologically condense at all space-time sheets having projection to given region of space-time so that this option makes sense only near the boundaries of space-time sheet of a given system. Also p-adic phase transition increasing the size of the space-time sheet could take place and the liberated energy would correspond to the reduction of zero point kinetic energy. Particles could be transferred from a portion of magnetic flux tube portion to another one with different value of magnetic field and possibly also of Planck constant h_{eff} so that cyclotron energy would be liberated. In the following only the "dropping" option is discussed.

Emergence of membrane bounded structures

Self-organization in many-sheeted space-time is expected to automatically lead to the generation of the ordered water phases which would have evolved to the gel phase defining in turn a natural predecessor of the membrane bounded structures. Self-organization would have also led to the emergence of membrane structures containing liquid crystal water stabilizing also DNA nucleotides.

In fact, the TGD inspired model for high T_c super-conductivity as quantum critical super-conductivity involving simultaneously two kinds of super-conductivities in a narrow range of temperatures around critical temperature (presumably $T \simeq 37$ °C) predicts correctly the double-layered structure of cell membrane and the length scales involved [K6, K7]. A fractal hierarchy of super-conductivities and cell membrane like structures is predicted corresponding to the dark matter hierarchy and p-adic length scale hierarchy [K15]. Josephson junctions and corresponding Josephson currents are in a crucial role in the model for the hierarchy of generalized EEGs responsible for the communication to and control by magnetic body.

According to unexpected findings about behavior of the cell membrane [I104] discussed from TGD viewpoint in [K44], the usual picture based on pumps and channels for ions is not correct. Rather, cell interior is in gel phase in which water is in structured phase around charged biopolymers intermediate between ice and water. One implication of this is stabilization of RNA and DNA polymers since hydrolysis is impossible due to the lack of free water molecules. Cell membrane would have guaranteed the long term stability of gel phase.

Second function of the membrane like structure consisting of lipids or perhaps even DNA or RNA molecules could relate to the topological quantum computation and memory in the manner discussed in [K17]. The phase transitions changing the length of the wormhole magnetic flux tubes defining the braid strands and making possible TQC would also make possible biocatalysis via reconnection of flux tubes and via $\hbar$ changing phase transitions changing the length of flux tube.

In this framework water and lipids molecules playing the role of lipids could have been present in very early stage since they emerge as a result of self-organization process and are not genetically determined.

Did life evolve in Mother Gaia's womb?

The proposed framework poses strong conditions on pre-biotic environment and one ends up to to interpretations for the notion of Mother Gaia's womb, which are by no means mutually exclusive.

1. Mother Gaia's womb as underground seas?

Braiding in the proposed sense requires the presence negatively charged polymers and membranes consisting of lipids or their analogs. Water seems to be necessary but also gel phase is needed since free water induces de-polymerization. The coherent structure of gel would be due to the braiding of distant molecules. The phase transitions of gel phase are good candidates for a basic mechanism of bio-control and would stabilize these polymers via the formation of structured water around them preventing hydrolysis. The developing life forms should be shielded from UV radiation and meteor bombardment.

The combination of these constraints leads to the idea that life as we define it could have evolved in the womb of Mother Gaia in underground seas with the Earth's crust shielding from UV and meteors. The necessary ingredients of biomolecules, in particular phosphates making possible phosphorylation making DNA and RNA charged and appearing also in hydrophilic ends of phospholipids, would have dissolved to the water from the ground. Cambrian revolution would have meant the burst of these highly developed life-forms to the Earth surface and resulting as a phase transition increasing the value of Planck constant for Earth's space-time sheet by a factor of two would have occurred. This would also provide a justification of Expanding Earth theory explaining the strange finding that the continents fits nicely together to form a single super continent covering entire Earth's surface if the radius of Earth is one half of its recent value and actually the same as the recent radius of Mars, which is now known to contain reservoirs of underground water.

2. Mother Gaia's womb as mantle-core boundary?

What about the period before the life in underground seas?

1. The plasma like aspects of cytoplasm suggests that some kind of plasma phase must have been present. Also the postulated Bose-Einstein condensates of bosonic ions at dark magnetic flux quanta represent kind of quantum plasma.

2. Plasmoids involving magnetic flux tubes and charged particles could have been predecessors of more complex molecular life forms and could have developed in the interstellar space. Their metabolism could have been based on universal metabolic energy quanta. Simple metabolic cycles and short term chemical storage of energy based on fusion and decay of simple molecules induced by say UV radiation from the nearby stars might have developed during this era. Quite high temperatures can be considered so that after the interstellar period this kind of life forms could have survived and developed in the hot interior of planets receiving their metabolic energy from radiation by high temperature plasma. A possible candidate for the womb of Mother Gaia is the mantle-core boundary, where intensive self-organization processes are expected to take place.

3. Ultimately the charged molecules must have come in contact with ordinary water in underground seas. One can imagine that the polymerization of the charged molecules and the formation of structured water around them stabilizing them and giving rise to a gel phase took place simultaneously in presence of metabolic energy feed.

The primordial womb containing plasmoid like life forms could have been located somewhere below the boundary at which $k = 137$ atomic space-time sheets transform to very hot $k = 131$ space-time sheets: this should occur when the thermal de Broglie wave length becomes equal to the p-adic length scale $L(131)$. The transition occurs above the crust-mantle boundary (1300 K). Mantle-core boundary (4000 K) is a good candidate for a seat of high-T life forms.

The dropping of O, C, N ions from the hot $k = 131$ space-time sheets to larger space-time sheets generates light at visible frequencies replacing solar light so that even intra-terrestrial counterpart of photosynthesis could develop. The dropping of oxygen atoms could make also possible development of oxygen based metabolism.

Magnetic flux quantum structure of the magnetosphere acting as a nervous system and a metabolic circuitry of the magnetic Mother Gaia could make possible controlled metabolism already during the pre-biotic period and allow to circumvent these difficulties.

Model for the genetic code

The emergence of genetic code is one of the basic mysteries of models for pre-biotic life. The exact A-G symmetry and slightly broken T-C symmetry of the genetic code strongly suggest that the

evolution of the triplet code occurred as a fusion of singlet and doublet codes. One ends up with a detailed model for how this happened by studying the structure of tRNA molecule carrying in its fossilized parts detailed information about the evolution of the code.

Nanno-bacteria [I130, I93] might correspond to some predecessor of the recent genetic code. Nanno-bacteria accompany mineral structures and actively manipulate them: this conforms with the view that mineral interfaces have been indeed important for the evolution of polymers.

Introns are the basic mystery of DNA. TGD predicts that language is a universal phenomenon appearing at level of eukaryotes. Memes represented as sequences of 21 DNA triplets and expressing themselves as field patterns associated with MEs would realized this universal language.

What makes possible the coherence of bio-chemical activities?

In TGD Universe the control of genome by magnetic body relies on magnetic flux sheets traversing through DNA strands [**?**, K15]. The model implies a generalization of the notion of gene. Super-genes correspond to sequences of genes inside single organism belonging to single magnetic flux sheet and organize like text lines at a page of a book. The expression of super-genes as an intentional action of magnetic body occurs therefore coherently at the level of entire organs. This explains to the miraculous coherence of bio-chemical activities at the level of single organism. Also hyper-genes involving genomes of several organisms, not necessary belonging to even same species, become possible. Collective gene expression at this level makes possible the development of co-operation and social structures and are predicted to be present already at the bacterial level.

Braiding defined by magnetic flux tubes of their wormhole counterparts carrying dark variants of charged particles seem to represent especially important part of the magnetic body and this leads to models of topological quantum computation and bio-catalysis.

5.3.3 Pre-Biotic Chemistry And New Physics

The emergence of symbolic representations at dark matter level is certainly the most fascinating possibility suggested by dark matter hierarchy.

Overall view

The most important implications can be deduced readily.

1. The dropping of ions and atoms between space-time sheets involves a liberation of zero point kinetic energy. By p-adic length scale hypothesis these energies define a fractal hierarchy of universal metabolic currencies which have not changed at all during evolution and are the same in the entire universe. The presence of the metabolic machinery from the beginning helps enormously in the attempts to understand how life has evolved.

2. Chiral selection resulting in bio-polymers having a definite handedness is a deep mystery in standard physics framework. TGD predicts entire hierarchy of standard model physics meaning scaled up variants of electro-weak and color physics and dark variants of these. The hierarchy of dark weak gauge bosons predicted by TGD imply strong parity breaking effects in arbitrarily long length scales above atomic length scales, and the presence of the chiral selection supports the view that also dark weak bosons play key role in bio-control. Indeed, charge entanglement generated by W MEs would be in central position in TGD based model for how magnetic bodies control biological bodies.

3. The emergence of life means emergence of symbolic representations (including names), and also what might be called "molecular sex". Formation of wormhole magnetic flux tubes between biomolecules having quark pair and its conjugate is an attractive candidate for this process and means coding of DNA nucleotides to quarks and antiquarks appearing as dark matter at the flux tubes. This leads to a new view about bio-catalysis based on the temporary dropping of the liberated proton to a larger space-time sheets and ensuing liberation of metabolic energy quantum kicking the complex formed by reactants over the potential wall separating it from the final state. A new view about water and its role in bio-catalysis

emerges. Stability considerations allow a general model for how first bio-polymers able to replicate emerged.

Dark matter and the emergence of symbolic representations at molecular level

The most important new physics element of pre-biotic chemistry has been already discussed and corresponds to the presence of dark matter hierarchy suggesting new views about hydrogen bond, water, and catalytic action. A highly attractive hypothesis is that symbolic representations at molecular level in the sense that quarks and antiquarks code for DNA nucleotides [K17] and also for amino-acids [K2].

Evolution of pre-biotic chemistry as a sequence of bifurcations

In his article "Biocosmology" [I64] Chris King discusses biochemistry from the point of view of mathematician using the notions of symmetry breaking and bifurcation. This discussion allows for a physicists to get a wider perspective to the complexities of biochemistry. In the following I modify the arguments of King to TGD framework. The first basic new element is that generation of new space-time sheets corresponds to a sequence of symmetry breakings.

Besides hydrogen C, N, and O atoms with charges 6, 7, and 8 are the most important elements appearing in basic bio-monomers. The bonds with hydrogen are formed between 1s and $2p^3$ orbitals. The covalent bonds between C, N, and O atoms are the bonds appearing in various bio-monomers like ribose. Also peptide bonds between C and N in amino-acid sequence are covalent bonds. In standard chemistry one can characterize the atom in given molecule by its electronegativity telling how effectively it attracts electrons.

Electronegativity increases in the sequence C, N, O so that the bonds are more and more polar. Also Si, P, and S in the next row of the periodic table form covalent bonds but the bond energy tends to be lower which reflects itself as lower boiling points. For instance, the boiling point of H_2S is below the freezing point of water). Consider now the bifurcations.

1. Polar-non-polar bifurcation is fundamental in biology. Non-polar molecules are hydrophobic and are not water-soluble whereas polar molecules are hydrophilic and water-soluble. For instance, the formation of biological membranes is based on hydrophobic character of the second ends of lipids. A rough characterization of amino-acids is by polar-non-polar dichotomy. Also DNA base stacking is based on polarity.

2. Second bifurcation corresponds to acid-base dichotomy. Acids are able to act as donors of positive and bases donors of negative charge. For instance, this allows to classify polar amino-acids to acidic and basic ones. A working hypothesis worth of studying is that many-sheeted physics is involved in the sense that the protons in acid and electrons in base have dropped to some larger space-time sheet from the atomic space-time sheet.

3. The third bifurcation corresponds to that between second and third row of the periodic table that is Na^+-K^+ and Mg^{++}-Ca^{++} bifurcations. The covalent bonds involving K and Ca are in general weaker. Na^+ concentration is higher outside cell whereas K^+ concentration is higher inside cell. Same applies to gel phase, a possible predecessor of cell membrane bound regions. Mg^{++} acts as stabilizer of polymers and Ca^{++} ions are key players in cellular and intracellular control. In particular, Ca^{++} waves appear in extremely wide range of frequencies and conduction velocities.

4. The fourth bifurcation corresponds to the d-orbital elements forming a catalytic group. Almost all transition elements Mn, Fe, Co, Cu, Zn are essential biological trace elements, promote pre-biotic synthesis and are optimal in their catalytic ligand-forming capacity and valency transitions. For instance, Zn^{2+} catalyzes RNA polymerization in pre-biotic synthesis and occurs in both polymerases and DNA binding proteins.

5. The fifth bifurcation corresponds to chiral symmetry breaking not easy to understand in standard model predicting extremely small parity breaking. There is empirical evidence such as circular polarization of light from the region of star formation in the constellation of Orion suggests that parity breaking occurs also in interstellar space. Also the amino-acids in Murchison meteorite were found to be dominantly left handed.

In TGD Universe the interpretation of bifurcations is not quite the same as in the world obeying standard chemistry.

1. The polar-non-polar bifurcation corresponds to hydrophilic-hydrophobic dichotomy. The model for protein folding and bio-catalysis relies on the hypothesis that wormhole flux tubes connect conjugate amino-acids. This process is analogous to base pairing. Stating it roughly, amino-acid and its conjugate correspond hydrophilic and hydrophobic amino-acid. This bifurcation is thus important from the point of view of molecular symbolism and bio-catalysis if is based on the coding of DNA are nucleotides and amino-acids by quarks and antiquarks at the ends of wormhole magnetic flux tubes connecting them to other molecules. The emergence of wormhole magnetic flux tubes could be seen almost as a definition of emergence of life. This might have happened already during prebiotic molecular evolution if water molecules have been present from the beginning.

2. Acid-non-acid bifurcation brings in protons and there is obviously a connection with the role of protons in the basic mechanisms of metabolism and catalysis. What is also essential is the role of negative charge of bio-polymers making bio-polymers critical against local deformations so that a wide repertoire of catalytic actions using $\hbar$ changing phase transitions of wormhole magnetic flux tubes and their reconnections becomes possible. Phosphate ions would not serve as batteries of metabolic energy but make bio-polymers sensitive to catalytic actions.

3. Fifth bifurcation is difficult to understand in standard physics framework but is consistent with the presence long ranged weak fields predicted by TGD and possibly associated with dark matter. This bifurcation is not the last one in TGD Universe since already plasmoids identified as rotating magnetic systems break parity because the sign of the charge density generated by the induced radial ohmic current depends on the orientation of rotation and only the second orientation is favored energetically. W MEs induce charge entanglement giving rise to plasma oscillation patterns in turn inducing various physiological waves. This mechanism can be used as a control tool by magnetic bodies at various levels of hierarchy. Long range weak forces due to the exotic ionization of atomic nuclei could provide a tool for controlling conformations of nucleic acid polymers. Same applies to kaolinite clays consisting of Al, Si, O suggested to be of biological importance (Al can have three different states at a given lattice site): in this case the state of Al atoms in the lattice might be manipulated using weak forces.

4. The hierarchy of bifurcations defines also a hierarchy of decreasing cyclotron frequencies. The cyclotron frequencies would be associated with both with Bose-Einstein condensates of ordinary and exotic bosonic ions at magnetic flux sheets. For the bosonic ions cyclotron frequencies in the $B_{end} = 2B_E/5$ are in alpha band and in TGD Universe they play a fundamental role in communications to and control by magnetic body using hierarchy of generalized EEGs. Ca^{++} and other waves associated with bosonic ions are of special importance in the bio-control by magnetic body using plasmoids and plasma oscillation patterns.

What selected the bio-molecules?

The extremely low probabilities for the selection of bio-molecules from a super-astrophysical number of alternatives represents one of the bottleneck problems of biology relying on the prevailing view about biochemistry. The notion of braid could resolve this problem.

Suppose that the presence of braids distinguishes between living and dead matter, that the four nucleotides are mapped to colored braid strands (that is to 2 quarks + 2 anti-quarks), and that a given amino-acid is mapped in a non-deterministic manner to one of the 3-braids associated with the DNA triplets coding for it. Braids could be associated besides DNA, amino-acids, and lipids also to other bio-molecules and define more general analogs of genetic codes as correspondences between bio-molecules able to react.

The implication would be that the step of catalytic reactions bringing together the catalyst and reactants would occur by a temporary reduction of Planck constant only for subsets of bio-molecules connected by braid strands and the pattern of braid strands involved would define the

geometro-dynamical pattern of the reaction. The outcome would be a selection of very restricted subsets of bio-molecules able to form reaction networks and of reaction pathways. This would imply Darwinian selection of subsets of bio-molecules able to co-exist and dramatically enhance the probability for the emergence of life as we know it.

One challenge is to predict what kind of braids can begin from a given bio-molecule, say nucleotide or amino-acid. The physicist's guess would be that the (electromagnetic only?) interaction energy between bio-molecule and given pattern of wormhole contacts having quark and anti-quark at its throats should select the preferred braids as minima of the interaction energy. How closely the presence of hydrogen bond relates to this is also an interesting question.

Polymerization, dehydration, phosphorylation, and new physics

The generation of phosphate polymers and polymers in general occurs by dehydration which quite generally seems to involve dropping of a proton to larger space-time sheet and liberation of metabolic energy quantum. It is interesting to find how one could understand these processes in TGD framework. Since the notion of wormhole magnetic flux tube playing a central role in the model of DNA as topological quantum computer and in the model of bio-catalysis, it is natural to look whether the basic steps of these processes could be understood in this conceptual framework.

1. $ATP \to ADP$ process

AMP, ADP, ATP are phosphorylated RNA nucleosides [I3] and the hydrolysis of ATP to ADP [I5] plays a key role in the metabolism. Obviously also the molecules XMP, X=U, C, G are important biologically. Each PO_3 in ATP corresponds to one unit of negative charge except for the last one which carries two units of negative charge. According to the standard chemistry $ATP \leftrightarrow ADP$ corresponds to the hydrolysis

$$ATP^{4-} + H_2O \leftrightarrow ADP^{2-} + P_i$$

where P_i denotes orthophosphate HPO_4^{-2}. In ADP the last phosphate group is $HO-PO_2^{-2}$ rather than $O = PO_2^{-2}$ as in the case of ATP.

The actual process is however much more complex than this.

1. The process involves several steps such that energy is liberated in two steps in which the change of Gibbs free energy is $\Delta G = .42$ eV and $\Delta G = .31$ eV making altogether.73 eV, which should closely relate to the liberated metabolic energy.

2. Three protons are accelerated in electric field during the generation of ATP. The interpretation would be in terms of driving of electrons from larger space-time sheet to $k = 137$ atomic space-time sheet. If the larger space-time sheet corresponds to $k = 139$, the increment of the zero point kinetic energy of proton is $(1 - 1/4) \times \times E_0(137) = .375$ eV for $E_0(137) = .5$ eV of metabolic energy quantum. Three protons would give net zero point kinetic energy increment of 1.125 eV which is higher than $\Delta G_{tot} = .73$ eV. The explanation of the discrepancy should relate to Coulomb binding energy of protons with ATP and F_1. This interpretation conforms with the observation that the liberated energy is higher for the third proton.

Consider now a more detailed model for the process. The binding of ATP to the catalytic site involves several steps.

Step 1: The binding $ATP + F_1 \to$ATP$\cdot F_1$ to the catalyst site is a complex process involving the break-up of the hydrogen bonds between cellular water and ATP molecule and cell water and catalyst site and generation of hydrogen bonds between catalyst site and ATP molecule. In TGD framework this means that protons can be kicked to and dropped back from atomic space-time sheets. Only the net number of protons dropped however matters.

This process involves liberation of Gibbs free energy about $\Delta G_{ATP} = .42$ eV. It was earlier believed that this energy is liberated instantaneously but the findings about the behavior of the F_1 motor coupled to dissipative load, lead Oster and Wang to suggest that the process is more complex and starts from a loose binding and ending up to a strong binding [I123].

Step 2 Hydrolysis: $F_1\cdot$ATP$\to F_1\cdot$ADP$\cdot P_i$. The change of free energy is small during this step: $\Delta G \sim 0$.

Step 3: Ortophosphate is released from the catalyst site: $F_1 \cdot \mathrm{ADP} \cdot P_i \to F_1 \cdot ADP + P_i$. Free energy $\Delta G \sim .31$ eV is liberated at this step.

Step 4: ADP is released from the catalyst site: $F_1 \cdot \mathrm{ADP} + P_i \to F_1 + ADP + P_i$. $\Delta G \sim 0$ holds true also for this process.

This picture suggests that the notion of the high energy phosphate bond is not quite correct as suggested also by some empirical findings [D11, D5], [I106]. The metabolic energy could be stored as the zero point kinetic energy of protons rather than in phosphate bonds. Perhaps one fundamental function of phosphates would be to make DNA and RNA polymers charged in turn making possible the formation of wormhole magnetic flux tubes and braiding making possible a wide repertoire of catalytic actions. Phosphorylation of say protein could mean a reconnection process for magnetic flux tubes with flux tubes attached to O= atom transferred from ATP to the target to which phosphate is attached.

2. Model of $ATP \to ADP$ based on wormhole magnetic flux tubes

Consider first the basic philosophy behind model.

1. In the model of DNA as topological quantum computer XMPs, $X = A, T, C, G$ can be connected to oxygen atoms by wormhole magnetic flux tubes having quark and antiquark at opposite throats of wormhole contact and charge conjugated quark-anti-quark pairs at the ends of the flux tubes. Dark u quark and its charge conjugate code for A, T and d quark and its conjugate for G, C so that the conjugation for nucleotides corresponds to charge conjugation for quarks and $A - G$ and $T - C$ symmetries of the third nucleotide of the codon to isospin symmetry.

2. Basic bio-catalytic processes are identified as a reconnection of the wormhole magnetic flux tubes and change of the length of the flux tube induced by the change of the value of Planck constant associated with it. It would not be too surprising if this kind of mechanism were involved also in $ATP \to \mathrm{ADP} + P_i$. The reason for the special role of ATP among XTP might be that the positive charge $q(u) = 2/3$ of u-quark maximizes the attractive interaction between u quark and phosphate.

3. Flux tubes connect to oxygen atoms in the proposed model of bio-catalysis and protein folding [K2]. The model is relies on ideas inspired by the model of DNA as topological quantum computer [K17]. In this model hydrogen bonds are assumed to correspond or to be accompanied by (wormhole) magnetic flux tubes. Also flux tubes connecting acceptor atoms or molecules of hydrogen bonds are assumed to be connected long flux tubes and represent genuinely new physics. Examples of acceptors are $O =$ atoms in phosphates and amino-acids and aromatic rings in DNA and also in some amino-acids. The model for protein folding has tight connections with existing chemistry and leads to a very simple criterion for the formation of hydrogen bond between $N - H$ and $O =$ in the constant part of amino-acid and to a proposal for the folding code.

4. DNA as TQC model gives further constraints. The structure of the phospholipids suggest that in the case DNA nucleotides long flux tubes connect the aromatic ring of the nucleotide to the $O =$ atom at the hydrophilic end of the lipid acting as a standard plug which in turn can be connected to another acceptor and eventually terminates to a donor of hydrogen bond. The detailed charge structure of the aromatic ring(s) should determine the quark-nucleotide correspondence. The connection line to the lipid could involve several intermediate $O =$ plugs and the first plug in the series would be the $O =$ atom of the monophosphate of the nucleotide. Not surprisingly, phosphorylation would be absolutely essential for the operation of DNA as topological quantum computer. $O = -O =$ flux tubes could also act as switches inducing a shortcut of the flux tube connection by reconnecting with a hydrogen bond connecting two water molecules. This is an essential step in the model for how DNA acts as topological quantum computer.

A possible model (perhaps the simplest one found hitherto) for the reaction $ATP \to ADP + P_i$ is based on the assumption that it splits a flux tube connection defining strand of a braid defining topological quantum computation. A change of the hardware of topological quantum computer would be therefore in question.

1. Suppose that ATP defines a standard plug in flux tube connections. This would mean that aromatic ring and the oxygen atoms $O = 1$, $O =_2$, and $O =_3$ of the phosphates are connected by magnetic flux tubes to some molecules. These flux tubes represent genuinely new physics in accordance with the fact that "high energy phosphate bonds" are not really understood in the standard chemistry. Suppose that the flux tube associated with $O =_2$ connects it with $O =_3$ and defines the somewhat mysterious high energy phosphate bond. This bond would be formed during cellular breathing and the metabolic energy would go the formation of the magnetic flux tube between $O =_2$ and $O =_3$. Suppose that $O =_1$- the innermost O has a flux tube connecting it to catalyst in this case F_1.

2. At Step 1 F_1 and ATP molecule would find each other. This would be due to the shortening of the magnetic flux tube connecting them and associated with the innermost phosphate. This would liberate.42 eV of metabolic energy.

3. At Step 2 hydrolysis would induce $F_1 \cdot \mathrm{ADP} \cdot P_i \rightarrow F_1 \cdot ADP + P_i$. Since no energy is released at this step, there is temptation to conclude that a reconnection of $O_2 - O_2$ fluc tube and a flux tube associated with catalyst occurs. ADP and P_i fors now a high energy bond with catalyst. the reconnection of $(O =_2) - (O =_3)$ flux tube with the hydrogen bond connecting two water molecules leads to the disappearance of this flux tubes so that the incoming and outgoing the flux tubes are shortcut by $(O =_2) - -H - (OH)$ *resp.* $(O =_3) - -H - (OH)$ hydrogen bonds (connection to ground is the analog in circuit theory). This would correspond in the usual terminology the liberation of the third phosphate: $ATP \rightarrow ADP + P_i$. P_i however remains at the end of flux tube to be attached later to another ADP. The resulting bonds to water molecules would have low energy and the liberated energy would be usable metabolic energy. In this case the function of the splitting would be purely energetic.

4. One can imagine also a function related to information processing. P_i could be also attached to some other molecule in phosphorylation process so that the outcome would be a reconnection in the web of magnetic flux tubes. Phosphorylation is infeed known to play a key role in activation and deactivation of proteins and in the formation of signal pathways. In the case of AMP associated with DNA there would be only single flux tube involved and it could connect DNA nucleotide to nuclear or cell membrane.

5. The process involves also hydration. $(OH)^-$ ion joins to the third P to give P_i^{-3} and H^+ to $O - P$ in second P to give $H^+ - O$ in ADP^{-1}. The exchange of electron would lead to the final state $ADP^{-2} + P_i^{-2}$.

A possible model for the dropping of protons would be following.

1. It is absolutely essential to realize that F_1 is an open system and that naive thermodynamic considerations can lead to misunderstandings. In particular, the notion of high energy phosphate bond does not make sense. The source of the metabolic energy is the chemical energy used to drive protons to the atomic space-time sheets of F_1. The function of the large negative charge of ATP is to increase the rate for the binding of ATP^{-4} to F_1. In the classical picture the binding to F_1 is followed by the dropping of two protons to larger space-time sheet. The value of the metabolic quantum could be reduced from .5 eV to about .21 eV by the Coulomb energy of proton with PO^{4-}. The Coulomb binding energy of the remaining protons at F_1 with $ADP + P_i$ is smaller and the dropped proton liberates larger energy about .31 eV. In quantum picture the division of the process to this kind of sequence might not be a good approximation.

2. One function of the $ATP \rightarrow ADP$ would be to induce the dropping of the third proton from F_1 space-time sheet. Second function would relate to the topological quantum computation like process since the decay would correspond to a splitting of a braid strand coming to the aromatic ring of A and proceeding along string defined by the ring and three $O =:$ s of phosphates and continuing further. This would make possible TQC as a braiding for both halves of the split flux tubes. After the reconnection the total braid structure would be different. Quite generally, reconnection process would make possible to modify the hardware of topological quantum computer.

3. The reason for why P_i leaves the catalyst site and proton is dropped (step 2) should be the in-stabilization of the bound state of positively charged proton with $ADP^{-2} + P_i^{-2}$ which does not have so strong Coulomb interaction energy with proton as ATP^{-4} As a consequence, proton can drop to the larger space-time sheet.

4. What remains open are the details of the transformation of the chemical energy to zero point kinetic energy of protons. Remote metabolism suggests that protons send negative energy phase conjugate photons to the geometric past inducing a transition of an energy carrying molecule to a lower energy state (zero energy ontology gives justification for this picture). This would mean the failure of the standard description in terms of reaction kinetics. The catabolism of nutrients is the eventual provider of the metabolic energy and the coenzyme nicotinamid adenic dinucleotide NAD^+ [I30] receives electron and the energy liberated in the catabolic reaction. In the proposed framework it is not an surprising that NAD^+ is analogous to RNA dinucleotide (perhaps as remnant from RNA era when dinucleotides defined the 2-codon code) and consists of two phosphates and adenine and nicotinamide nucleosides. The oxidation reaction $NADH \to NAD^+$ in turn liberates this energy. Protons could gain their energy by sending negative energy photons to $NADH$. Negative energy photons would propagate along "topological light rays" parallel to the flux tubes connecting the system in a precisely targeted manner to NADH aromatic rings. Alfven waves propagating along magnetic field lines would be the standard electrodynamics counterpart for these topological light rays.

Many details of the process remain open but it would seem that the key ideas of TGD based quantum vision about living matter are fused together in rather detailed manner in this picture.

3. Polymerization of DNA and RNA

The polymerization of RNA and DNA by dehydration involves the fusion of $PO_4H_2^{2-}$ phosphate molecule with ribose. In this process the stub...-O-H of the phosphate ion combines with H-O-C-... stub of ribose (here C is the carbon atom not belonging to the ribose cycle). This gives rise to..-O-$(H\text{-}O)^-$-C-... plus proton dropping to a larger space-time sheet and liberating metabolic energy quantum. Too large negative charge of three units makes the complex unstable and $(H\text{-}O)^-$ ion splits out. Metabolic energy quantum might be also used in the process.

DNA as TQC model would suggest a possible interpretation. Perhaps the polymerization creates flux tube connections from nucleotides to to other molecules -say lipid molecules of the nuclear membrane or some catalyst molecule- via the attached O= attached to phosphate. Also the phosphorylation of proteins could involve this kind of reconnection process creating flux tube connection of protein with some other molecule.

Hydration de-stabilizes long polymers unless there is a continual feed of protons to the atomic space-time sheets. This could be achieved by irradiation with photons with energy equal to the metabolic energy currency. Situation changes also if water is ordered/structured water, in liquid crystal form, or as ice, and therefore unable to provide the water molecules needed for the hydration. Stabilization of RNA and DNA polymers could be achieved in this manner in gel phase.

Clay structures are known to act as catalyzers of RNA polymerization. The general model of catalysis based on the recombination and $\hbar$ changing transition for magnetic flux tubes should explain also this.

Why DNA is stable inside cell nucleus?

Inside membrane bound surface both DNA and RNA nucleotides and polymers are stable. The un-stability of the DNA nucleotides and polymers outside membrane bound surfaces could involve many-sheeted physics.

1. What one expects that DNA transforms to RNA unless it is inside a membrane bound region. A possible reason is that water molecule is needed to transform DNA to RNA but not available inside membrane bound structure where water is structure water in gel phase.

2. In the case of A, G, and C nucleotides DNA$\to$ RNA transformation means simply an addition of one oxygen atom to the de-oxyribose ring, that is replacement of one C-H with C-O-H.

If ordinary water is present this could be achieved by the dissociation of the water molecule to $OH^- + H^+$ followed by the replacement of C-H in the de-oxyribose cycle with C-OH^- so that a negative1ly charged ribose results. The outcome is free hydrogen atom. If H^+ drops to a larger space-time sheet, the liberated zero point kinetic energy is of order .5 eV. This process is basically the same which should occur when single ATP molecule is utilized in metabolism.

3. In the case of T nucleotide also CH_3 group differentiating T from U must be de-attached. This is achieved if the hydrogen atom from the water molecule is taken by the de-attached CH_3 group to give CH_4 molecule. As a result a negatively charged U results. Inside cell nucleus or in gel phase this process is not favored because the water is in liquid crystal form and it costs energy to take the needed H_2O molecule from it.

5.3.4 Could High Energy Phosphate Bond Be Negentropic Bond With Negative Binding Energy?

Most people assign the word "love" to the word "life" as their first association. There is a notable exception to this: scientists including biologists. Un-educated layman might however wonder whether one can understand life without identifying any physical counterpart for this notion (, which could be replaced with that of compassion, sex, or ability to act synergetically or just X if some of these notions sounds less un-scientific). Certainly the word "love" stimulates a deep feeling of disgust in a reductionistically conditioned scientist. But isn't the duty of scientist to win this kind of feelings and try to see whether this identification might be possible after all? The prize could be high: the understanding of what distinguishes between living and dead matter could change the entire culture. Who knows, maybe it could be possible to identify some poorly understood fundamental biological process allowing a quantitative model using a guess for what this physical correlate could be. The basic step of metabolism is at the core of life and indeed poorly understood, and I shall argue that the identification of the negentropic entanglement as the counterpart for the notion of love could allow to model quantitatively what happens in this process.

Basic ideas

Before continuing general motivating comments about implications of negentropic entanglement (see **Fig.** `http://tgdtheory.fi/appfigures/cat.jpg` or **Fig. ??** in the appendix of this book) are in order.

1. Ordinary bound states are stable because they have positive binding energy. One can visualize this kind of binding as a jail: the second particle resides near the bottom of a potential well. Organized marriage is a social analogy for this situation. Negentropic entanglement makes possible bound states for which binding energy can have and perhaps even has always a wrong sign. The state is not prevented from decaying to free particles in state function reduction by energy conservation: Negentropy Maximization Principle (NMP) [K32] takes care that they remain correlated. The social analogy would be a voluntary marriage based on love. Partners are completely free to leave but want to stay together. One implication could be explanation for the stability of highly charged basic molecules of life such as DNA and ATP.

2. The presence of the negentropic entanglement implies the directedness of the biological processes since the outcome of the state function reduction would be far from random since the behavior of negentropic bonds could be almost deterministic. In the case of time-like entanglement this would select only particular initial final state pairs so that determinism would emerge also in this sense and could lead to almost deterministic irreversible cellular automaton behavior characteristic for the living matter very different from the reversible determinism of classical physics and very difficult to understand in quantum context.

3. The determinism would of course be only partial and would allow volition not spoiled by randomness of quantum jump. This would provide a general explanation for the ability of the living matter to overcome the second law basically implied by quantum randomness

predicted by the standard quantum theory. This would happen in time scales shorter than the time scale of the appropriate causal diamond (CD) only but one would have hierarchy of CD meaning that in arbitrary long time scales there are levels of hierarchy at which second law is broken. The hierarchy of Planck constants would be also crucial since it would allow zooming up to arbitrarily long time scale. Non-equilibrium thermodynamics and cellular automaton models could be seen as phenomenological descriptions for the actual breaking of second law in the intersection of real and p-adic worlds.

4. High energy negentropic bonds need not be present only in phosphates. O=s are are present in all important biomolecules. Phosphates are present in DNA. Each peptide bond in amino-acid polymer contains O=. Also sugars contain it. Maybe O= indeed acts as a universal plug defining then ends of negentropic flux tube bonds between biomolecules. For instance, protein folding for which a possible model is discussed in [K2] from different view point could be more or less deterministic cellular automaton like process if the bonds are negentropic. Negentropic entanglement would also guarantee the stability of the folding pattern. Certainly the assumption that the process is random -as standard quantum theory would suggest- leads to Levinthal paradox stating that the rate of the process is quite too slow. The simplest possibility is that the flux tube bonds are between O=s of subsequent amino-acids before folding and the folding process involves formation of reconnections possibly drawing by a reduction of Planck constant certain amino-acids near to each other. O=s could also act as plugs connecting protein to other biomolecules. One must however notice that many neurotransmitters, hallucinogens, and alcohol having strong effects on consciousness have O-H groups instead of O=s. This inspires the question what happens to the flux tube in O=$\leftrightarrow$ O-H process.

General formulation of the model

Consider now the model. High energy phosphate bond (see `http://tinyurl.com/yar7zv7j`) [I18] assigned with the two outer-most phosphates of ATP (see `http://tinyurl.com/clnu4`) [I3] is fundamental for the basic processes in living matter. The $ATP \to ADP + P_i$ liberates metabolic energy loaded to ATP in the cellular respiration process (see `http://tinyurl.com/yyvrbp`) [I8] or its equivalent and occurs again and again and defines a kind of Karma's cycle in living matter. The phosphate bond is assumed to have a high energy content liberated as ATP is hydrated to ADP (see `http://tinyurl.com/5w7cud`) [I2] and phosphate ion (see `http://tinyurl.com/2xbv3y`) $P_i = PO_4^{3-}$ [I37]. The notion of high energy phosphate bond has been however challenged as being meaningless [D11, D5], [I106].

1. One can of course consider a high energy bond for which the interaction potential looks like a well at the top of mountain and spin glass degeneracy of quantum TGD would certainly allow to consider this kind of notion. I do not know whether models realizing this idea concretely have been really constructed.

2. My earlier proposal for $ATP \to ADP + P_i$ process is inspired by the notion of many-sheeted space-time and p-adic length scale hypothesis making sense in the intersection of real and p-adic worlds and involves the dropping of protons (or electrons) to larger space-time sheets and driven back in oxidative metabolism. The energy liberated in this process corresponds to the zero point kinetic energy of protons (or electrons), which is smaller at the larger space-time sheet. The maximum value of zero point kinetic energy is predicted to be $E_0 \simeq .5$ eV for $k = 137$ in the case of proton and for $k = 148$ in the case of electron (for electron the energy would be by a factor $2^{-11}m_p/m_e \simeq .94$ smaller).

   In many-sheeted space-time particles topologically condense at all space-time sheets having projection to given region of space-time so that this option makes sense only near the boundaries of space-time sheet of a given system. Also p-adic phase transition increasing the size of the space-time sheet could take place and the liberated energy would correspond to the reduction of zero point kinetic energy. Particles could be transferred from a portion of magnetic flux tube portion to another one with different value of magnetic field and possibly also of Planck constant h_{eff} so that cyclotron energy would be liberated. In the following only the "dropping" option is discussed.

3. With an inspiration coming from DNA as topological quantum computer model [K17] I have also proposed that the magnetic flux tubes connecting bio-molecules to each other define a kind of Indra's net plays a key role in the biological information processing. For instance, topological quantum computations could be realized in terms of braids formed by flux tubes [K17, K2]. O=: s associated with phosphates wold serve as universal plugs to which flux tubes could be connected connecting intronic nucleotides and lipid layers of nuclear or cell membrane. In particular, the innermost O= of ATP could be connected by a flux tube to any biomolecule needing metabolic energy- say some catalyst or the F_1 machine central for energy metabolism. The reduction of Planck constant would bring ATP and biomolecule near each other and lead to a formation of a weakly bound state making catalytic processes possible. The outer O=: s of the ATP molecule could be connected by a flux tube to each other, which could be rather long loop. This flux tube could provide the new physics realization of the high energy phosphate bond.

4. ATP (P_i) has 4 (3) units of negative charge and at least ordinary layman might wonder why this does not induce instability. Similar problem is encountered in the case of DNA, which contains two units of negative charge per nucleotide. This particular problem is regarded as completely real. The idea about life as something in the intersection of real and p-adic worlds [**?**] raises the question whether these high energy states could be made possible by the presence of negentropic bonds- most naturally associated with the flux tubes with large $\hbar$. This love marriage would stabilize ATP, ADP, and DNA and other charged biomolecules. The presence of phosphates would be a clear-cut signature of this stabilization mechanism. Also proteins involve phosphates playing a key role in the bio-control: typically phosphorylation activates or de-actives the protein and is also involved with the generation of signal pathways. Why this happens would be easy to understand in Indra's net model.

5. In $ATP \to ADP + P_i$ transformation the energy carried by the negentropic bonds would be liberated but leave the flux tube bonds negentropic. Cell respiration would take care of the loading of the batteries with negentropic metabolic energy. This would involve also the kicking of protons back to the smaller space-time sheets. Also the molecular lovers ADP and P_i would find each other again as the Planck constant for the flux tube connecting them would be reduced during the cellular respiration transform ADP and P_i back to ATP.

Quantitative estimates

Consider now a more detailed model for $ATP \to ADP + P_i$. The binding of ATP to the catalytic site involves several steps. I have described them in the previous section and in the following add to this template the interpretation suggested by the proposed picture.

1. **Step 1** : The binding $ATP + F_1 \to ATP \cdot F_1$ to the catalyst site is a complex process involving the break-up of the hydrogen bonds between cellular water and ATP molecule and cell water and catalyst site and generation of hydrogen bonds between catalyst site and ATP molecule. In TGD framework this means that protons can be kicked to and dropped back from atomic space-time sheets. Only the net number of protons dropped however matters.

   This process involves a liberation of Gibbs free energy per single attachment, which is about $\Delta g_{ATP} = .42$ eV. It was earlier believed that this energy is liberated instantaneously but the findings about the behavior of the F_1 motor coupled to dissipative load, lead Oster and Wang to suggest that the process is more complex and starts from a loose binding and ending up to a strong binding [I123].

   Comment: One can question the assumption that strong binding is generated. Instead of binding proton or electron would be dropped to a larger space-time sheet and liberate zero point kinetic energy.

   (a) The simplest interpretation in the proposed picture is that the negentropic flux tube connecting ATP and F_1 molecule and behaving as high energy phosphate bond associated with the innermost O= is contracted via the reduction of Planck constant. Then proton is dropped from $k = 137$ space-time sheet to a much larger space-time sheet and liberates metabolic energy quantum $E(137) \simeq .5$ eV. Another possibility is that electron

at $k = 148$ space-time sheet is dropped. This process would replace the instantaneous generation of binding energy and in zero energy ontology the time scale for this process would correspond to the time scale of appropriate causal diamond (CD).

(b) Instead of single particle energy macroscopic Gibbs energy $G = E + PV - TS$ is the useful notion now since macroscopic quantities of matter are studied and pressures and temperature are typically constant in the situations considered ($dG = -SdT + VdP$). G is minimized for constant T and P prevailing in the situation considered.

(c) In the attachment of ATP to catalyst S is reduced and a good guess is that volume is not affected so that PV term does not change. From this one can deduce that the liberated energy per catalyst particle -call it $\Delta e = e_i - e_f = \Delta g - T\Delta s$ (i and f refer to initial and final states) satisfies $\Delta e > \Delta g = .42$ eV.

(d) One must estimate the value of Δe. The attachment reduces the kinetic energy of relative motion of catalyst and ATP to zero. If it makes sense to speak about thermal equilibrium for ATP an catalyst in translational degrees of freedom the reduction of kinetic energy is $\Delta e_K = 3T/2$, which is of order.045 eV at room temperature. Whether this energy remains in the catalyst-ATP system or is it liberated in the process is not clear. The energy liberated in the dropping of the proton or electron gives a contribution $\Delta e = E_0 = .5$ eV. This gives the condition

$$\Delta g_1 = E_0 + 3T/2 - T\Delta s = .42 \ \ eV \ \ . \tag{5.3.1}$$

If the liberated kinetic energy remains in the system, the first guess is $\Delta e = E_0 = .5$ eV, where E_0 is the nominal value of zero point kinetic energy. This would give for $T\Delta s$ the estimate $T\Delta s = .08$ eV about 3 times thermal energy corresponding to three translational degrees of freedom. This looks rather reasonable order of magnitude estimate.

(e) NMP suggests-maybe even requires- that the bond remains negentropic. The binding energy associated with ATP- catalyst binding could be small- of the order of thermal energy about .045 eV.

2. **Step 2** Hydrolysis: $F_1 \cdot ATP \to F_1 \cdot ADP \cdot P_i$. The change of free energy is small during this step: $\Delta G \sim 0$.

Comment: The simplest option explaining the fact that the change of energy is small is that hydrolysis leaves the flux tube between outer O=: s of ATP intract and removes only the P-O-P bond. This flux loop could have rather large $\hbar$.

3. **Step 3** : Ortophosphate is released from the catalyst site: $F_1 \cdot ADP \cdot P_i \to F_1 \cdot ADP + P_i$. Free energy $\Delta G \sim .31$ eV is liberated at this step.

Comment: The simplest option is that the negentropic flux tube liberates its energy but remains negentropic. The increase of Planck constant might be involved.

(a) The value of Δe is now smaller than ΔG, which suggests that the metabolic energy quantum in the case of proton corresponds to $\Delta e = E(139) \simeq .25$ eV. The average change of kinetic energy can be assumed to be equal to thermal energy in final state and is same as above. This gives the condition

$$\Delta g_2 = E_0/2 - 3T/2 + T\Delta s = .32 \ \ eV \ \ .$$

(b) By adding this equation with the similar equation for Step 1 (see Eq. 5.3.1) one obtains the condition

$$\Delta g_1 + \Delta g_2 = 3E_0/2 = .74 \ \ eV \ \ .$$

This gives $E_0 = .49$ eV so that the model seems to be internally consistent.

4. **Step 4** : ADP is released from the catalyst site: $F_1 \cdot ADP + P_i \rightarrow F_1 + ADP + P_i$. $\Delta G \sim 0$ holds true also for this process.

   Comment: $\hbar$ increases back to the original value for the innermost flux tube which could it still have small positive energy and be negentropic.

The model would predict that ADP and P_i and remain highly correlated (connected by flux tubes) as do also AXP and F_1. These predictions should be testable by marking ADP and P_i of ATP with the same "color" (say radioactively) and finding whether the colors of ADP and P_i remain the same during the subsequent cycles or whether they mix immediately. These love affairs at molecular level could be modified only by reconnections of flux tubes as also in human relationships. For instance, two ADPs could exchange their P_is or F_1s. Negentropic entanglement could guarantee the highly organized and directed nature of basic bio-catalytic processes.

5.3.5 Water Memory And Braids

There are several grand visions about TGD Universe. One of them is as a topological quantum computer in a very general sense. This kind of visions are always oversimplifications but the extreme generality of the braiding mechanism suggest that also simpler systems than DNA might be applying TQC.

Water memory: general considerations

With few exceptions so called "serious" scientists remain silent about the experiments of Benveniste and others relating to water memory [I53, I55, I71, I72] in order to avoid association with the very ugly word "homeopathy".

The Benveniste's discovery of water memory initiated quite dramatic sequence of events. The original experiment involved the homeopathic treatment of water by human antigene. This meant dilution of the water solution of antigene so that the concentration of antigene became extremely low. In accordance with homeopathic teachings human basophils reacted on this solution.

The discovery was published in Nature and due to the strong polemic raised by the publication of the article, it was decided to test the experimental arrangement. The experimental results were reproduced under the original conditions. Then it was discovered that experimenters knew which bottles contained the treated water. The modified experiment in which experimenters did not possess this information failed to reproduce the results and the conclusion was regarded as obvious and Benveniste lost his laboratory among other things. Obviously any model of the effect taking it as a real effect rather than an astonishingly simplistic attempt of top scientists to cheat should explain also this finding.

The model based on the notion of field body and general mechanism of long term memory allows to explain both the memory of water and why it failed under the conditions described.

1. Also molecules have magnetic field bodies acting as intentional agents controlling the molecules. Nano-motors do not only look co-operating living creatures but are such. The field body of molecule contains besides the static magnetic and electric parts also dynamical parts characterized by frequencies and temporal patterns of fields. To be precise, one must speak both field and relative field bodies characterizing interactions of molecules. Right brain sings-left brain talks metaphor might generalize to all scales meaning that representations based on both frequencies and temporal pulse with single frequency could be utilized.

   The effects of complex bio-molecule to other bio-molecules (say antigene on basofil) in water could be characterized to some degree by the temporal patterns associated with the dynamical part of its field body and bio-molecules could recognize each other via these patterns. This would mean that symbolic level in interactions would be present already in the interactions of bio-molecules.

   If water is to mimic the field bodies of molecules using water molecule clusters, at least vibrational and rotational spectra, then water can produce fake copies of say antigenes recognized by basofils and reacting accordingly.

   Also the magnetic body of the molecule could mimic the vibrational and rotational spectra using harmonics of cyclotron frequencies. Cyclotron transitions could produce dark photons,

whose ordinary counterparts resulting in de-coherence would have large energies due to the large value of $\hbar$ and could thus induce vibrational and rotational transitions. This would provide a mechanism by which molecular magnetic body could control the molecule. Note that also the antigenes possibly dropped to the larger space-time sheets could produce the effect on basofils.

2. There is a considerable experimental support for the Benveniste's discovery that bio-molecules in water environment are represented by frequency patterns, and several laboratories are replicating the experiments of Benveniste as I learned from the lecture of Yolene Thomas in the 7: th European SSE Meeting held in Röros [J11]. The scale of the frequencies involved is around 10 kHz and as such does not correspond to any natural molecular frequencies. Cyclotron frequencies associated with electrons or dark ions accompanying these macromolecules would be a natural identification if one accepts the notion of molecular magnetic body. For ions the magnetic fields involved would have a magnitude of order.03 Tesla if 10 kHz corresponds to scaled up alpha band. Also Josephson frequencies would be involved if one believes that EEG has fractally scaled up variants in molecular length scales.

3. Suppose that the representations of bio-molecules in water memory rely on pulse patterns representing bit sequences. The simplest realization of bit would be as a laser like system with bit 1 represented by population inverted state and bit 0 by the ground state. Bits could be arranged in sequences spatially or by variation of zero point energy defining the frequency: for instance increase of frequency with time would define temporal bit sequence. Many-sheeted lasers are the natural candidates for laser like systems are in question since they rely on universal metabolic energy quanta. Memory recall would involve sending of negative energy phase conjugate photons inducing a partial transition to the ground state. The presence of metabolic energy feed would be necessary in order to preserve the memory representations.

Water memory in terms of molecular braidings

It is interesting to look water memory from the point of view of TQC. Suppose that the molecules and water particles (space-time sheet of size of say cell length scale) are indeed connected by color flux tubes defining the braid strands and that splitting of the braid strands can take place so that water flow can gives rise to a braiding pattern and TQC like process.

The shaking of the bottle containing the diluted homeopathic remedy is an essential element in the buildup of water memories also in the experiments of Benveniste [I71]. Just like the vigorous flow of sol near the inner monolayer, this process would create a water flow and this flow creates a braiding pattern which could provide a representation for the presence of the molecules in question. Note that the hardware of braiding could carry information about molecules (cyclotron frequencies for ions for instance.

The model for the formation of scaled down variants of memories in hippocampus discussed above suggests that each half period of theta rhythm corresponds to TQC followed by a non-computational period during which the outcome of TQC is expressed as 4-D nerve pulse patterns involving cyclotron frequencies and Josephson frequency. Josephson currents at the second half period would generate dark Josephson radiation communicating the outcome of the calculation to the magnetic body. Entire hierarchy of EEGs with varying frequency scale would be present corresponding to the onion like structure of magnetic body. This pattern would provide an electromagnetic representation for the presence of the antigene and could be mimicked artificially [I72], [J11].

This picture might apply be the case also in the case of water memory.

1. The shaking might drop some fraction of antigene molecules to dark space-time sheets where they generate a dark color magnetic field. Because of the large value of Planck constant super-conductivity along color flux tubes running from molecular space-time sheets could still be present.

2. TGD based model of super conductivity involves double layered structures with same p-adic length scale scale as cell membrane [K6]. The universality of p-adic length scale hierarchy this kind of structures but with a much lower voltage over the bilayer could be present

also in water. Interestingly, Josephson frequency $ZeV/\hbar$ would be much lower than for cell membrane so that the time scale of memory could be much longer than for cell membrane for given value of $\hbar$ meaning longer time scale of memory recall.

3. Also in the case of homeopathic remedy the communication of the result of TQC to the magnetic body would take place via Josephson radiation. From the point of view of magnetic body Josephson radiation resulting in shaking induced TQC induced would replace the homeopathic remedy with a field pattern. The magnetic bodies of basophils could be cheated to produce allergic reaction by mimicking the signal representing the outcome of this TQC. This kind of cheating was indeed done in the later experiments of Benveniste involving very low frequency electromagnetic fields in kHz region allowing no identification in terms of molecular transitions (magnetic body and cyclotron frequencies) [I72].

Why experimenter had to know which bottle contained the treated water?

Why experimenter had to know which bottle contained the treated water? The role of experimenter eliminates the possibility that the (magnetic bodies of) clusters of water molecules able to mimic the (magnetic bodies of) antigene molecules electromagnetically are present in the solution at geometric now and produce the effect. The earlier explanation for experimenter's role was based on the idea that memory storage requires metabolic energy and that experimenter provides it. The vision about living matter as topological quantum computer (TQC) suggests a variant of this model in which experimenter makes possible the recall of memories of water represented as braiding patterns and realized via TQC.

1. Does experimenter provide the metabolic energy needed to store the memories of water?

What could be then the explanation for the failure of the modified experiment? Each memory recall reduces the occupation of the states representing bit 1 and a continual metabolic energy feed is needed to preserve the bit sequence representations of antibodies using laser light systems as bit. This metabolic energy feed must come from some source.

By the universality of metabolic energy currencies population inverted many-sheeted lasers in living organisms define the most natural source of the metabolic energy. Living matter is however fighting for metabolic energy so that there must be some system willing to provide it. The biological bodies of experimenters are the best candidates in this respect. In this case experimenters had even excellent motivations to provide the metabolic energy. If this interpretation is correct then Benveniste's experiment would demonstrate besides water memory also psychokinesis and direct action of desires of experimenters on physics at microscopic level. Furthermore, the mere fact that we know something about some object or direct attention to it would mean a concrete interaction of our magnetic with the object.

2. Does experimenter make possible long term memory recall?

The alternative explanation is that experimenter makes possible long term memory recall which also requires metabolic energy.

1. If braiding pattern represents, the water memory the situation changes since the robustness of the braiding pattern suggests that this representation is still in the geometric past (which is replaced with a new one many times). If the dark variants of molecules created in the process are still in the water, the braid representation of water memories could be available even in the geometric now but it is better to not make this assumption. The challenge is to understand how this information can be made conscious.

2. What is certainly needed is that the system makes the TQC again. This would mean a fractal quantum jump involving unitary U process and state function reduction leading to the generation of generalized EEG pattern. Only the sums and differences of cyclotron frequency and Josephson frequency would matter so that the details of the flow inducing braiding do not matter. The shaking process might be continuing all the subjective time in the geometric past so that the problem is how to receive information about its occurrence. Experimenter might actually help in this respect since the mechanism of intentional action initiates the action in the geometric past by a negative energy signal.

3. If the magnetic body of the water in the geometric now can entangle with the geometric past, TQC would regenerate the experience about the presence of antigene by sharing and fusion of mental images. One can however argue that water cannot have memory recall in this time scale since water is quite simple creature and levels with large enough $\hbar$ might not be present. It would seem that here the experimenter must come in rescue.

4. The function of experimenter's knowledge about which bottle contains the homeopathic solution could be simply to generate time-like entanglement in the required long time scale by serving as a relay station. The entanglement sequence would be *water now - experimenter now - water in the past* with "now" and "past" understood in the geometric sense. The crucial entanglement bridge between the magnetic body of water and experimenter would be created in the manufacturing of the homeopathic remedy.

   Note that this explanation does not exclude the first one. It is quite possible that experimenter provides also the metabolic energy to the bit representation of water memories possibly induced by the long term memory recall.

This picture is of course just one possible model and cannot be taken literally. The model however suggest that magnetic bodies of molecules indeed define the braiding; that the generalized EEG provides a very general representation for the outcome of TQC; that liquid flow provides the manner to build TQC programs - and also that shaking and sudden pulses is the concrete manner to induce visible-dark phase transitions. All this might be very valuable information if one some day in the distant future tries to build topological quantum computers in laboratory.

5.3.6 How Bio-Polymers Were Associated With Their Dark Counterparts?

The experiments of Pollack [L15] demonstrating what he calls fourth phase of water is characterized by negatively charged regions - exclusion zones (EZs). The stoichiometry of water inside EZ is $H_{1.5}O$. TGD based model assumes that part of protons in these regions have been transferred to to magnetic flux tubes were they form sequences identifiable as dark nuclei. The surprising finding is that a simple model for dark proton allows to assign its states to multiplets for which numbers of states are those assignable to DNA, RNA, and tRNA codons, plus amino-acids. Also the vertebrate genetic code can be realized in a simple manner. This leads to a vision about prebiotic life as dark life evolved in water before the ordinary life. Dark life would be present also in ordinary life forms.

If one believes that dark proton sequences [K24] define the counterparts of DNA, RNA, tRNA, and amino-acids realized at magnetic flux tubes, the question is how this form of life was transformed to the bio-chemical life.

The article "Hydrogen cyanide polymers, comets and the origin of life" (`http://tinyurl.com/ybfuwneq`, thanks to Ulla for the link) helped me to discover a new big gap in my knowledge about biology and this in turn led to a more detailed vision about how the transition could have taken place. HCN is everywhere and Miller demonstrated in his classic experiments that 11 out of 20 amino-acids emerged in presence of HCN. It has been later found that well over 20 amino-acids were produced. (`http://tinyurl.com/y9at46fe`). In my own belief system amino-acids could have appeared first as concrete something "real" and DNA as symbolic representations of this something "real". First at dark matter level and then biochemically.

In TGD Universe one can imagine - with inspiration coming partially from Pollack's experiments [L15] (`http://tinyurl.com/oyhstc2`) - that dark variants DNA, RNA and amino-acids were realized first as dark proton sequences at flux tubes- dark nuclei - I call them just dark DNA, RNA and amino-acids although dark proton sequences are in question. The genetic machinery involving translation and transcription was realized as dark variant and dark DNA was a symbolic representation for dark amino-acids.

How did this dark life give rise to bio-chemical life as its image? This is the question! I can only imagine some further questions.

1. Was this process like master teaching to a student a skill? Master does it first, and then student mimics. If so, the emergence of amino-acids, mRNA and DNA polymers would *not* have been purely chemical process. Dark variants of these polymers would have served

as templates for the formation of ordinary basic biopolymers, for transcription, and for translation. These templates might have been necessary in order to generate long RNA and DNA sequences: mere chemistry might have not been able to achieve this. Without dark polymers one obtains only bio-monomers, with dark polymers as template one obtains also bio-polymers. Dark polymers would have been the plan, biopolymers the stuff used to build.

2. Are dark DNA, RNA, amino-acids, etc indeed still there and form binary structures with their biochemical variants as I have indeed proposed?

3. Are dark translation and transcription processes still an essential part of ordinary translation and transcription? Master-student metaphor suggest that these dark processes actually induce them just like replication of magnetic body could induce the replication of DNA or cell. Visible chemistry would only make visible the deeper "dark chemistry". Apologies for all biochemists who have done heroic work in revealing chemical reaction paths!

How the process assigning biochemical life to dark life could have proceeded? The minimalistic guess is that the only thing that happened was that dark life made itself gradually visible! As a consciousness theoretician I have a temptation to see religious statements as hidden metaphors, at least they provide an excellent manner to irritate skeptics: Dark matter - the "God" made us- the biological life - to its own image.

1. First dark amino-acid sequences were accompanied by ordinary amino-acid sequences so that the dark translation process had now a visible outcome. At this step the presence of HCN was crucial and made the step unavoidable. Also the presence of template was necessary.

2. Dark mRNA got a visible counterpart in the same manner: the presence of template made possible long RNA polymers. The translation remained basically dark process but made visible by mRNA.

3. Dark DNA got a visible companion: again the presence of the template was - and still is - crucial.

What about generation of DNA and RNA? It is known that in reducing atmosphere DNA and RNA nucleobasis are obtained in an environment believed to mimick prebiotic situation: the presence of HCN and ammonia are necessary (`http://tinyurl.com/y9at46fe`). Reducing atmosphere `http://tinyurl.com/yc62g22f` does not oxidize, in other worlds does not contain oxygen and other oxidizing agents and can contain also actively reducing agents such as hydrogen, carbon monoxide. There are however some problems.

1. There is evidence that early Earth atmosphere contained less reducing molecules than thought in times of Miller. If life emerged in the underground water reservoirs as TGD strongly suggests, the usual atmosphere was absent and there are good hopes about reducing atmosphere.

2. The experiments using reducing gases besides those used in Miller's experiments produce both left and right handed polymers so that chiral selection is missing. This is not a surprise since weak interactions generate extremely small parity breaking for visible matter. If dark proton strings or even dark nuclei are involved, the Compton length of weak gauge bosons can be of the order of atomic length scale or even longer and weak interactions would be as strong as electromagnetic interactions. Therefore chiral selection becomes possible. The simplest option is that chirality selection occurred already for the helical magnetic flux tubes and induced that of biopolymers.

5.3.7 Two steps towards understanding of the origins of life

Two highly interesting findings providing insights about the origins of life have emerged and it is interesting to see how they fit to the TGD inspired vision.

The group led by Thomas Carell has made an important step in the understanding the origins of life. They have identified a mechanism leading to the generation of purines A and G which besides pyrimidines A,T (U) are the basic building bricks of DNA and RNA. The crucial step is to

make the solution involved slightly acidic by adding protons. For year later I learned that a variant of Urey-Miller experiment with simulation of shock waves perhaps generated by extraterrestrial impacts using laser pulses generates formamide and this in turn leads to the generation of all 4 RNA bases.

These findings represent a fascinating challenge for TGD inspired quantum biology. The proposal is that formamide is the unique amide, which can form stable bound states with dark protons and crucial for the development of life as dark matter-visible matter symbiosis. Pollack effect would generate electron rich exclusions zones and dark protons at magnetic flux tubes. Dark protons would bind stably with unique amine leaving its chemical properties intact. This would lead to the generation of purines and the 4 RNA bases. This would be starting point of life as symbiosis of ordinary matter and dark matter as large $h_{eff}/h = n$ phases of ordinary matter generated at quantum criticality induced by say extraterrestrial impacts. The TGD based model for cold fusion and the recent results about superdense phase of hydrogen identifiable in TGD framework as dark proton sequences giving rise to dark nuclear strings provides support for this picture.

There is however a problem: a reductive environment (with ability to donate electrons) is needed in these experiments: it seems that early atmosphere was not reductive. In TGD framework one can imagine two - not mutually exclusive - solutions of the problem. Either life evolved in underground oceans, where oxygen concentration was small or Pollack effect gave rise to negatively charged and thus reductive exclusion zones (EZs) as protons were transferred to dark protons at magnetic flux tubes. The function of UV radiation, catalytic action, and of shock waves would be generation of quantum criticality inducing the creation of EZs making possible dark $h_{eff}/h = n$ phases.

The first step: binding of dark protons to formamido-pyrimidine

I learned about very interesting discovery related to the problem of understanding how the basic building bricks of life might have emerged. RNA (DNA) has nucleotides A,G,C,U (T) as basic building bricks.

The first deep question is how the nucleotides A,G,C,U, and T emerged.

1. There are two types of nucleotides. Pyrimidines C and T/U (see `http://tinyurl.com/k3vxl9b`) have single carbon 6-cycle. Purines A and G (see `http://tinyurl.com/odvqw2p`) in turn have single 6-single and 5-cycle fused attached together along one side. Purines are clearly more complex than pyrimidines.

2. U.K. chemist John Sutherland demonstrated a plausible sequence of steps leading to the emergence of pyrimidines. Purines turned out to be more problematic. Leslie Orgel and colleagues suggested a possible pathway but it produces purines in too tiny amounts.

Now a group led by Thomas Carell in Ludwig Maximilian University have found a more plausible mechanism [I73] (see `http://tinyurl.com/z65kpyo`).

1. Carell and colleagues studied the interaction of biomolecule formamido-pyrimidine (FaPy) with DNA and found that it also reacts to produce purines. Could FaPys have served as predecessors of purines? (For formamide see `http://preview.tinyurl.com/lwqyqnu` and for the class of chemical compounds known as amines see `http://tinyurl.com/mad6c2u`).

2. The first step would have been a copious production of amino-pyrimidines containing several chemical groups known as amines. The problem is that the are so many amines and they normally react indiscriminantly to produce many different compounds. One wants mostly purines so that only one critical amine is wanted.

3. When Carell and his team added some acid to the solution to decrease its pH, a miracle happened. The extra protons from acid attached to the amines of the amino-pyrimidine and made them non-reactive. There was however one exception: just the amine giving rise to purine in its reactions! The reactive amine also readily bonded with formic acid acid (see `http://tinyurl.com/lmstt7n`) or formamide. Hence it seems that one big problem has been solved.

The second challenge is to understand how the building bricks of RNA and DNA combined to form longer polymers and began to replicate.

1. One prevailing vision is that so called RNA world preceded the recent biology dominated by DNA. The goal has been to achieve generation of RNA sequence in laboratory. Unlike DNA RNA sequences are not stable and long sequences are difficult to generate. DNA in turn replicates only inside cell and the presence of what is known as ordered water seems to be essential for this.

2. This step might involve new physics and chemistry and I have considered the possibility that the new physics involves magnetic bodies and dark proton sequences as a representation of the genetic code at the level of dark nuclear physics. There is no need to add that the fact that dark proton states provide representations for RNA, DNA, tRNA, and amino-acids [K24, L2] looks like a miracle and I find still difficult to believe that it is true and for genetic code. Also the representation of vertebrate code emerges in terms of correspondences of dark proton states.

   This suggests that the replication of DNA and takes place at the level of dark proton sequencies - dark nuclear strings - serving as a dynamical template for the biological replication. Also transcription and translation would be induced by dark process. Actually all biochemical processes could have as template the dynamics of molecular magnetic bodies and biochemistry would be kind of shadow of deeper dynamics.

3. There is actually support for dark proton sequences. Quite recently I learned about the article of Leif Holmlid and Bernhard Kotzias [L26] (see `http://tinyurl.com/hxbvfc7`) about the superdense phase of hydrogen. In TGD superdense phase has interpretation as dark proton sequences at magnetic flux tubes with the Compton length of dark proton coded by $h_{eff}/h \simeq 2^{11}$ to electron's Compton length [L17]. Remarkably, it is reported that the superdense hydrogen is super-conductor and super-fluid at room temperatures and even above: this is just what TGD predicts.

   The dark protons in TGD inspired quantum biology [L19] should have much longer Compton length of order of the distance between nucleotides in DNA sequences in order to serve as templates for chemical DNA. This gives a dark Compton length of order $\simeq 3.3$ Angstroms from the fact that there are 10 codons per 10 nm. This gives $h_{eff}/h \simeq 2^{18}$.

One can return back to the first step in the genesis of DNA and RNA. The addition of protons to the solution used to model prebiotic environment to make it slightly acidic was the key step. Why?

1. Here cold fusion might help. Cold fusion is claimed to take place in electrolysis involving ionization and charge separation. The electric fields used in electrolysis induce ionization and thus charge separation. For me it has however remained a mystery how electric fields, which are extremely tiny using the typical strength of molecular electric field as standard are able to induce a charge separation. Of course, every chemist worth of his salt regards this as totally trivial problem. I am however foolish enough to consider the possibility that some new physics might be involved.

2. The mechanism causing charge separation could be analogous to or that discovered by Pollack as he irradiated water bounded by a gel phase [L15] [L15]: in the recent case the electric field would take the role of irradiation as a feeder of energy. Negatively charged exclusion zones (EZs) were formed and 1/4 of protons went somewhere.

   The TGD proposal is that part of protons went to magnetic flux tubes and formed dark proton sequences identifiable as dark nuclear strings. The scaled down nuclear binding energy favours the formation of dark nuclear strings perhaps proceeding as analog of nuclear chain reaction. This picture allows to ask whether dark proton sequences giving rise to a fundamental representation of the genetic code could have been present already in water [L19]!

3. How DNA/RNA could have then formed? Could the protons making the solution acidic be dark so that the proton attaching to the amine would be dark? Could it be that for

all amines except the right one the proton transforms to ordinary proton and destroys the chemical reactivity. Could the attached dark proton remain dark just for the correct amine so that the amine would remain reactive and give rise to purine in further reactions? Could A,G,C,T and U be those purines and pyrimidines - or even more general biomolecules - for which the attachment to dark proton does not transform it to ordinary proton and in this manner affect dramatically the chemical properties of the molecule? What is the condition for the preservation of the darkness of the proton?

Second step: Could shock waves due to extraterrestrial impacts have produced RNA bases?

About year later I learned about a further interesting finding related to the prebiotic evolution (see the popular article at `http://tinyurl.com/m8npeor`). The conclusion of the research article (see [I79]) is that that the extraterrestrial impacts on Earth's early atmosphere might have generated all 4 RNA bases (see `http://tinyurl.com/kxxc7db`). Also now the formamide is involved and my layman guess is that the motivation for this comes from the experiment of Carell et al [I73] (see `http://tinyurl.com/z65kpyo`) discussed above. If formamide is generated then it becomes possible to generate formamido-pyridine and from this the RNA bases can be generated.

The experiment was a modern version of Urey-Miller experiment originally intended to simulate the situation at the surface of the early atmosphere modelled as a mixture a water H_2O, carbon-monoxide CO, and ammonium NH_3. The shock waves generated by the impacts were modelled in the experiment using terawatt laser pulses.

In the original Urey-Miller experiment amino-acids were generated. In the modern version of the experiment it was found that also formamide $CONH_3$ is formed, whose presence under suitable circumstances can lead to the generation of all 4 RNA bases. The presence of UV radiation, shock waves caused by extraterrestrial collisions, or of catalyst is the necessary condition.

In TGD Universe the additional condition could guarantee quantum criticality accompanied by dark $h_{eff}/h = n$ phases leading to the generation of dark protons and their stable binding with formamido-pyrimidine. The stable binding would not be possible for other amido-pyrimidines since dark protons would transform to ordinar protons for them. All 4 RNA bases would emerge from formamido-pyrimidine. All basic molecules of life could be produced in the reductive atmosphere.

The atmosphere was assumed to be reductive and this is a problem: the best that one can hope is that the early atmosphere was weakly reductive. Chemical compound is reductive (see `http://tinyurl.com/m9cqnob`) if it tends to donate electron. Reduction means receiving electron - and in chemistry hydrogen atom. To obtain a reducing atmosphere (see `http://tinyurl.com/lx4tat2`) one should remove oxygen from it. It however seems that the early atmosphere has contained oxygen and was oxidative rather than reductive. How could one overcome the problem?

1. In the experiment of Carell et al protons were added to reduce the pH of water. The basic experimental rule is that this makes the environment more reductive. The TGD proposal is that it led to a formation of dark proton-amine pair for the amine leading to the formation of purine. Charge separation by Pollack effect [L15] [L19] leading to the generation of dark proton sequences (dark nuclei) at magnetic flux tubes could have been due to the IR radiation, and maybe also by UV radiation, catalytic action, or by shock waves. The presence of electrons in the exclusion zones (EZs) could have made them electron donors and therefore reductive.

   The addition of protons in the experiment of Carell reducing the pH of water could have induced a transformation of dark protons at magnetic flux tube to ordinary protons. Dark protons bound to the amines would have transformed to ordinary protons and inducing their chemical inactivity. Only for the amine formamide serving as a precursor of purine the dark proton-amine bound state was stable and remained chemically reactive since dark proton did not affect the properties of visible matter part of the compound. Symbiosis between dark and ordinary matter began. This view conforms also with the vision about the pairing of DNA/RNA and dark DNA/RNA formed by sequences of proton triplets representing DNA/RNA codons [L21]. DNA is indeed negatively charged and dark proton could neutralize it but allow it to remain chemically active.

2. Second possibility is suggested by the conjecture that prebiotic life evolved in the crust of Earth, perhaps in the underground oceans or regions related to volcanoes [L45, L19]. The content of oxygen of this environment could have been much lower than at the surface making it reductive: it would not be possible to even talk about atmosphere. But where did the metabolic energy come from? Could volcanic energy emitted as dark long wave photons with energies in the range of bio-photon energies help here? There are indeed a theories assuming that first life forms emerged from volcanoes. These problems are discussed in [L45, L19] from TGD viewpoint. Note that these two explanations do not exclude each other.

5.3.8 Could the replication of mirror DNA teach something about chiral selection?

I received a link to a very interesting popular article (see `http://tinyurl.com/zqgutdv`) from which I learned that short strands of mirror DNA and mirror RNA - known as aptamers - have been be produced commercially for decades - a total surprise to me. Aptamers bind to targets like proteins and block their activity and this ability can be utilized for medical purposes.

Now researchers at Tsinghua University of Beijing have been able to create a mirror variant of an enzyme - DNA polymeraze - catalyzing the transcription of mirror DNA to mirror RNA also replication of mirror DNA [I143]. What is needed are the DNA strand to be replicated or transcribed, the mirror DNA nucleotides, and short primer strand (see `http://tinyurl.com/j3o8cyx`) since the DNA polymeraze starts to work only if the primer is present. This is like recalling a poem only after hearing the first few words.

The commonly used DNA polymerase containing about 600 amino-adics is too long to be built up as a right-handed version and researchers used a much shorter version: African swine fever virus having only 174 amino-acids. The replication turned out to be very slow. A primer of 12 nucleotides was extended to a strand of 18 nucleotides in about 4 hours: 3/2 nucleotides per hour. The extension to a strand of 56 nucleotides took 36 hours making 44/36= 11/9 nucleotides per hour. DNA and its mirror image co-existed peacefully in a solution. One explanation for the absence of mirror life is that the replication and transcription of mirror form was so slow that it lost the fight for survival. Second explanation is that the emergence of mirror forms of DNA polymerase and other enzymes was less probable.

Can one learn anything about this?

1. Chiral selection is one of the deep mysteries of biology. Amino-acids are left-handed and DNA and RNA double strands form a right-handed screw. One can assign handedness with individual DNA nucleotides and with DNA double strand but web sources speak only about the chirality of double strand. If the chirality of the DNA nucleotides were not fixed, it would have been very probably discovered long time ago as an additional bit doubling the number of DNA letters.

2. What could be the origin of the chirality selection? Second helicity could have been loser in the fight for survival and the above finding supports this: fast ones eat the slow ones like in market economy. There must be however a breaking of mirror symmetry. Weak interactions break of mirror symmetry but the breaking is extremely small because the weak bosons mediating weak interaction are so massive that the length scale in which the breaking of mirror symmetry matters is of order 1/100 times proton size. This breaking is quite too small to explain chiral selection occurring in nano-scales: there is discrepancy of 8 orders of magnitude. The proposal has been that the breaking of mirror symmetry has been spontaneous and induced by a very small seed. As far as I know, no convincing candidate for the seed has been identified.

According to TGD inspired model chiral selection would be induced from that in dark matter sector identified in terms of phases of ordinary matter with non-standard value of Planck constant $h_{eff}/h = n$ [K75, K76]. In living matter dark matter would reside at magnetic flux tubes and control ordinary matter. TGD predicts standard model couplings, in particular weak parity breaking. For $h_{eff}/h = n$ the scale below which weak bosons behave as massless particles implying large parity breaking is scaled up by n. Large parity breaking for dark matter becomes possible in even biological length scales for large enough h_{eff}.

The crucial finding is that the states of dark proton regarded as part of dark nuclear string can be mapped naturally to DNA, RNA, tRNA, and amino-acid molecules and that vertebrate genetic code can be reproduced naturally [K24]. This suggests that genetic code is realized at the level of dark nuclear physics and induces its chemical variant. More generally, biochemistry would be kind of shadow of dark matter physics. A model for dark proton sequences and their helical pairing is proposed and estimates for the parity conserving and breaking parts of Z^0 interaction potential are deduced.

Dark matter and chirality selection

In TGD framework the hierarchy of Planck constants suggests an explanation for the chirality selection.

1. In TGD Universe the new physics of quantum biology involves magnetic bodies and dark proton sequences as a representation of the genetic code at the level of dark nuclear physics. The crucial observation is that dark proton states provide representations for RNA, DNA, tRNA, and amino-acids [K24, L2] and there is also natural map between DNA and amino-acid type states giving rise to vertebrate genetic code. This looks like a miracle and I find still difficult to believe that it is true. A The extreme slowness of the wrong-handed DNA replication as compared to the ordinary replication means large breaking of parity symmetry. This is possible to understand in terms of weak interactions only if they are dark in DNA length scales so that weak bosons are effectively massless and weak interactions are as strong as electromagnetic interactions.

   This suggests that the replication of DNA and takes place at the level of dark proton sequencies - dark nuclear strings - serving as a dynamical template for the biological replication. Also transcription and translation would be induced by dark processes. Actually all biochemical processes could have as template the dynamics of molecular magnetic bodies and biochemistry would be kind of shadow of dark matter physics.

   If this is the case, then chiral selection would take place the selection at the level of dark nuclear strings and induce that the level of biochemistry. If dark and ordinary chiralities fit together like hand and glove. Dark matter at magnetic bodies could control the behavior of ordinary matter. By parity breaking the dark weak binding energy between members of proton pairs in the dark DNA strand consisting of a pair of helical dark proton strings is higher for the second helical chirality and would favour this chirality. A very naive thermodynamical estimate is that the ratio of the densities of two chiralities is proportional to the Boltzmann exponent $exp(-\Delta E_B/T)$. The transition to thermodynamical equilibrium can be however very slow so that thermodynamical argument need not make sense.

2. There is experimental support for dark proton sequences. Leif Holmlid and Berhard Kotzias [L26] (see `http://tinyurl.com/hxbvfc7`) have published an article about the superdense phase of hydrogen proposed to make possible to overcome the Coulomb wall making cold fusion impossible in the textbook Universe. In TGD superdense phase has interpretation as dark proton sequences at magnetic flux tubes with the Compton length of dark proton coded by $h_{eff}/h = n_{eff} \simeq 2^{11}$ to electron's Compton length [L17]. Remarkably, it is reported that the superdense hydrogen is super-conductor and super-fluid at room temperatures and even above: this is just what TGD predicts.

   The dark protons in TGD inspired quantum biology (see `http://tinyurl.com/lwxdl7y`) should have much longer Compton length of the order of the distance between nucleotides in DNA sequences in order to serve as templates for chemical DNA. This gives a dark Compton length of order $\simeq 3.3$ Angstroms from the fact that there are 10 codons per 10 nm. This would give $n_{eff,p} \simeq 2^{18}$. The safest manner to estimate the dark binding energy is by scaling the binding energy about $E_B \simeq 7$ MeV per nucleon by $1/n_{eff,p}$ to give $E_{B,d} = E_B/n_{eff,p} = 28$ eV.

3. Further evidence for the importance of dark protons in biology comes from the recent finding of the group led by Thomas Carell related to the understanding the origins of life [I73] (see `http://tinyurl.com/z65kpyo`). For TGD inspired model see [L24], [K19]. Carell et al

have identified a mechanism leading to the generation of purines A and G, which besides pyrimidines A,T (U) are the basic building bricks of DNA and RNA. The crucial step is to make the solution involved slightly acidic by adding protons.

In TGD inspired quantum biology this suggest that the protons in the acidic water are dark and that the attachment of the dark protons to the amines of the amino-pyrimidine transforms them to ordinary protons and makes the amino-pyrimidine non-reactive. There would be however one exception: the amine which reacts further to give purines as a reaction product. In this case the proton would remain dark and the chemical properties of the amine would remain intact. This suggests that DNA nucleotides and DNA strands can attach to dark protons or are accompanied by them.

Model for the replication of DNA

One can consider a detailed model for the replication as induced by the addition of dark protons to dark proton sequence representing dark DNA strand. The added dark protons would be accompanied or attached with the DNA nucleotides as suggested by the work of Carell et al.

1. In the replication and transcription of DNA the basic step would be the addition of dark proton to an increasing dark proton sequence. The need for primer means that there must already exist a dark proton sequence. In the presence of prime the attractive dark nuclear binding energy of the added dark proton with the prime would make the dark fusion rate higher. The addition of dark protons could proceed like a dark nuclear chain reaction. It would be made possible by the dark nuclear binding energy per proton scaling like $1/h_{eff,p}$.

   For the ordinary nuclei the binding energy per nucleon would be of the order of 7 MeV (note that charge independence of strong interactions holds in good approximation). The scaling down by $h_{eff}/h = 2^{18}$ would give $E_B \simeq 4$ eV, which corresponds to UV photon energy. Note that bio-photons assumed to correspond dark photons with same energy have energies in visible and UV range.

2. Dark nuclear energy cannot explain parity breaking. The axial part of dark weak energy between dark protons belonging to dark strand and its conjugate and having nuclei acids and its conjugate as a chemical "shadow" must be also involved. Two values of h_{eff} are involved: $h_{eff,p}$ assignable to the flux tubes containing dark protons parallel to DNA strands and $h_{eff,W}$ assignable to the transversal flux tube connecting dark protons associated with different dark strands.

   One of the assumptions of the TGD inspired model of cold fusion [L17, L26] is that the weak scale is scaled up from weak boson Compton length to about atomic length scale. This would require $h_{eff,W}/h = n_{eff,W}$ for weak bosons to be roughly

$$n_{eff,W} \simeq \frac{m_Z}{m_p} \times n_{eff,p} \simeq 91 \times n_{eff,p}$$

   so that one would have $n_{eff,W} \simeq 2^{25}$. If this is the case weak interactions are of essentially same strength as em interaction below the scaled up Compton scale of order 3 Angstroms. This makes it possible to talk about classical Z^0 Coulomb potential and about spin dependent parity breaking Z^0 force. These two interaction energies sum up and this reduces the binding energy per proton in double strand for the other chirality.

3. The parity conserving Z^0 Coulomb interaction energy between two protons at different strands connected by a flux tube is given by the expression

$$\begin{aligned} &V_{PC}(r_{12}) = -kV(r_{12}) \ , \quad V(r_{12}) = \tfrac{\hbar}{r_{12}} \ , \\ &k = \alpha_Z Q_Z^2(p) \ , \qquad \alpha_Z = \tfrac{\alpha}{sin^2(\theta_W)cos^2(\theta_W)} \ , \quad Q_Z(p) = 1/4 - sin^2(\theta_W) \ . \end{aligned} \tag{5.3.2}$$

Here units $\hbar = 1$, $c = 1$ are used. r_{12} refers to the distance between dark protons at magnetic flux tubes assignable to DNA strands. Base pair thickness is about .34 nm and thickness of DNA double strand is about 2 nm. r_{12} could be between these two limits.

4. The spin dependent and parity non-conserving Z^0 interaction potential for Dirac spinors proportional to the gradient of the Z^0 Coulomb potential can be written as

$$V_{PNC} = \alpha_Z Q_Z^A(p) Q_Z^V(p) \gamma_5 V(r_{12}) \ . \tag{5.3.3}$$

Here $Q_Z^A = I_{3,A}/2 = 1/4$ is the axial weak charge of proton. The vectorial charge of proton is $Q_Z(p) = 1/4 - sin^2(\theta_W) \simeq 0.02$ so that it is much smaller than $Q_Z^A(p)$. Hence the axial force dominates by a factor $10^2/8 \sim 12.5$ for a given relative position. Usually the axial part becomes very small by symmetries as one estimates quantum averages but in the recent situation one cannot expect this since the positions of dark protons are in the first approximation fixed.

5. Using non-relativistic correspondence following from $\gamma_5 = \gamma_0\gamma_1\gamma_2\gamma_3$ and $(\gamma_5)^2 = -1$: this equation holds true also for $(\gamma^0\gamma^k p_k(m)$, and one has

$$\gamma_5 \to \frac{\overline{\sigma}\cdot p}{m_p} \ .$$

Here $\overline{\sigma}$ denotes Pauli sigma matrices expressible as $\gamma^0\gamma^i$). Using the replacement $p \leftrightarrow i\hbar_{eff,W}\nabla$ one can write V_{PNC} as the sum of the axial energies of the two protons

$$\begin{aligned} V_{s_1,s_2} &= V_{s_1} + V_{s_2} \ , \\ V_{s_i} &= \frac{\hbar_{eff,W}}{m_p}\overline{\sigma}_i\cdot\nabla_i V_{PC}(r_{12}) = (-1)^i \frac{k n_{eff,W}\hbar}{m_p}\hbar\frac{\overline{\sigma}_i\cdot\overline{r}_{12}}{r_{12}^2} \ . \ i = 1,2 \ . \end{aligned} \tag{5.3.4}$$

The parity breaking part of Z^0 force is proportional to $n_{eff,W}$ from the expression of momentum operator in terms of gradient operator so that dark matter physics makes itself visible and increases further the magnitude of parity breaking. The potential energy changes sign in reflection $\overline{r}_{12} \to -\overline{r}_{12}$. This gives

$$\begin{aligned} V_{s_1,s_2} &= -\frac{\alpha_Z}{4}(\frac{1}{4} - sin^2(\theta_W))\frac{n_{eff,W}\hbar}{m_p r_{12}}\frac{(\overline{\sigma}_1 - \overline{\sigma}_2)\cdot\overline{r}_{12}}{r_{12}}\frac{\hbar}{r_{12}} \\ &= \frac{1}{4}\frac{1}{(\frac{1}{4} - sin^2(\theta_W)}\frac{n_{eff,W}\hbar}{m_p r_{12}}\frac{(\overline{\sigma}_1 - \overline{\sigma}_2)\cdot\overline{r}_{12}}{r_{12}}V_{PC}(r_{12}) \ . \end{aligned} \tag{5.3.5}$$

6. For the vectorial part one has

$$V_{PC} = -\alpha_Z(\frac{1}{4} - sin^2(\theta_W))^2 V(r_{12}) \ . \tag{5.3.6}$$

The order of magnitude is about $V_Z = .16/x$ eV.

7. The condition that r_{12} corresponds to dark Compton length of proton implies in the first approximation $\frac{n_{eff,p}}{m_p r_{12}} = 1$ so that $n_{eff,W}$ proportionality gives factor $m_Z/m_p \simeq 91$. The order of magnitude parity breaking potential is the value potential at distance in the range $r_{12} \in [3.4, 2]$ nm. Let us expres the horizontal distance between the paired dark protons as $r_{12} = x$ Angstroms. This gives for the axial part

$$\begin{aligned} V_{s_1,s_2} &= \frac{1}{4}\frac{1}{(\frac{1}{4} - sin^2(\theta_W)}\frac{m_Z}{m_p}(\overline{\sigma}_1 - \overline{\sigma}_2)\cdot\frac{\overline{r}_{12}}{r_{12}}V_{PC}(r_{12}) \\ &\simeq .5\times 10^2 \times 91 \times \frac{V_{PC}(r_{12})}{x} \times (\overline{\sigma}_1 - \overline{\sigma}_2)\cdot\frac{\overline{r}_{12}}{r_{12}} \quad . \end{aligned} \tag{5.3.7}$$

The order or magnitude for the axial part is roughly $4550/x$ times larger than for the vectorial part. V_{PNC} is proportional to $1/x^2$ and V_{PC} to $1/x$. The condition that the states are spin eigenstates requires that spin quantization axes must be chosen along the flux tube connecting the dark protons. This is rather natural choice.

This would give for the axial part order of magnitude $V_{PNC} \sim 728/x^2$. For 2 nm distance one would obtain $V_{PNC} \sim 1.82$ eV. For 1 nm distance one would have $x = 10$ and this would give $V_{PNC} \simeq 7.28$ eV. For this value $V_{PC} \simeq 16$ meV, which is of same order of magnitude as thermal energy $kT/2$ at room temperature.

8. The process of adding dark protons to the increasing DNA sequence must be possible irrespectively of the direction of spin. The spin eigenvalue in the direction of the horizontal axis connecting the members of dark proton pair is assumed to be opposite for the members of the dark proton pairs of dark double strand. This assumption comes from the model of the dark genetic code. This demands that V_{NPC} is considerably smaller than strong binding energy E_B. For 1 nm distance one has $V_{PNC} \simeq 7.28$ eV considerably smaller than $E_B \simeq 28$ eV.

9. What is the relation of the fermionic chirality to the geometric chirality? The reflection for dark protons induces the reflection of the entire helix turning also its direction. The reflection permutes the dark protons of each pair since their positions are related by reflection in the plane orthogonal to z-axis $(x_2, y_2) = (-x_1, -y_1)$. One has $(x_1, y_1, z) \leftrightarrow (x_2, y_2, -z)$. A further rotation of π in say (x, z)-plane around say y-axis is symmetry and gives $(x_2, y_2, -z) \rightarrow (-x_2, y_2, z) = (x_1, -y_1, z)$. Hence the net effect is $(x_1, y_1, z) \rightarrow (x_1, -y_1, z)$ and DNA strand with an opposite screw direction is generated.

The model of dark genetic code motivates the assumption that the dark protons of the pair are spin eigenstates for the spin projection along the axis connecting the members of the pair. The direction of the spin quantization axis changes in reflection from that given by (x_1, y_1) to that given by $(x_1, -y_1)$ so that the states are not anymore eigenstates of the spin projection along this axis. Thus the fermionic chirality indeed correlates with the chirality of double strand and the two chiralities are in physically different position.

What happens at the level of classical fields? Kähler magnetic field transforms like angular momentum in reflections and rotations as is easy to see from its expression in terms of vector potential. Hence it does not change its direction in reflection but changes its direction in the rotation. Hence the magnetic flux along flux tube changes to opposite in the reflection. This also affects the physics and induces effects at the level of dark strong interactions. The magnetic energy is of form $s \cdot B$ and vanishes classically. Quantum mechanically it does not vanish since s is operator and one can wonder what this implies physically.

Differences between standard model and TGD based description

The above estimate relies on standard model, which is quantum field theory in Minkowski space, and one can wonder what new elements TGD brings in. I do not try to estimate the effects in TGD framework but just list the differences.

1. In TGD framework space-time is 4-surface in $M^4 \times CP_2$ and this description must be replaced with a description using 8-D imbedding spinors. At space-time level massive M^4 Dirac equation $p_k\gamma^k\Psi = m\Psi$ is replaced by 8-D chiral symmetry implying separate conservation of quark and lepton numbers with the analog of massless Dirac equation for the Kähler-Dirac gamma matrices, which are superpositions of M^4 and CP_2 gamma matrices. K-D gamma matrices are contractions of canonical momentum current densities of Kähler action with the imbedding space gamma matrices. If the action is volume term, one obtains induced gamma matrices. The twistorialization of TGD by replacing the imbedding space with the product of twistor spaces of M^4 and CP_2 and lifting space-time surfaces to their twistor spaces with induced twistor structure leads to the addition of volume term to Kähler action [K79]. This term corresponds to cosmological constant and is extremely small in the recent cosmology.

2. One can decompose K-D gamma matrices to their M^4 and CP_2 parts: $\Gamma^\alpha = \Gamma^\alpha_{M^4} + \Gamma^\alpha_{CP_2}$ and write the K-D equation as $\Gamma^\alpha_{M^4} D_\alpha \Psi = -\Gamma^\alpha_{CP_2}\Psi$. The presence of $\Gamma^\alpha_{CP_2}$ parts breaks conservation of M^4 chirality and serves as a signal for massivation. This operator is kind of mass operator acting non-trivial in electroweak spin degrees of freedom assignable to CP_2 and the action of its square is analogous to the action of mass squared operator.

   The understanding of particle massivation at this level does not seem however possible and the proper approach relies of p-adic thermodynamics for super-Virasoro representations for which ground states are characterized by the modes of imbedding space spinors which are massless in 8-D sense and are eigenstates of M^4 mass squared operator with eigenvalues determined by CP_2 spinor Laplacian [K30]. Its action on M^4 chirality is same as action of mass in massive Dirac equation in M^4.

3. In the case of M^4 Dirac equation the multiplication of massive Dirac equation with γ_5 using anti-commutativity of γ_5 and γ_k gives $\gamma^k p_k \gamma_5 \Psi = -m\gamma_5\Psi$ instead of$p_k\gamma^k\Psi = m\Psi$. TGD framework γ_5 anti-commutes with $\Gamma^\alpha_{M^4}$ but commutes with $\Gamma^\alpha_{CP_2}$ so that also now one has similar equation $\Gamma^\alpha_{M^4} D_\alpha \Psi = +\Gamma^\alpha_{CP_2}\Psi$.

5.4 Model For The Hierarchy Of Josephson Junctions

As far as hierarchy of EEGs and its generalizations is considered the hierarchy of Josephson junctions assignable to cell membrane itself is relevant. Dark matter hierarchy and p-adic fractality allow to imagine a fractal hierarchy of structures analogous to cell membrane with arbitrarily large thickness. One can even imagine scaled up variants of cell membrane with different p-adic length scale and value of Planck constant but possessing same membrane potential as ordinary cell membrane. The generalization of the imbedding space helps to understand what is involved and is discussed in Appendix.

5.4.1 The Most Recent Model For The Generation Of Nerve Pulse

For some time ago I learned [J1, J2, J18, J19, J21] (thanks to Ulla Mattfolk) that nerve pulse propagation seems to be an adiabatic process and thus does not dissipate: the authors propose that 2-D acoustic soliton is in question. Adiabaticity is what one expects if the ionic currents are dark currents (large $\hbar$ and low dissipation) or even supra currents. Furthermore, Josephson currents are oscillatory so that no pumping is needed. Combining this input with the model of DNA as topological quantum computer (TQC) [K17] leads to a rather precise model for the generation of nerve pulse.

1. The system would consist of two superconductors- microtubule space-time sheet and the space-time sheet in cell exterior- connected by Josephson junctions represented by magnetic flux tubes defining also braiding in the model of TQC. The phase difference between two super-conductors would obey Sine-Gordon equation allowing both standing and propagating soliton solutions. A sequence of rotating gravitational penduli coupled to each other would be the mechanical analog for the system. Soliton sequences having as a mechanical analog penduli rotating with constant velocity but with a constant phase difference between them would generate moving kHz synchronous oscillation. Periodic boundary conditions at the

ends of the axon rather than chemistry determine the propagation velocities of kHz waves and kHz synchrony is an automatic consequence since the times taken by the pulses to travel along the axon are multiples of same time unit. Also moving oscillations in EEG range can be considered and would require larger value of Planck constant in accordance with vision about evolution as gradual increase of Planck constant.

2. During nerve pulse one pendulum would be kicked so that it would start to oscillate instead of rotating and this oscillation pattern would move with the velocity of kHz soliton sequence. The velocity of kHz wave and nerve pulse is fixed by periodic boundary conditions at the ends of the axon implying that the time spent by the nerve pulse in traveling along axon is always a multiple of the same unit: this implies kHz synchrony. The model predicts the value of Planck constant for the magnetic flux tubes associated with Josephson junctions and the predicted force caused by the ionic Josephson currents is of correct order of magnitude for reasonable values of the densities of ions. The model predicts kHz em radiation as Josephson radiation generated by moving soliton sequences. EEG would also correspond to Josephson radiation: it could be generated either by moving or standing soliton sequences (latter are naturally assignable to neuronal cell bodies for which $\hbar$ should be correspondingly larger): synchrony is predicted also now.

3. The previous view about microtubules in nerve pulse conduction can be sharpened. Microtubular electric field (always in the same direction) could explain why kHz and EEG waves and nerve pulse propagate always in same direction and might also feed energy to system so that soliton velocity could be interpreted as drift velocity. This also inspires a generalization of the model of DNA as TQC sine also microtubule-cell membrane systems are good candidates for performers of TQC. Cell replication during which DNA is out of game seems to require this and microtubule-cell membrane TQC would represent higher level TQC distinguishing between multi-cellulars and mono-cellulars.

4. New physics would enter in several manners. Ions should form Bose-Einstein cyclotron condensates. The new nuclear physics predicted by TGD [L2], [L2] predicts that ordinary fermionic ions (such as K^+, Na^+, Cl^-) have bosonic chemical equivalents with slightly differing mass number obtained by replacing one or more neutral color flux tubes connecting nucleons of neutral atom with a charged one. Anomalies of nuclear physics and cold fusion provide experimental support for the predicted new nuclear physics. Electronic supra current pulse from microtubules could induce the kick of pendulum inducing nerve pulse and induce a small heating and expansion of the axon. The return flux of ionic Josephson currents would induce convective cooling of the axonal membrane. A small transfer of small positive charge into the inner lipid layer could induce electronic supra current by attractive Coulomb interaction. The exchange of exotic W bosons which are scaled up variants of ordinary $W^{\pm}$ bosons is a natural manner to achieve this if new nuclear physics is indeed present.

5.4.2 Quantum Model For Sensory Receptor

This original model of nerve pulse and EEG was still based on the implicit assumption that the space-time sheet carrying the Josephson currents is far from vacuum. The model for sensory receptor and sensory qualia however led to a the proposal that the space-time sheet in question is near vacuum extremal [K21, K43]. Near vacuum extremal property does not affect the general structure of the model in an essential manner.

1. The only change [K43, K44] is the replacement of charges ± 1 of ions with effective charges given as

$$Q_{eff} = -\frac{Z-N}{2p} + 2Z + q_{em} \quad . \tag{5.4.1}$$

Z and N denote nuclear charge and neutron number. $p = sin^(\theta_W)$ corresponds to Weinberg angle. For K^+, Cl^-, Na^+, Ca^{++} one has $Z = (19, 17, 11, 20)$, $Z - N = (-1, -1, -1, 0)$,

Table 5.1: Table gives the prediction of the model of photoreceptor for the Josephson energies for typical values of the membrane potential. For comparison purposes the energies E_{max} corresponding to peak sensitivities of rods and cones, and absorption ranges for rods are also given. R, G, B, W refers to red, green, blue, white. The values of Weinberg angle parameter $p = sin^2(\theta_W)$ are assumed to be .23 and.0295. The latter value is forced by the fit of Josephson energies to the known peak energies.

Ion	Na^+	Cl^-	K^+	Ca^{+2}
$E_J(.04\ mV, p = .23)/eV$	1.01	1.40	1.51	1.76
$E_J(.065\ V, p = .23)/eV$	1.64	2.29	2.69	2.73
$E_J(40\ mV, p = .0295)/eV$	1.60	2.00	2.23	1.68
$E_J(50\ mV, p = .0295)/eV$	2.00	2.49	2.79	2.10
$E_J(55\ mV, p = .0295)/eV$	2.20	2.74	3.07	2.31
$E_J(65\ mV, p = .0295)/eV$	2.60	3.25	3.64	2.73
$E_J(70\ mV, p = .0295)/eV$	2.80	3.50	3.92	2.94
$E_J(75\ mV, p = .0295)/eV$	3.00	3.75	4.20	3.15
$E_J(80\ mV, p = .0295)/eV$	3.20	4.00	4.48	3.36
$E_J(90\ mV, p = .0295)/eV$	3.60	4.50	5.04	3.78
$E_J(95\ mV, p = .0295)/eV$	3.80	4.75	5.32	3.99
Color	R	G	B	W
E_{max}	2.19	2.32	3.06	2.49
energy-interval/eV	1.77-2.48	1.97-2.76	2.48-3.10	

and $q_{em} = (1, -1, 1, 2)$. **Table 5.1** gives the values of Josephson energies for some values of resting potential for $p = sin^(\theta_W) = .0295$ reproducing the frequencies of peak sensitivity for photoreceptors. Rather remarkably, they are in IR or visible range.

2. The energies are in UV and visible range. Hence one can consider also Josephson junctions with considerably lower membrane potentials of order mV are possibly without losing the thermal stability. For instance, one could consider $k = 151, 157, 163, 167$ Josephson junctions with a membrane potential scaling as $1/L(k)$. For $k = 167$ the energies would be scaled down by a factor $2^{-(167-151)/2} = 2^{-8}$ giving for $V_{eff} = .09$ V a photon energy somewhat below the thermal energy at room temperature. On the other hand, the fact that Josephson junctions with a vanishing Z^0 field are at the verge of thermal instability suggests that also they might be present in living matter.

3. From **Table 5.1** one can evaluate the value of Planck constant for a given Josephson frequency for various ions. For $f_J = 5$ Hz giving a first estimate for neuronal Josephson frequency and V=-55 mV corresponding to the critical voltage for the generation of action potential one obtains the values $r = \hbar/\hbar_0 = (1.51, 1.89, 2.11, 1.59) \times 2^{46}$ for $(Na^+, Cl^-, K^+, Ca^{++})$. For V=-70 mV corresponding to the resting potential of neuron and same Josephson frequency one obtains $r = (0.961.201.341.01) \times 2^{47}$. For Ca^{++} ion r is very near to a power of 2. A good mnemonic is that the Josephson energies of biologically important ions vary in an interval, which is in a reasonable approximation half octave $(E_J(K^+)/E_J(Na^+) = 1.3958 \simeq \sqrt{2} \simeq 1.4142)$.

It interesting to try to interpret the resting potentials of various cells in this framework in terms of the Josephson frequencies of various ions. **Table 5.1** gives the values of Josephson frequencies of basic biological ions for typical values of the membrane potential.

1. The maximum value of the action potential during nerve pulse is +40 mV so that Josephson frequencies are same as for the resting state of photoreceptor. Note that the time scale for nerve pulse is so slow as compared to the frequency of visible photons that one can consider that the neuronal membrane is in a state analogous to that of a photoreceptor.

2. For neurons the value of the resting potential is -70 mV. Na^+ and Ca^{++} Josephson energies 2.80 eV and 2.94 eV are in the visible range in this case and correspond to blue light. This does not mean that Ca^{++} Josephson currents are present and generate sensation of blue at neuronal level: the quale possibly generated should depend on sensory pathway. During the hyper-polarization period with -75 mV the situation is not considerably different.

3. The value of the resting potential is -95 mV for skeletal muscle cells. In this case Ca^{++} Josephson frequency corresponds to 4 eV metabolic energy quantum.

4. For smooth muscle cells the value of resting potential is -50 mV. In this case Na^+ Josephson frequency corresponds to 2 eV metabolic energy quantum.

5. For astroglia the value of the resting potential is -80/-90 mV for astroglia. For -80 mV the resting potential for Cl^- corresponds to 4 eV metabolic energy quantum. This suggests that glial cells could also provide metabolic energy as Josephson radiation to neurons.

6. For all other neurons except photo-receptors and red blood cells Josephson photons are in visible and UV range and the natural interpretation would be as bio-photons. The bio-photons detected outside body could represent sensory leakage. An interesting question is whether the IR Josephson frequencies could make possible some kind of IR vision.

5.4.3 The Role Of Josephson Currents

The general vision is that Josephson currents of various ions generate Josephson photons having dual interpretations as bio-photons and EEG photons. Josephson photons can in principle regenerate the quale in the neurons of the sensory pathway. In the case of motor pathways the function would be different and the transfer of metabolic energy by quantum credit card mechanism using phase conjugate photons is suggested by the observation that basic metabolic quanta 2 eV *resp.* 4 eV are associated with smooth muscle cells *resp.* skeletal muscle cells.

As already found in the previous section, the energies of Josephson photons associated with the biologically important ions are in general in visible or UV range except when resting potential has the value of -40 mV which it has for photoreceptors. In this case also IR photons are present. Also the turning point value of membrane potential is +40 mV so that one expects the emission of IR photons.

Josephson photons could be used to communicate the qualia to the magnetic body.

1. If Josephson currents are present during the entire action potential, the entire range of Josephson photons down to frequencies of order 2 kHz range is emitted for the standard value of $\hbar$. The reason is that lower frequencies corresponds to cycles longer than the duration of the action potential. The continuum of Josephson frequencies during nerve pulse makes it possible to induce cyclotron transitions at the magnetic body of neuron or large structure. This would make possible to communicate information about spatial and temporal behavior of the nerve pulse pattern to the magnetic body and build by quantum entanglement a sensory map.

2. The frequencies below 2 kHz could be communicated as nerve pulse patterns. When the pulse rate is above $f = 28.57$ Hz the sequence of pulses is experienced as a continuous sound with pitch f. f defines the minimum frequency for which nerve pulses could represent the pitch and there remains a 9 Hz long range to be covered by some other communication method.

3. The cyclotron frequencies of quarks and possibly also of electron would make possible a selective reception of the frequencies emitted during nerve pulse. Same applies also to the Josephson frequencies of hair cell (, which does not fire). If the value of Planck constant is large this makes possible to communicate the entire range of audible frequencies to the magnetic body. Frequency would be coded by the magnetic field strength of the flux tube. Two options are available corresponding to the standard ground state for which Z^0 field is very weak and to almost vacuum extremals. For the first option one as ordinary cyclotron frequencies. The cyclotron frequency scales for them differ by a factor

Table 5.2: Cyclotron frequencies of quarks and electron in magnetic field $B_{end} = .2$ Gauss for standard vacuum with very small Z^0 field and nearly vacuum extremal.

fermion	$f_c(e)/MHz$	$f_c(u)/MHz$	$f_c(d)/MHz$
standard	.564	.094	.019
nearly vacuum extremal	8.996	2.275	.947

$$r(q) = \frac{Q_{eff}(q)}{Q_{em}(q)} = \frac{\epsilon(q)}{2pQ_{em}(q)} + 1 \ , \quad \epsilon(u) = -1 \ , \epsilon(d) = 1 \tag{5.4.2}$$

from the standard one. For $p = .0295$ one obtains $(r(u), r(d), r(e) = (24.42, 49.85, 15.95)$. The cyclotron frequencies for quarks and electron with masses m(u)=2 MeV, m(d)=5 MeV, and m(e)=.5 MeV are given by **Table 5.2** for the two options. If one assumes that B_{end} defines the upper bound for field strength then he standard option would require both d quark and electron. Gor $d$quark with kHz CD the upper bound for cyclotron frequencies would be 20 kHz which corresponds to the upper limit of audible frequencies.

4. Besides cyclotron frequencies also the harmonics of the fundamental frequencies assignable to quark and electron CDs could be used and in case of musical sounds this looks a highly attractive option. In this case it is now however possible to select single harmonics as in the case of cyclotron transitions so that only the rate of nerve pulses can communicate single frequency. Lorentz transform sub-CD scales up the frequency scale from the secondary p-adic time scale coming as octave of 10 Hz frequency. Also the scaling of $\hbar$ scales this frequency scale.

5.4.4 What Is The Role Of The Magnetic Body?

The basic vision is that magnetic body receives sensory data from the biological body- basically from cell membranes and possibly via genome - and controls biological body via genome. This leaves a huge amount of details open and the almost impossible challenge of theoretician is to guess the correct realization practically without any experimental input. The following considerations try to clarify what is involved.

Is magnetic body really needed?

Libet's findings and the model of memory based on time mirror (see **Fig.** `http://tgdtheory.fi/appfigures/timemirror.jpg` or **Fig. ??** in the appendix of this book) hypothesis suggests that magnetic body is indeed needed. What is the real function of magnetic body? Is it just a sensory canvas? The previous considerations suggest that it is also the seat of geometric qualia, in particular the pitch of sound should be coded by it. It would be relatively easy to understand magnetic body as a relatively passive sensory perceiver defining sensory map. If one assumes that motor action is like time reversed sensory perception then sensory and motor pathways would be just sensory pathways proceeding in opposite time directions from receptors to the various layers of the magnetic body. Brain would perform the information processing.

Certainly there must exist a region in which the motor and sensory parts of the magnetic body interact. What comes in mind is that these space-time sheets (or actually pairs of space-time sheets) are parallel and generate wormhole contacts between them. This interaction would be assignable to the region of the magnetic body could receive positive energy signals from associative sensory areas and send negative energy signals to motor motor neurons at the ends of motor pathways wherefrom they would propagate to premotor cortex, supplementary motor cortex and to frontal lobes where the abstract plans about motor actions are generated.

Is motor action time reversal of sensory perception in zero energy ontology?

One could argue that the free will aspect of motor actions does not conform with the interpretation as sensory perception in reversed direction of time. On the other hand, also percepts are selected -say in binocular rivalry [J12]. Only single alternative percept need to be realized in a given branch of the multiverse. This makes possible metabolic economy: for instance, the synchronous firing at kHz frequency serving as a correlate for the conscious percept requires a lot of energy since dark photons at kHz frequency have energies above thermal threshold. Similar selection of percepts could occur also at the level of sensory receptors but quantum statistical determinism would guarantee reliable perception. The passivity of sensory perception and activity of motor activity would reflect the breaking of the arrow of time if this interpretation is correct.

What magnetic body looks like?

What magnetic body looks like has been a question that I have intentionally avoided as a question making sense only when more general questions have been answered. This question seems however unavoidable now. Some of the related questions are following. The magnetic flux lines along various parts of magnetic body must close: how does this happen? Magnetic body must have parts of size at least that defined by EEG wavelengths: how do these parts form closed structures? How the magnetic bodies assignable to biomolecules relate to the Earth sized parts of the magnetic body? How the personal magnetic body relates to the magnetic body of Earth?

1. The vision about genome as the brain of cell would suggest that active and passive DNA strands are analogous to motor and sensor areas of brain. This would suggests that sensory data should be communicated from the cell membrane along the passive DNA strand. The simplest hypotesis is that there is a pair of flux sheet going through the DNA strands. The flux sheet through the passive strand would be specialized to communicate sensory information to the magnetic body and the flux sheet through the active strand would generate motor action as DNA expression with transcription of RNA defining only one particular aspect of gene expression. Topological quantum computation assignable to introns and also electromagnetic gene expression would be possible.

2. The model for sensory receptor in terms of Josephson radiation suggests however that flux tubes assignable to axonal membranes carry Josephson radiation. Maybe the flux tube structures assigned to DNA define the magnetic analog of motor areas and flux tubes assigned with the axons that of sensory areas.

3. A complex structure of flux tubes and sheets is suggestive at the cellular level. The flux tubes assignable to the axons would be parallel to the sensory and motor pathways. Also microtubules would be accompanied by magnetic flux tubes. DNA as topological quantum computer model assumes and the proposed model of sensory perception and cell membrane level suggests transversal flux tubes between lipids and nucleotides. The general vision about DNA as brain of cell suggest flux sheets through DNA strands.

   During sensory perception of cell and nerve pulse the wormhole flux tube connecting the passive DNA strand of the first cell to the inner lipid layer would recombine with the flux tube connecting outer lipid layer to some other cell to form single flux tube connecting two cells. In the case of sensory organs these other cells would be naturally other sensory receptors. This would give rise to a dynamical network of flux tubes and sheets and axonal sequences of genomes would be like lines of text at the page of book. This structure could have a fractal generalization and would give rise to an integration of genome to super-genome at the level of organelles, organs and organism and even hypergenome at the level of population. This would make possible a coherent gene expression.

4. This vision gives some idea about magnetic body in the scale of cell but does not say much about it in longer scales. The CDs of electrons and quarks could provide insights about the size scale for the most relevant parts of the magnetic body. Certainly the flux tubes should close even when they have the length scale defined by the size of Earth.

Additional ideas about the structure follow follow if one assumes that magnetic body acts a sensory canvas and that motor action can be regarded as time reversed sensory perception.

1. If the external world is represented at part of the magnetic body which is stationary, the rotation of head or body would not affect the sensory representation. This part of the magnetic body would be obviously analogous to the outer magnetosphere, which does not rotate with Earth.

2. The part of the magnetic body at which the sensory data about body (posture, head orientations and position, positions of body parts) is represented, should be fixed to body and change its orientation with it so that bodily motions would be represented as motions of the magnetic , which would be therefore analogous to the inner magnetosphere of rotating Earth.

3. The outer part of the personal magnetic body is fixed to the inner magnetosphere, which defines the reference frame. The outer part might be even identifiable as the inner magnetosphere receiving sensory input from the biosphere. This magnetic super-organism would have various life forms as its sensory receptors and muscle neurons. This would give quantitative ideas about cyclotron frequencies involved. The wavelengths assignable to the frequencies above 10 Hz would correspond to the size scale of the inner magnetosphere and those below to the outer magnetosphere. During sleep only the EEG communications with outer magnetic body would remain intact.

4. Flux quantization for large value of $\hbar$ poses an additional constraint on the model.

   (a) If Josephson photons are transformed to a bunch of ordinary small $\hbar$ photons magnetic flux tubes can correspond to the ordinary value of Planck constant. If one assumes the quantization of the magnetic flux in the form

   $$\int BdA = n\hbar$$

   used in super-conductivity, the radius of the flux tube must increase as $\sqrt{\hbar}$ and if the Josephson frequency is reduced to the sound frequency, the value of $\hbar$ codes for the sound frequency. This leads to problems since the transversal thickness of flux tubes becomes too large. This does not however mean that the condition might not make sense: for instance, in the case of flux sheets going through DNA strands the condition might apply.

   (b) The quantization of magnetic flux could be replaced by a more general condition

   $$\oint (p - ZeA)dl = n\hbar \ , \tag{5.4.3}$$

   where p represents momentum of particle of super-conducting phase at the boundary of flux tube. In this case also $n = 0$ is possible and poses no conditions on the thickness of the flux tube as a function of $\hbar$. This option looks reasonable since the charged particles at the boundary of flux tube would act as sources of the magnetic field.

   (c) Together with the Maxwell's equation giving $B = ZeNv$ in the case that there is only one kind of charge carrier this gives the expression

   $$N = \frac{2m}{RZ^2e^2} \tag{5.4.4}$$

   for the surface density N of charge carrier with charge Z. R denotes the radius of the flux tube. If several charge carriers are present one has $B = \sum_k N_k Z_k e v_k$, and the condition generalizes to

   $$N_i = \frac{2m_i v_i}{RZ_i \sum_k Z_k v_k e^2} \ . \tag{5.4.5}$$

   It seems that this condition is the most realistic one for the large $\hbar$ flux sheets at which Josephson radiation induces cyclotron transitions.

What are the roles of Josephson and cyclotron photons?

The dual interpretation of Josephson radiation in terms of bio-photons and EEG photons seems to be very natural and also the role of Josephson radiation seems now relatively clear. The role of cyclotron radiation and its interaction with Josephson radiation are not so well understood.

1. At least cell membrane defines a Josephson junction (actually a collection of them idealizable as single junctions). DNA double strand could define a series of Josephson junctions possibly assignable with hydrogen bonds. This however requires that the strands carry some non-standard charge densities and currents- I do not know whether this possibility is excluded experimentally. Quarks and antiquarks assignable to the nucleotide and its conjugate have opposite charges at the two sheets of the wormhole flux tube connective nucleotide to a lipid. Hence one could consider the possibility that a connection generated between them by reconnection mechanism could create Josephson junction.

2. The model for the photoreceptors leads to the identification of bio-photons as Josephson radiation and suggests that Josephson radiation propagates along flux tubes assignable to the cell membranes along sensory pathways up to sensory cortex and from there to motor cortex and back to the muscles and regenerates induced neuronal sensory experiences.

3. Josephson radiation could be used quite generally to communicate sensory data to/along the magnetic body: this would occur in the case of cell membrane magnetic body at least. The different resting voltages for various kinds of cells would select specific Josephson frequencies as communication channels.

4. If motor action indeed involves negative energy signals backwards in geometric time as Libet's findings suggest, then motor action would be very much like sensory perception in time reversed direction. The membrane resting potentials are different for various types of neurons and cells so that one could speak about pathways characterized by Josephson frequencies determined by the membrane potential. Each ion would have its own Josephson frequency characteristizing the sensory or motor pathway.

The basic questions concern the function of cyclotron radiation and whether Josephson radiation induces resonantly cyclotron radiation or vice versa.

1. Cyclotron radiation would be naturally associated with the flux sheets and flux tubes. The simplest hypothesis is that at least the magnetic field $B_{end} = .2$ Gauss can be assigned with the some magnetic flux quanta at least. The model for hearing suggests that B_{end} is in this case quantized so that cyclotron frequencies provide a magnetic representation for audible frequencies. Flux quantization does not pose any conditions on the magnetic field strength if the above discussed general flux quantization condition involving charged currents at the boundary of the flux quantum are assumed. If these currents are not present, $1/\hbar$ scaling of B_{end} for flux tubes follows.

2. The assumption that cyclotron radiation is associated with the motor control via genome is not consistent with the vision that motor action is time reversed sensory perception. It would also create the unpleasant question about information processing of the magnetic body performed between the receival of sensory data and motor action.

3. The notion of magnetic sensory canvas suggests a different picture. Josephson radiation induces resonant cyclotron transitions at the magnetic body and induces entanglement of the mental images in brain with the points of the magnetic body and in this manner creates sensory maps giving a third person perspective about the biological body. There would be two kind of sensory maps. Those assignable to the external world and those assignable to the body itself. The Josephson radiation would propagate along the flux tubes to the magnetic body.

4. There could be also flux tube connections to the outer magnetosphere of Earth. It would seem that the reconnections could be flux tubes traversing through inner magnetosphere to poles and from there to the outer magnetosphere. These could correspond to rather low cyclotron frequencies. Especially interesting structure in this respect is the magnetic flux sheet at the Equator.

5.4.5 Dark Matter Hierarchies Of Josephson Junctions

The hierarchy of Josephson junctions assignable to cell membrane and characterized by values of Planck constant provides a rather nice model for cell membrane but one can consider also more general dark hierarchies of Josephson junctions. This model conforms with the general vision that living matter processes information by locating it to various pages of the "Big Book".

Maximization of Planck constant in quantum control and communication in living matter

The sectors of the imbedding space for which CD and CP_2 are replaced with their n_a- *resp.* n_b-fold coverings define the most promising candidates concerning the understanding of living matter, at least the quantum control of living matter. The reason is that the value of the Planck constant is maximized and given by $r = \hbar/\hbar_0 = n_a n_b$. Also the number of pages with same Planck constant would be finite unlike for the more general option allowing rational values of Planck constant. In particular, infinite number of pages with the standard value of Planck constant would be possible and this might lead to mathematical difficulties.

Experimental constraints allow to consider also the possibility that only covering spaces are possible. One must be however very cautious in making hasty conclusions. If also factor spaces are allowed one can have G_a or G_b as discrete and exact symmetry groups at the level of dark matter and these symmetries would be manifested as approximate symmetries of the visible matter topologically condensed around the dark matter.

1. In M^4 degrees of freedom since the restriction to the orbifold $\hat{M}^4/G_a$ is equivalent to the exact G_a-invariance of dark matter quantum states. Molecular rotational symmetries correspond typically to small groups G_a and might relate to this symmetry. Small values of n_a would not affect dramatically the value of Planck constant if n_b is large.

2. $G_a = Z_n$, $n = 5, 6$ are favored for molecules containing aromatic cycles. Also genuinely 3-dimensional tetrahedral, octahedral, and icosahedral symmetries appear in living matter.

In the sequel only integer values of Planck constant will be considered. An especially interesting hierarchy corresponds to ruler and compass integers expressible as a product of power of two and distinct Fermat primes (see Appendix). The reason is that these integers correspond to number theoretically very simple quantum phases. This hierarchy includes as a special case powers of two and one can imagined a resonant interaction between p-adic length scale hierarchy and hierarchy of Planck constants.

Dark hierarchy of Josephson junctions with a constant thickness

The model for EEG relies on fractal hierarchy of cell membrane like structures with a fixed thickness and membrane potential. Therefore cell membrane thickness is not scaled by $\hbar$ as one might naively expect. Same applies to magnetic flux tubes: this is possible since the condition for the quantization of magnetic flux can be replaced with a more general one if one allows charged currents at the boundaries of flux quanta [K43]. In this model the value of $\hbar$ becomes a measure for the evolutionary level of cell and neurons in hippocampus, associative regions of cortex and their motor counterparts, and frontal lobes are expected to correspond to the largest values of $\hbar$ measuring also the time scale of long term memory and planned action. Note that cell membrane corresponds to twin primes $k = 149$ and $k = 151$ with $k = 151$ defining a Gaussian Mersenne so that it is indeed very special.

Page of a book is rather precise metaphor for the magnetic flux sheet going through a linear array of strings of nuclei and also for a collection flux tubes parallel to axons. This raises several questions. Do the lines of the text of this book correspond to axons in neural circuits? Do the pages correspond to larger structures formed by the axons?

The quantum model for qualia [K43] implies that Josephson radiation travels through flux tubes parallel to sensory pathways and there could be also a horizontal organization of the neurons-at least at the level of sensory receptors in the sense that magnetic flux tubes connecting DNA nucleotides to lipids of cell membrane fuse to form longer flux tubes between DNA nucleotides of different cells when sensory receptor is active. Axons could thus be seen as the analogs of text

Table 5.3: Twin primes define especially interesting candidates for double membrane like structures defining Josephson junctions. Also included the pair $(137, 13^2 = 169)$ although $k = 169$ is not prime. The two largest scales could relate to structures appearing in brain.

$(k, k+2)$	$(137, 139)$	$(149, 151)$	$(167, 169 = 13^2)$	$(179, 181)$
$L_e(k)$	.78 A	5 nm	$2.5\mu m$	.32 mm
$(k, k+2)$	$(191, 193)$,	$(197, 199)$		
$L_e(k)$	1 cm	8 cm		

lines which however can interact with each other. Similar organization would appear at the level of flux sheets traversing through DNA strands.

Books are made for reading and one can thus ask whether the book metaphor extends. Could the observed moving brain waves scanning cortex relate to the "reading" of the information associated with these sheets of book by the magnetic body and does our internal speech correspond to this "reading" ? One is also forced to ask whether these brain waves are induced by waves propagating along magnetic flux quanta of the magnetic body of Earth or personal magnetic body in the case that it has components other than magnetic flux sheets serving as Josephson junctions.

An objection against a fractal hierarchy of Josephson junctions with thickness scaling as $\hbar$

One can consider also a hierarchy of Josephson junctions with a scaled up thickness proportional to $\hbar$ instead of constant thickness. If these junctions have same voltage at all levels of the hierarchy a resonant interaction between various levels of the hierarchy would become possible.

One can represent common sense objections against this idea. The electric field involved with the higher levels of Josephson junction hierarchy is very weak: something like 10^{-7} V/m for lito-ionospheric Josephson junctions (of thickness about 176 km from the scaling of the cell membrane thickness by $\lambda^4 = 2^{44}$) which might be responsible for EEG. The electric field of the Earth at space-time sheets corresponding to ordinary matter is much stronger: about $10^2 - 10^4$ V/m at the surface of Earth but decreasing rapidly as ionosphere is approached being about.3 V/m at 30 km height. The estimate for the voltage between ionosphere and Earth surface is about 200 kV [F45].

The many-sheeted variant of Faraday law implies that on order to have a voltage of order.08 V over lito-ionospheric Josephson junction at dark matter space-time sheet, the voltage over ionospheric cavity must be almost completely compensated by an opposite voltage over litosphere so that lito-ionospheric double layer could be seen as a pair of capacitor plates in a radial electric field of order 10^{-7} V/m generated by the charge density in sub-litospheric part of Earth. This condition requires fine-tuning and therefore looks unrealistic.

A natural distance scale in which the electric field is reduced would correspond to 10-20 km thick layer in which whether phenomena are present. The mirror image of this layer would be Earth's crust. The cell membrane counterpart would be a dipole layer like charge density between the lipid layers of the cell membrane. Note that the electric field at dark matter space-time can be constant. However, as far as Josephson junction is considered, it is only the net voltage what matters.

5.4.6 P-Adic Fractal Hierarchy Of Josephson Junctions

p-Adic length scale hypothesis allows to imagine a hierarchy of Josephson junctions at least in length scales regarded usually as biologically relevant. The voltage through the junction need not however be same as for the ordinary cell membrane anymore. Twin primes are especially interesting since they would naturally correspond to pairs of structures analogous to a pair of lipid layers defining cell membrane.

In particular, twin primes abundant in the p-adic length scale range assignable to living matter could define double layered structures acting as Josephson junctions.

Also Gaussian Mersennes define highly interesting p-adic length scales and the length scale range between cell membrane thickness and the size of cell contains as many as four Gaussian Mersennes corresponding to $k = 151, 157, 163, 167$. Only the smallest one is associated with a twin prime but p-adic length scale hypothesis allows also non-prime values of k.

The possibility of a p-adic hierarchy of membrane like structures accompanied by Josephson junctions

One can imagine the existence of fractally scaled up variants of cell membrane defining hierarchy of Josephson junctions possibly realized as magnetic flux tubes. The possible existence of this hierarchy is however not relevant for the model of EEG in its recent form.

The first hierarchy correspond to the p-adic length scales varying in the range of biologically relevant p-adic length scales $L(k)$ involving membrane like structures. Twin primes $(k, k+2)$ are good candidates here (Table 3). Second hierarchy corresponds to dark matter hierarchy for which length scales come as $\sqrt{r}L(k))$, $r = \hbar/\hbar_0$. Later the question which values of r are favored will be discussed.

The size of cell nucleus varies in the range $(L(169) = 5\ \mu m, 2L(169) = 10\ \mu m)$. This is consistent with the assumption that cell nucleus provides the fundamental representation for this block. This would mean that at least the multiply coiled magnetic flux quantum structures associated with DNA appear as fractally scaled up copies.

Each dark matter level corresponds to a block of p-adic length scales $L(k)$, $k = 151, ..., 169$. Also new length scales emerge at given level and correspond to $L(k)$, $k > 169$. The dark copies of all these length scales are also present. Hence something genuinely new would emerge at each level.

Fractal hierarchy of magnetic bodies assignable to cell

Second hierarchy corresponds to a dark matter hierarchy involving values of Planck constant. The original hypothesis was that the values of Planck constant comes as $r \equiv \hbar/\hbar_0 = 2^{11k}$ of given p-adic length scale assignable to biological membrane like structure. A possible justification for the hypothesis is that the ratio of electron and proton masses is rather near to 2^{11} and that this number appears in quantum TGD in the role of fundamental constant. This hypothesis is however un-necessarily restrictive and it is better to consider at least the values of r given as products of two ruler and compass integers n_F expressible as a product of distinct Fermat primes and some power of two. The justification comes from the number theoretic vision about evolution and number theoretical simplicity of the phases $q = exp(i2\pi/n_F)$ (Appendix).

The emergence of a genuinely new structure or function in evolution would correspond to the emergence of new level in this fractal hierarchy. Quantum criticality would be essential: phases corresponding different values of Planck constant would compete at quantum criticality.

The flux sheet or tubes through cell membranes should integrate to larger structures at the higher levels of dark matter hierarchy implying the integration of sensory inputs from a large number of cells to single coherent input at higher levels of dark matter hierarchy. One can think two options: the sensory inputs from cell membranes are communicated directly to the magnetic body or via the DNA. The second option would require that the flux sheets or tubes starting from cell membrane traverse also the DNA.

5.5 Physical Model For Genetic Code And Its Evolution

The original number theoretic models for genetic realized on the idea that genetic code has deeper number theoretical significance. The neglect of some obvious physical inputs however generated some pseudo problems. These models however led to what I believe is the correct track concerning the understanding of the prebiotic evolution. The original model for the evolution of genetic code as a fusion of singlet and doublet codes to triplet code has been discussed in [**?**]. The model to be discussed here is obtained from this model by some dramatic simplifications.

The basic questions are following.

1. What were the physical counterparts of the pre-amino-acids and pre-tRNAs for singlet and doublet codes?

2. How the triplet code emerged from the singlet and doublet codes? How the tRNA molecules evolved and how the amino-acids replaced pre-amino-acids?

3. Can one identify singlet and doublet life-forms or at least some predecessors of triplet life forms as existing life-forms?

In an attempt to answer these questions p-adic length scale hypothesis and the vision about the molecular evolution as a sequence of spontaneous symmetry breakings induced by the generation of new space-time sheets serve as valuable guide lines. The following biological input is needed.

1. RNA world [I142] as a model for pre-biotic evolution allows to identify pre-amino-acids as RNA sequences (RNA_1 for short) differing somehow from the ordinary RNA sequences (RNA_2 for short). 1-code was associated with the transformation of $RNA_2 \rightarrow RNA_1$ and 2-code in the simplest case with the transcription of RNA_2 to its conjugate.

2. The cross like structure of tRNA molecule identifiable as a composite of its singlet and doublet predecessors allows to read directly the main steps in the evolution of the triplet code as a fusion of singlet and doublet codes and also gives detailed and highly non-trivial information about RNA_1.

3. The reverse transcriptase, appearing in retro-viruses like HIV and acting also as a transcriptase [J3], provides the mechanism transforming RNA sequences to DNA sequences inside pre-nucleus so that DNA→RNA code emerged and also evolved rapidly since reverse transcriptase makes a lot of errors.

4. The basic idea is that the fusion of $tRNA_1$ and $tRNA_2$ to to $tRNA_3$, the recent tRNA, made $RNA_2 \rightarrow RNA_1$ and $RNA_2 \rightarrow RNA_2$ transformations impossible and the amino-acids originally catalyzing the attachment of RNA_2 doublet in RNA_2 transcription began to be attached to a growing amino-acid sequence and mRNA→ amino-acid part of genetic machinery was established. The emergence of reverse transcriptase brought in DNA. DNA as topological quantum computer idea generalized to RNA context provides tight additional conditions on the course of events: in particular, membrane like structures, most naturally consisting of RNA_1 should have been present already at RNA era.

5. Nanno-bacteria claimed to be even the dark bio-matter are excellent candidates for singlet and doublet life-forms or at least, predecessors of the recent life-forms. There are reasons to believe that RNA era is still continuing inside cell nucleus.

Second group of questions relates to the quantum control of the translation process. There are many questions also now.

1. What makes a codon stopping codon?

2. What is behind the symmetries of the code with respect to the third codon.

3. What is the origin of breaking of the canonical A-T, C-G rules for mRNA-tRNA association?

The model for the transition from RNA era to RNA-amino-acid era allows to answer these questions and te DNA as TQC picture leads to a physical interpretation of these symmetries and their breaking.

5.5.1 RNA World

The hypothesis that pre-biotic life before the emergence of the cell membrane structures was RNA dominated (the notion of RNA world) is based on a strong empirical evidence summarized in detail in [I64]. For instance, only RNA can be generated spontaneously in the absence of cell membrane bounded structures. There is also a lot of support for the ability of RNA to take care of functions

like replication, translation, and transfer (see the [I64] and references therein). Ribozymes could even replace enzymes as RNA based catalyzing agents so that even amino-acids might be unnecessary in RNA world and the system could consist of RNA only. This of course does not mean that this system could yet realize genetic code and evolve.

An important implication is that pre-amino-acids might be identifiable as $2', 5'$ RNA, which was produced in the classical experiments of Leslie Orgel at 1980s mimicking primordial ocean. There are however also other candidates and the structure of tRNA more or less fixes identification to a high degree.

Ontogeny recapitulates phylogeny principle suggests that if RNA coded RNA during primordial period, the remnants of these RNAs could still exist and be coded by specific genes. This is indeed the case [I116] (for an article about RNA genes and RNA world see [I138]). RNA genes were discovered already 1990 in the genome of Caenorhabditis elegans, the small nematode worm but it took years to realize that they do not code proteins but small RNA molecules that somehow turn off other genes that play a role in worm development. Later these small RNA coding genes were found in flies, mollusks, fish, and even humans. As many as 200 microRNA genes in C. elegans were known at time of the writing of the article, which would represent about 1 percent of the genes of its genes. There is also evidence that centrosomes possess their own genome based on RNA rather than DNA [I9].

5.5.2 Programming Of Bio-Molecular Self Assembly Pathways From TGD Point Of View

The beautiful results (for a popular summary see [I127]) about programming of bio-molecular self assembly - described above - when combined with the earlier model for the pre-biotic evolution - inspire interesting insights about the role of braiding in translation. The basic observation is that the structure of tRNA- although more complex than that of hairpin- has much common with that of hairpins. Therefore it is interesting to look this structure from the point of view of TGD. For instance, one can find whether the notions of braiding, anomalous em charge and quark color could provide additional insights about the structure and function of tRNA.

The brief summary of the resulting picture is as follows. According to the TGD based model of pre-biotic evolution, 3-code should have resulted as a fusion of 1- and 2- codes to 3-codes involving fusion of $tRNA_1$ and $tRNA_2$ to $tRNA_3 \equiv tRNA$. Second hypothesis is that during RNA era the function of $tRNA_2$ was to generate RNA_2 double helix from single RNA strand and that amino-acids catalyzed this process. The considerations that follow strongly suggest that $tRNA_1$ was involved with a non-deterministic generation of new RNA sequences essential for the evolution. After the establishment of 3-code these two process fused to a deterministic process generating amino-acid sequences. RNA era could still continue inside cell and play an important role in evolution.

There is an interesting work about programming bio-molecular self assembly pathways [I40]. The catalytic self assembly of complexes of nuclei acids is carried out automatically by a program represented implicitly as a mixture of linear DNA strand acting as catalyst and so called hairpin DNA: s containing three nucleation sites a_t, b_t, c_t - so called toeholds.

Key ideas

The basic idea is that a set of bio-molecular reactions can be programmed to occur in a desired order by using a generalization of lock and key mechanism. The simplest self assembly pathway can be specified by a collection of keys and locks. In the beginning there is only one key and the this key fits to only one door, which leads into a room with several doors. The lock eats the key but gives one or more keys. If the room contains several doors to which the keys fits, the reaction corresponds to addition of several branches to the already existing reaction product. By continuing in this manner one eventually ends up to the last room and at the last step the lock gives back the original key so that it can act as a catalyst.

The translation of this idea to a program defining self assembly pathway is following.

1. DNA hairpin define key structural element of the self-assembly program. Hairpin is a single-stranded DNA strand in meta-stable configuration having form A+B+C [I107] such that B

forms a loop and C is a palindrome [I35] . The formal expression for palindromy is $C = A_t^*$: this means that C read backwards (C_t) is conjugate A^* of A implying that A and C running in opposite direction can form a double helix (duplex) by hydrogen bonding. As catalytic a^* acting as key forms a double helix with a, the hairpin molecule opens to a linear DNA molecule and energy is liberated. In this process original key is lost but the two other toeholds b_t and c_t contained by the hairpin become available as keys. Each hairpin in the mixture of catalyst and hairpin molecules has its own lock and two keys.

2. The process of opening new doors continues until all hairpin molecules are used. The key given by the last lock must be catalyst strand a^*. The outcome is a molecule consisting of pieces of DNA strands and can possess a very complex topology. For instance, the formation trees and star like structures can be easily programmed.

3. To run this program one needs only an optimal mixture of catalyst molecule and hairpin DNA molecules. In the applications discussed in [I40] hairpins have length of order 10 nm which corresponds to $L_e(151) = \sqrt{5}L(151)$ defining also cell membrane thickness. That $L_e(151)$ corresponds also to the length of 30-nucleotide sequence defining the codon of the code associated with Mersenne prime $M_{61} = 2^{61} - 1$ might not be an accident. The simplest applications are autocatalytic formation of DNA dublex molecules and of branched junctions, nucleated dendritic growth, and autonomous locomotion of a bipedal walker.

The basic idea in the realization of the autonomous motion of bipedal walker is to cheat the walker to follow a track marked by food. The walker literally eats the food and receives in this manner the metabolic energy needed to make the step to the next piece of food. The menu contains two kinds of hairpins (see **Fig. 5.1**): hairpins A attached regularly along the desired path of the walker (second DNA strand) and hairpins B but not attached to the strand. The front leg l of the walker attaches to A and this catalyzes the formation of the duplex $A \cdot B$ as a waste and the liberated metabolic energy allows to make a step in which hind leg becomes the front leg.

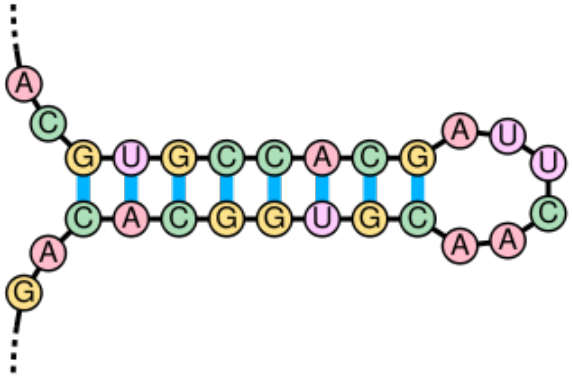

Figure 5.1: The structure of DNA hairpin (stem loop)

TGD view about the situation

The possibility to program the self-assembly relies on the almost deterministic realization of the lock and key mechanism. The presence of braid strands could make this possible.

1. Consider first the hypothesis about the cancelation of anomalous DNA charge. The palindromic character of A means that the neck of the hairpin has vanishing anomalous em charge and also vanishing color charge is possible. Hence palindromes are favored in TGD Universe. The circular piece B is not in general color singlet. It could have braid strands connecting

it to it to some other DNA or nuclear membrane but this is not necessary. Same applies to the toehold a_t at the end of the other strand of neck.

2. The attachment of the lock to key could be seen as a process in which a braid consisting of magnetic flux tubes connecting lock and key strands (DNA and its conjugate) is formed spontaneously and followed by a phase transition reducing $\hbar$ contracting the flux tubes and in this manner guiding the key to the lock.

If one assumes that only paired nucleotides of single DNA strand possess braid strands, one must assume the same for mRNA. As a consequence one would loose the nice interpretation for the formation of AAA... tail of mRNA as a manner to guarantee integer valuedness and small value (or even vanishing) of the anomalous em charge. If there is braid strands associated with entire mRNA, it could end at the nuclear membrane. In this case the transfer of tRNA to mRNA during translation by a phase transition reducing $\hbar$ of braid strands could be initiated by the fusion of the braid strand ends coming from mRNA codon and from its conjugate codon at tRNA at nuclear membrane.

5.5.3 The Archeology Of TRNA Molecules As A Guideline

The study of the structure of the ordinary tRNA molecule is of considerable help in the attempts to guess what might have been its predecessor.

The structure of the tRNA molecule

The shape of the tRNA molecule [I50] in 2-D representation is that of cruciform.

1. tRNA molecule has a cross like appearance, and decomposes into a body coded by tRNA gene and an acceptor stem which is same for all amino-acids and added separately and can be replaced during the lifetime of the tRNA molecule. Acceptor stem, to which the amino-acid is attached with the mediation of amino-acyl-tRNA synthase, can be said to be a passive component and is same for all tRNAs so that its structure does not determine which amino-acid is attached to it. The stem is not coded by genes and contains 4 nucleotides.

2. tRNA molecule can be seen as single RNA strand just as hairpin. The five stems are double helices analogous to the necks of the hairpin. Strand begins at $5'$ end of the acceptor stem directed upwards. The second strand of acceptor stem continues as a toehold ending to $3'$ end of tRNA. The toehold has at its end ACC to which the amino-acid (rather than conjugate DNA) attaches.

3. tRNA molecule (see **Fig. 5.2**) contains three arms with hairpin structure. A arm containing the anticodon is directed downwards. D and T arms are horizontal and directed to left and right. Between T arm and A arm there is additional variable hairpin like structure but with highly degenerate loop is degenerate. It has emerged during evolution.

4. The structure of tRNA minus anticodon depends on anti-codon which conforms with the fact T and D arms are related to the binding of amino-acid so that their nucleotide composition correlates with that of anticodon.

5. Anticodon arm contains the anticodon of mRNA codon and thus corresponds to RNA. For doublet part of the mRNA codon the correspondence is 1-1 but for the third nucleotide the correspondence is more complex due to wobble base pairing to be discussed below. Wobble base pairing indeed leads to the recent simplified model for the evolution of the triplet code as a fusion of 1-code and 2-code.

Wobble base pairing

The phenomenon of wobble base pairing [I54] is very important. There are only about 40 tRNA molecules instead of 61 which means that one-to-one map between mRNA nucleotides and tRNA conjugate nucleotides is not possible. Crick suggests that so called wobble base pairing resolves the

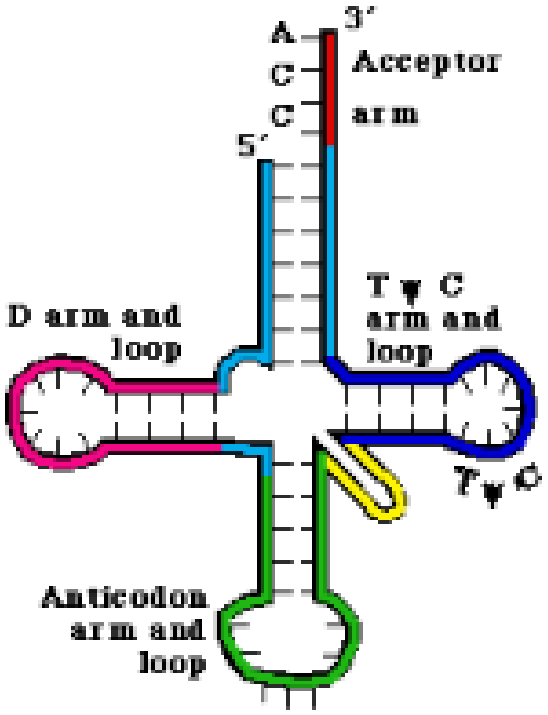

Figure 5.2: The structure of tRNA

problem. What happens that the first nucleotide of anticodon is either A, G, U, or I(nosine) [I21]. The base-pairings for third nucleotide are $\{A-U, G-C, U-\{A,G\}, I-\{U,A,C\}\}$. The explanation for the non unique base pairing in the case of U is that its geometric configuration is quite not the same as in ordinary RNA strand. I is known to have 3-fold base pairing.

Minimization of the number of tRNAs requiring that only three mRNA codons act as stopping signs predicts that the number of tRNAs is 40.

1. It is convenient to classify the 4-columns of code table according to whether all four codons code for the same amino-acid ($(T,C,A,G) \to X$, whether 4-column decomposes into two doublets: $[(T,C),(A,G)] \to [X,Y]$, or whether it decomposes to triplet and singlet ($[(T,C,A),G] \to [ile, met]$). There are also the 4-columns containing stop codon: $[(U,C),(A,G)] \to [(tyr,tyr),(stop,stop)]$ and $[(U,C),A,G] \to [(cys,sys),stop,trp]$. Mitochondrial code has full A-G and T-C symmetries whereas for vertebrate nuclear code 3 4-columns break this symmetry.

2. Consider first 4-columns for which the doublet symmetry is broken. $[tyr,tyr,top,stop]$ column must correspond to first tRNA nucleotide which is A or G (tyr). The absence of anti-codons containing U implies stop codon property. For $[cys,sys,stop,trp]$ one must have A, G and C but U is not allowed. ile-met column can correspond to tRNAs with I and C as the first nucleotide.

3. For 4-columns coding for two doublet amino-acids the minimal set of first tRNA codons is $\{A,G,U\}$. For completely symmetric 4-columns the minimal set of tRNA codons is $\{I,U\}$. Thus $\{A,G,U,I\}$ would replace $\{A,G,U,C\}$.

4. There are 9 completely symmetric 4-columns making 18 tRNAs, 5 doublet pairs making 15 tRNAs, ile-met giving 2 tRNAs, and the columns containing stopping codons giving 5 tRNAs. Altogether this gives 18+15+2+5= 40. Also the deviations from the standard code can be understood in terms of the properties of tRNA.

Consider the interpretation of wobble base pairing in TGD framework assuming the braiding picture and the mapping of nucleotides to quarks. The completely symmetric 4-columns correspond

to unbroken isospin and matter-antimatter asymmetries. 4-columns decomposing into doublets result from the breaking of matter-antimatter asymmetry at quark level. ile-met column corresponds to the breaking of both symmetries. The base pairings of I obviously break both symmetries.

The non-unique based pairing of U and I means that they cannot correspond to a unique quark or anti-quark in braiding U pairs with both A and G so that the braid strands starting from these RNA nucleotides must both be able to end to tRNA U. Hence tRNA U is not sensitive to the isospin of the quark. This non-uniqueness could relate to the assumed anomalous geometric character of the binding of U codon to tRNA sequence. The braid strands beginning from U, A, and C must be able to end up to I so that I can discriminate only between $\{U, C, A\}$ and G.

Anomalous em charge and color singletness hypothesis for tRNA

One can test also whether the vanishing of anomalous em charge of tRNA leads to testable predictions. One can also try understand translation process in terms of the braiding dynamics. One must distinguish between the states of tRNA alone and tRNA + amino-acid for which braidings are expected to be different.

Before continuing it must be made clear that braiding hypothesis is far from being precisely formulated. One question is whether the presence of the braiding could distinguish between matter in vivo and vitro. For instance, the condition that anomalous em charge is integer valued or vanishing for DNA hairpins in vivo gives strong condition on the loop of the hairpin but or hairpins in vitro there would be no such conditions. Second point is that amino-acids and I and U in tRNA_1 could carry variable anomalous em charge allowing rather general compensation mechanism.

1. tRNA without amino-acid

1. The minimal assumption is that braiding hypothesis applies only to the stem regions of tRNA in this case. In this case the strands can indeed begin from strand and end up to conjugate strand. The possibility of color singletness and vanishing of total anomalous em charge are automatically satisfied for the stem regions as a whole in absence of non-standard base pairings. In general the acceptor stem contains however $G*U$ base pair which is matter-antimatter asymmetric but breaks isospin symmetry and gives unit anomalous charge for the acceptor stem. Also other stems can contain $G*U$, $U*G$ pairings as also $P*G$ and $L*U$ pairings (P and L denote amino-acids Pro and Leu). The study of concrete examples [I42] shows that single G*U bond is possible so that anomalous em charge can be non-vanishing but integer valued for double strand part of tRNA. Suppose that a given amino-acid can have anomalous of any codon coding for it. If P in $G*P$ pair has the anomalous em charge of the codon CCG, $G*P$ pair has vanishing anomalous em charge. If L corresponds to CUA the value of anomalous em charge is integer.

2. The anomalous em charge in general fails to vanish for the loops of hairpins. For the braids possibly associated with the loops of tRNA the strands can only end up to tRNA itself or nuclear membrane. If there are no braid strands associated with these regions, there is no color or anomalous em charge to be canceled so that the situation trivializes. On the other hand, in the case of tRNA I and U associated with the first nucleotide of the anticodon of tRNA can have a varying value of anomalous em charge. Therefore integer valued em charge and color singletness become possible for tRNA. tRNA can also contain amino-acids. If the amino-acids can carry a varying anomalous em charge with a spectrum corresponding to its values for DNA codons coding it, also they could help to stabilize tRNA by cancelling the anomalous em charge.

2. tRNA plus amino-acid

1. Amino-acyl tRNA synthetase, which is the catalyst inducing the fusion of amino-acid with ACC stem [I51], could have braid strands to both amino-acid and tRNA and have regions with opposite anomalous em charges compensating separately that of amino-acid and of the active part of tRNA. The required correlation of amino-acid with anticodon would suggest that both D and T loops and A-loop are included. The simplest option is however that the

anticodon is connected by braid to amino-acid so that braiding would define the genetic code at the fundamental level and the many-to-one character of genetic code would reflect the 1-to-many character of amino-acid-quark triplet correspondence. This hypothesis is easy to kill: for the portion of catalyst attaching to a given portion of DNA strand amino-acids and codons should have opposite anomalous em charges: $Q_a(amino) = -Q_a(codon)$.

2. After the catalysis involving reduction of $\hbar$ amino-acid and tRNA would form a system with a vanishing net anomalous em charge but with a braiding structure more complex than that before the fusion.

3. In the translation process the braiding structure of tRNA- amino-acid system should reorganize: the braid strands connecting anticodon with amino-acid are transformed to braid strands connecting it to mRNA codon with a subsequent reduction of $\hbar$ of braid strands bringing tRNA into the vicinity of mRNA. In the transcription the anticodon-codon braiding would be replaced with amino-acid-mRNA braiding forcing formation of the amino-acid sequence. It will be later found that the simpler option without this step corresponds to the earlier hypothesis according to which amino-acids acted originally as catalysts for the formation of RNA double helix.

4. tRNA is basically coded by genes which suggests that the general symmetries of the genetic code apply to to the variants of tRNA associated with same anticodon. Hence the variants should result from each other by isospin splits and modifications such as permutations of subsequent nucleotides and addition of AT and CG pairs not changing overall color and isospin properties. Also anomalous base pairs $X*Y$ can be added provide their net anomalous em charge vanishes.

5. tRNA has a complex tertiary (3-D) structure [I48] involving base pairing of distant nucleotides associated with the roots of the stem regions where tRNA twists sharply. This pairing could involve formation of braid strands connecting the nucleotides involved. The reduction of Planck constant for these strands could be an essential element of the formation of the tertiary structure.

The fossilized components of tRNA as record about the evolution of the recent form of the genetic code

The ordinary tRNA indeed seems to contain in its structure fossilized components providing a record about how the molecular evolution proceeded. tRNA_1 and tRNA_2 correspond naturally to the horizontal and vertical segment in the recent tRNA formed as a fusion of tRNA_1 and tRNA_2 to form a cross like structure (see figure above). Hence tRNA_1 and trNA_2 should represent in their structures the respective genetic codes.

1. tRNA_2 should contain both the conjugate of the coding RNA nucleotide attaching to RNA_2 plus the conjugate of the coded nucleotide to which RNA nucleotide was attached and then transferred to RNA_2 and added to the growing RNA sequence. This means that the structure of tRNA should help to deduce the doublet code experimentally. The pairs formed by the RNA triplet XYZ at the end of the anticodon arm of the ordinary tRNA and the pair formed by the triplet $X'Y'Z'$ and its conjugate on right and left sides of XYZ should provide detailed information about the doublet code. The pairs $XY - X'Y'$ should represent the doublet code apart from possible symmetry breaking effects. These effects might be induced at the level of $X'Y'Z'$-amino-acid correspondence level and thus not visible in the structure of tRNA.

2. The transition to the triplet code added one RNA nucleotide to both the exotic doublet $(XY)_2$ and the doublet $X'Y'$ and its conjugate coded by it. The exotic $2', 5'$ doublet plus the added singlet transformed to ordinary triplet. The simplest assumption is that these RNAs came from D arm and TψC arm. This is possible since all loops are physically near to each other. The structure of D and Tψ loops conforms with the assumption that the predecessor of the first *resp.* second loop has lost the coding *resp.* coded RNA. The structure of these loops forces also to conclude that all tRNA loops have been stem like structures before their deactivation just as the acceptor stem is. Deactivation of RNA_1 translation process must have

meant the completion of these stems to loops by addition of a conjugate of the conjugate of the coded RNA.

The components of tRNA as ribozymes which have acted originally as RNA polymerases

The mechanism of ribozyme catalyzed polymerization for both the exotic RNA with mono- *resp.* disphosphate backbones, and their their double strand can be guessed from the fact that the process can be seen as an unfaithful replication. Hence the tRNAs involved would play a role analogous to DNA polymeraze in the polymerization of DNA. The only difference is that, instead of the conjugate of the template strand, a copy of strand is reproduced and the copy can be un-faithful.

DNA replication utilizes the conjugate strand as a template and occurs with the mediation of DNA polymerase enzyme, which brings dXTP, $X = A, T, C, G$ rather than dXMP, to the vicinity of the DNA conjugate strand [I61]. The di-phosphate is cleaved out from dXTP and the liberated energy makes it possible to add the resulting dXMP to the growing DNA strand.

The prediction is that tRNA_1 and tRNA_2 have originally been ribozymes acting as exotic RNA polymerases. In the case of DNA strand dXMP pairs with its conjugate in the template strand by hydrogen bonds and $3', 5'$ bond is formed between monophosphate deoxiribose of previous nucleoside. In the case of exotic RNA strand the XMP associated with the tRNA pairs with its conjugate in the template RNA strand, $2', 5'$ bond with the ribose of the previous RNA unit is formed. tRNA is not so selective as a polymerase as DNA polymerase and this ultimately gives rise to the many-to-one correspondence crucial for the non-triviality of the genetic code.

1. RNA_2 consists of exotic RNA doublets with nucleotides connected by $2', 5'$ monophosphate bonds. tRNA_2 brings $2', 5'$ doublet $\mathrm{XMP}_2 \circ \mathrm{YTP}_2$ to the growing strand and glues it to the $5'$ position of the ribose in the already existing polymer. The YTP suffers the cleavage $\mathrm{YTP}_2 \to \mathrm{YMP}_2$ as in the case of DNA polymerization and the amount of metabolic energy provided by the cleavage is the same. The formation of $\mathrm{XMP}_2 \circ \mathrm{YTP}_2$ proceeds by gluing of XTP_2 to YTP_2 by a similar process so that the net metabolic energy used per nucleotide is essentially the same as in the ordinary DNA polymerization.

2. RNA_1 consists of exotic RNA singlets connected by $2', 5'$ diphosphate bonds. tRNA_1 brings XTP_2 near the growing strand, the cleavage $\mathrm{XTP}_2 \to \mathrm{XDP}_2$ occurs, and XDP_2 is glued to the $5'$ position of the ribose of the previous RNA nucleotide. The amount of metabolic energy provided by the cleavage is roughly one half of that in the case of RNA_2 polymerization, and this might partially explain why diphosphate exotic RNA strands are rare whereas monophosphate exotic DNA strands can be found inside cells. On the other hand, it is $ATP \to ADP$ cleavage, which usually occurs in the ordinary metabolism instead of $ATP \to$ AMP cleavage: only during a very intense metabolism $ATP \to$ AMP cleavage occurs. Since ATP metabolism is a functional fossil from a very early period of evolution, one might expect that $ATP \to$ ADP cleavage has in fact occurred naturally, if not even more naturally, also in the polymerization of $2', 5'$ RNA during (exotic) RNA era.

3. In the case of double exotic RNA strand of ordinary and exotic RNA the predecessor of the recent tRNA formed by $\mathrm{tRNA}_1 + \mathrm{tRNA}_2$ would be a ribozyme bringing energized singlet and doublet RNAs to the double strand acting as a template with tRNA_1 component catalyzing the cleavage of the monophosphate and tRNA_2 component catalyzing the cleavage of the diphosphate.

The crucial and testable prediction is that the ribozymes responsible for the exotic mono- and diphosphate $2', 5'$ RNA polymerization should have a strong resemblance with the two structural components of the recent tRNA. Furthermore, the replication catalyzed by these ribozymes should be unfaithful, perhaps in a manner consistent with the genetic code before the breaking of its symmetries. Ribozymes responsible for the ordinary RNA polymerization are known but I am not aware about how much is known about the corresponding ribozymes in the case of $2', 5'$ RNA. The building blocks of recent tRNA would however provide a good starting point for innovative RNA engineers. In any case, the very fact that this form of RNA does not even allow DNA, makes it a more natural candidate for the basic building block of RNA life than $3', 5'$ RNA.

From RNA world to RNA-tRNA world to RNA-DNA-tRNA world to DNA-RNA-protein world: how it went?

I encountered a highly interesting work [I76] (see http://tinyurl.com/y9ps2efz) related to the emergence of RNA world and I warmly recommend it to the reader (for a popular article see http://tinyurl.com/y7m3absu).

First a summary of basic terms for the possible reader of the article. There are three key enzymes involved in the process which is believed to lead to a formation of longer RNA sequences able to replicate.

1. Ribozyme is a piece of RNA acting as catalyst. In RNA world RNA had to serve also as a catalyst. In DNA world proteins took this task but their production requires DNA and transcription-translation machinery.

2. RNA ligase promotes a fusion of RNA fragments to a longer one in presence of ATP transforming to AMP and diphospate and giving metabolic energy presumably going to the fusion. In TGD fUniverse this would involve generation of an atom (presumably hydrogen) with non-standard value of $h_{eff} = n \times h$ having smaller binding energy scales so that ATP is needed. These dark bonds would be involved with all bio-catalytic processes.

3. RNA polymerase promotes a polymerization of RNA from building bricks. It looks to me like a special kind of ligase adding only single nucleotide to an existing sequence. In TGD Universe $h_{eff} = n \times h$ atoms would be involved as also magnetic flux tubes carrying dark analog of DNA with codons replaced with dark proton triplets.

4. RNA recombinase promotes RNA strands to exchange pieces of same length. Topologically this corresponds to two reconnections occurring at points defining the ends of piece. In TGD Universe these reconnections would occur for magnetic flux tubes containing dark variant of DNA and induce the chemical processes at the level of chemistry.

Self ligation should take place. RNA strands would serve as ligases for the generation of longer RNA strands. The smallest RNA sequences exhibiting self-ligation activity was found to be 40-nucleotide RNA and shorter than expected. It had lowest efficiency but highest functional flexibility to ligate substrates to itself. R18 - established RNA polymerase model - had highest efficiency and highest selectivity. What I can say about the results is that they give support for the notion of RNA world.

The work is related to the vision about RNA world proposed to precede DNA-RNA-protein world. Why I found it so interesting is that it relates to on particular TGD inspired glimpse to what happened in primordial biology.

In TGD Universe it is natural to imagine 3 or even 4 worlds.There are two scenarios: RNA world, RNA-tRNA world, and DNA-RNA-protein world and RNA world, RNA-tRNA world, DNA-RNA-tRNA world and DNA-RNA-tRNA-protein world.

Years ago I developed a rather detailed version of the idea about transition from RNA world to DNA-RNA-protein world [K19] but I did not realize the tRNA-RNA world as intermediate step (see http://tinyurl.com/y8ho27rq).

1. RNA world would contain only RNA. Protein enzymes would not be present in RNA world and RNA itself should catalyze the processes needed to for polymerization, replication, and recombination of RNA. Ribozymes are the RNA counterparts of enzymes. In the beginning RNA would itself act as ribozymes catalyzing these processes.

2. One can also try to imagine RNA-tRNA world. The predecessors of tRNA molecules containing just single amino-acid could have catalyzed the fusion of RNA nucleotide to a growing RNA sequence in accordance with the genetic code. The function of tRNA would thus been different: since the roles of RNA codon and amino-acid would have been changed from the usual. Amino-acid sequences would not have been present at this stage since there would be no machinery for their polymerisation.

3. One can consider a transition from this world to DNA-RNA-tRNA world. This would storage of genetic information to DNA from which it would have been transcribed by using polymerase consisting of RNA. This phase would have required the presence of cell membrane like structure since DNA is stabilized inside membranes or at them. Transition to this world should have involved reverse transcription catalyzed by RNA based reverse-transcriptase. Being a big evolutionary step, this transition should involve a phase transition increasing the value of $h_{eff} = n \times h$.

4. My earlier proposal has been that a transition from RNA world to DNA-RNA-protein world took place. The transition could have also taken place from DNA-RNA-tRNA world to world containing also amino-acid sequences and have led to rapid evolution of catalysis based on amino-acid sequences.

   The amino-acid sequences originating from tRNA originally catalyzing RNA replication stole the place of RNA sequences as the end products from RNA replication. The ribosome started to function as a translator of RNA sequences to amino-acid sequences rather than replication of them to RNAs! The roles of protein and RNA changed! Instead of RNA in tRNA the amino-acid in tRNA joined to the sequence! The existing machinery started to produce amino-acid sequences!

   Presumably the modification of ribosome or tRNA involved addition of protein parts to ribosome, which led to a quantum critical situation in which the roles of proteins and RNA polymers could change temporarily. When protein production became possible even temporarily, the produced proteins began to modify ribosome further to become even more favorable for the production of proteins.

   But how to produce the RNA sequences? The RNA replication machinery was stolen in the revolution. DNA had to do that via transcription to mRNA! DNA had to emerge before the revolution or at the same time and make possible the production of RNA via transcription of DNA to mRNA. The most natural options corresponds to "before", that is DNA-RNA-tRNA world. DNA could have emerged during RNA-tRNA era together with reverse transcription of RNA to DNA with RNA sequences defining ribozymes acting as reverse transcriptase. This would have become possible after the emergence of predecessor of cell membrane. After that step DNA sequences and amino-acid sequences would have been able to make the revolution together so that RNA as the master of the world was forced to become a mere servant!

   The really science fictive option would be the identification of the reverse transcription as time reversal of transcription. In zero energy ontology (ZEO) this option can be considered at least at the level of dark DNA and RNA providing the template of dynamics for ordinary matter.

How the copying of RNA strand to its conjugate strand catalysed by amino-acid of tRNA could have transformed to translation of RNA to amino-acid sequence? Something certainly changed.

1. The change must have occurred most naturally to tRNA or - less plausibly - to the predecessor of the ribosome machinery. The change in the chemical structure of tRNA is not a plausible option. Something more than chemistry is required and in TGD Universe dark matter localized at magnetic flux tubes is the natural candidate.

2. Evolution corresponds in TGD Universe gradual increase of $h_{eff} = n \times h$. A dramatic evolutionary step indeed took place. The increase of the value of $h_{eff} = n \times h$ for some structural element of tRNA could have occurred so that the catalysis for amino-acid sequence instead of that for RNA sequence started to occur.

3. The general model for bio-catalysis in TGD Universe involves a contraction of magnetic flux tubes by a reduction of h_{eff} and bringing together the reacting molecules associated with flux tubes: this explains the magic looking ability of biomolecules to find each other in the dense molecular soup. The reduction of h_{eff} for some dark atom(s) of some reacting molecules(s) to a smaller value liberates temporarily energy allowing to kick the reactants over a potential

wall so that the reaction can occur (atomic binding energies scale as $1/h_{eff}^2$). After than the liberated energy is absorbed and ordinary atom transforms back to dark atom.

In the recent case h_{eff} associated with a dark atom (or atoms) of tRNA could have increased so that the binding energy liberated would have increased and allowed to overcome a higher potential wall than before. If the potential wall needed to overcome in the fusion of additional amino-acid to a growing protein is higher than that in the fusion of additional RNA to a growing RNA sequence, this model could work.

4. The activation energy for the addition of amino-acid should be larger than that for RNA nucleotide. A calculated estimate for the activation energy for the addition of amino-acid is 63.2 eV (see `http://tinyurl.com/yab6dmrm`). An estimate for the activation energy for the addition of RNA nucleotide at the temperature range 37-13 C is in the range 35.6 -70.2 eV (see `http://tinyurl.com/y8xwpvvg`). An estimate for the activation energy for the addition of DNA nucleotide is 58.7 eV (see `http://tinyurl.com/yc8nr4kh`) The value in the case RNA would be considerably smaller than that in the case of amino-acids at physiological temperature. For DNA and amino-acid the activation energy would be somewhat smaller than for amino-acid. This is consistent with the proposed scenario. I am not able to decide how reliable these estimates are.

The natural first guess is that the dark atoms are hydrogen atoms. It is however not at all clear whether "ordinary" hydrogen atoms correspond to $n = h_{eff}/h = n = 1$.

1. Randell Mills [D3] has proposed his notion of hydrino atom to explain anomalous energy production and EUV radiation in 10-20 nm range taking place in certain electrolytic system and having no chemical explanation. The proposal of Mills is that hydrogen atom can make in presence of a catalyst a transition to a lower energy state with a reduced size. I have already earlier considered some TGD inspired models for hydrino. The resemblance with the claimed cold fusion suggests that the energy production involved in the two cases might involve the same mechanism.

   I have considered two models for the findings [L23]. The first model is a variant of cold fusion model that might explain the energy production and the observed radiation at EUV energy range. Second model is a variant of hydrino atom assuming that ordinary hydrogen atom corresponds to $h_{eff}/h = n_H > 1$ and that catalyst containing hydrogen atoms with lower value of $n_h < n_H$ could induce a phase transition transforming hydrogen atoms to hydrinos with binding energy spectrum scaled up by scaling factor $(n_H/n_h)^2$ and radii scaled down by $(n_h/n_H)^2$. The findings of Mills favour the value $n_H = 6$.

2. Suppose the transition corresponds to a transition analogous to photon emission so that it occurs between $\Delta J = 1$ transitions of hydrogen atom. There are two simple options: either the direction of electron spin change but orbital angular momentum remains unaffected or the angular momentum of electron changes by $\Delta L = 1$ but spin direction does not change.

   The simplest assumption is that the principal quantum numbers in the initial and final state are $n_i = 1$ and $n_f \geq n_i$. Assume first that initial state with $(n_{Hi}, n_i = 1)$ having $L_i = 0$ and final state with $(n_{Hf}, n_f \geq n_i)$.

3. The energy difference between the initial state with $(n_{Hi}, n_i = 1)$ and final state with (n_{Hf}, n_f). The initial binding energy is the ordinary binding of thought-to-be hydrogen atom in the ground state: $E_i = E_f(n_{Hf}/n_{Hi})^2 \simeq 13.6$ eV. Here E_f denotes the final ground state binding energy. The final state binding energy is $E_{fn_f} = E_f/n_f^2$.

   The liberated energy defining the order of magnitude for the activation energy (thermodynamical quantity) is given by

$$\Delta E = E_{fn_f} - E_i = \frac{E_f}{n_f^2} - E_f(\frac{n_{Hf}}{n_{Hi}})^2 = E_i\left[(\frac{n_{Hi}}{n_{Hf}})^2 n_f^{-2} - 1\right] \quad . \tag{5.5.1}$$

   The condition $\Delta E > 0$ gives

Table 5.4: The liberated energy in transition $(n_{Hi}, n_i = 1) \to (n_{Hf}, n_f = 2)$ in some cases.

(n_{Hi}, n_i)	(n_{Hf}, n_f)	$\Delta E/eV$
$(3,1)$	$(1,2)$	17.0
$(4,1)$	$(1,2)$	40.8
$(4,1)$	$(2,2)$	0.0
$(5,1)$	$(1,2)$	71.4
$(5,1)$	$(2,2)$	7.7
$(6,1)$	$(1,2)$	109.0
$(6,1)$	$(2,2)$	17.0

$$\frac{n_{Hi}}{n_{Hf}} > n_f \quad .$$

For $n_{Hi}/n_{Hf} = n_f$ one has $\Delta E = 0$. For instance, this occurs for $(n_{Hi}, n_{Hf}) \in \{(2,1), (6,3), (6,2)\}$ $\Delta E > 0$ condition gives $n_{Hi} > 2$.

4. Consider first $n_i = n_f = 1$ for which the spin direction of electron changes if the transition is analogous to photon emission. By putting $n_f = 1$ in Eq. 5.5.1 one obtains a formula for the transition energy in this case. For instance, $(n_{Hi}, n_i) = (6,1) \to (n_{Hf}, n_f) = (3,1)$ would correspond to $\Delta E = 40.8$ eV perhaps assignable to RNA polymerization and the transition $(n_{Hi}, n_i) = (7,1) \to (n_{Hf}, n_f) = (3,1)$ to $\Delta E = 60.4$ eV perhaps assignable to amino-acid polymerization and DNA polymerization. Note that $n_H = 6$ is supported by the findings of Mills.

5. Table 5.4 gives the liberated energies ΔE for transitions with $(n_i, n_f) = (1,2)$ in some cases. The transitions $(4,1) \to (1,2)$ resp. $(5,1) \to (1,2)$ might give rise to the activation energies associated with RNA resp. amino-acid polymerization.

6. If ordinary hydrogen atom and atoms in general correspond to $h_{eff}/h = n = 1$, the liberated energies would be below the ground state energy $E_0 = 13.6$ eV of hydrogen atom and considerably below the above estimates. For heavier atoms the binding energy scale would be Z^2-fold and already for carbon with $Z = 6$ by a factor 36 higher. It is difficult to obtain ΔE in the scale suggested by the estimates for the activation energies.

One could try to test whether tRNA could be modified to a state in which RNA is translates to RNA sequences rather than proteins. This would require a reduction of $h_{eff} = n \times h$ for the dark atom in question.

5.5.4 Recent Genetic Code As A Fusion Of Singlet And Doublet Codes?

There are several guidelines helping to answer the question how DNA-amino-acid translation might have emerged from singlet and doublet codes producing only RNA from RNA.

The following vision about evolution leading from RNA era to the recent DNA-RNA-amino-acid era inspired by a combination of RNA world vision [I142] with the detailed study of the structure of tRNA suggesting the presence of 1- and 2-codes during RNA era with the DNA as TQC vision suggesting the presence of cell membrane like structures as a necessary ingredient making possible topological quantum computation like processes already during RNA era. The recent model is considerably simpler than the earlier models [**?**].

RNA era and the transition to RNA-amino-acid era

1. Translation of mRNA to amino-acid sequences separates from the transcription of DNA to mRNA. One expects that during RNA two different kinds of RNAs, call them RNA_2 and RNA_1, analogous to mRNA and proteins existed. RNA_2 can be identified as the ordinary $3', 5'$ RNA acting in the role of mRNA. A natural candidate for RNA_1 playing the role of

proteins is $2', 5'$ RNA since it is generated in the experiments of Orgel and appears also in genomes. Of course, also other candidates can be considered and the structure of tRNA gives valuable information about the character of this RNA. The copying of RNA_2 to its conjugate was the counterpart of RNA replication. The transcription of RNA_2 to RNA_1 was the counterpart of translation.

2. The structure of tRNA, call it $tRNA_3$, gives valuable information about the course of events leading to the translation of mRNA to amino-acids. The cross like structure of $tRNA_3$ and the decomposition of RNA triplet appearing in it to 2-codon and 1-codon suggests that it resulted as a fusion of two hairpin like molecules $tRNA_1$ and $tRNA_2$. $tRNA_2$ brought pairs of nucleotides forming the 2-codon part of RNA triplet to the growing RNA_2 sequence during replication and 2-code was simply RNA conjugation. $tRNA_1$ was involved with transcription of RNA_2 to RNA_1 bringing RNA_1 nucleotides one-by own to the growing sequence. In $tRNA_3$ the third nucleotide does not quite correspond to ordinary RNA but to to A, G, U or I(nositol) and is believed to differ geometrically from ordinary nucleotide, and one can assume that these nucleotides were the building blocks of RNA_1 possibly appearing in $2', 5'$ form. The phenomenon of the wobble pairing can be assumed to have been present already during RNA era so that correspondence 1-code was not not 1-to-1 nor deterministic but given by the correspondence $\{U \to A, C \to G, \{A, G\} \to U, \{U, A, C\} \to I\}$ deduced from the number 40 of tRNAs and assigning unique 1-codon to only G could be interpreted as a many-to-one and non-deterministic correspondence generating new RNA sequences from existing ones. If there was RNA_2 sequence coding for $tRNA_1$, this sequence appearing in hairpin structure could have coded the inverse of the translation. As a consequence, the occurrence of transcription and its reversal generated a rapid evolution by creating new kinds of RNA_2 sequences.

3. From the fact that amino-acids are attached to the ACC stem of $tRNA_2$, one can guess that the role of amino-acids during RNA era was to catalyze the replication. If single amino-acid would have catalyzed the attachment of given RNA doublet to the growing sequence, there would be at most 16 amino-acids and genetic coded would not depend at all on the third nucleotide. This is indeed the case for roughly half of the code table (both matter antimatter symmetry and isospin symmetry with respect to third codon). For those mRNA codons for which A, G and T, C correspond to different amino-acids (breaking of matter antimatter asymmetry but isospin symmetry) two amino-acids catalyzed the attachment. Same amino-acid could also catalyzed two different attachments (ser, arg, leu for standard genetic code).

4. The crucial step was the fusion of the 1-code and 2-code to 3-code took place via fusion of $tRNA_1$ and $tRNA_2$ to $tRNA_3$ along their ends containing RNA_1 nucleotide and RNA_2 doublet which thus combined to RNA triplet. Presumably $tRNA_3$ in its original form was translated from a linear mRNA molecule and transformed spontaneously to the cross like shape because of the presence of palindrome structures in both. The original functions of tRNAs were not possible anymore since the triplet was not at the end of the molecule. The catalyzing amino-acid however was at the ACC end of and the function of $tRNA_3$ became to assist the translation of mRNA to amino-acid sequence. For those 3-codons for which single amino-acid catalyzed the fusion of 2-codon, a full matter antimatter and isospin symmetry resulted. For those 3-codons for which two amino-acids catalyzed the fusion, a breaking of matter antimatter symmetry took place in the sense that for given mRNA codon only the $tRNA_3$ corresponding to single amino-acid was stable. Isospin symmetry was broken only weakly or not at all (human mitochondrial code). Thus codons with A, G as third nucleotide almost always coded the first amino-acid and those with T, C as the third nucleotide the second one. Stopping codons resulted when all $tRNA_3$ corresponding to mRNA triplet were unstable. That same RNA can code for both amino-acid and act as a stop codon in certain situations, can be understood if the stability of corresponding $tRNA_3$ depends on the chemical environment.

Symbiosis with membrane bounded structures

In DNA as TQC picture nuclear and cell membranes make possible topological quantum computation. The magnetic flux tubes connecting DNA nucleotides to lipids of the cell membrane could also explain why DNA is stabile inside cell. The emergence of cell membranes consisting of lipids and generated via self-organization rather being coded by genes would have stabilized DNA generated in this manner during DNA-RNA-amino-acid era. Membrane bounded structures emerged when the space-time sheets corresponding to the p-adic length scale $k = 151$ emerged in the condensate.

Topological quantum computation should have taken place already during RNA era. This suggest that the counterpart of the cell membrane was present already at that time. Quite recently it was reported [I96] that DNA duplexes of length 6 to 20 base pairs can join to longer cylinders which in turn form liquid crystals and that the liquid crystal phase separates from the phase formed by single DNA strands. Long strands had been already earlier known to form liquid crystals. This encourages to think that also RNA duplexes are able to self-organize in this manner so that the analog of cell nucleus containing RNA double helices as genetic material could have existed already during RNA era.

The latter option would allow to distinguish between RNA_2 and RNA_1 used as building block of various structures. This suggests that RNA_1, which disappeared in the transition to RNA-amino-acid era, might have formed liquid membranes containing inside then RNA_2 such that RNA_2 nucleotides were connected by magnetic flux tubes to RNA_1 nucleotides. The minimal function of RNA_1 would have been to make possible the buildup of cell membrane. In this case the lengths of RNA_1 needed to be only of order $L_e(151) = 10$ nm. The sequences consisting of 30 RNA_1 base pairs would correspond roughly to the thickness of cell membrane and to the codon of M_{61} code. Lipid layer of thickness 5 nm would correspond to roughly 16 base pairs and to the codon assignable to M_{17}. If magnetic flux tubes indeed stabilize DNA, the presence of RNA_1 membrane might have been enough to stabilize also DNA so that RNA era could have been followed by DNA-RNA era and eventually by DNA-RNA-amino-acid era with RNA_1 membrane being replaced by double lipid layer membrane.

Reverse transcription of RNA to DNA

The basic problem was how to build DNA sequences which would later take the command. If one, in conflict with the Central Dogma, assumes the presence of the predecessor of the so called reverse RNA transcriptase [J3] associated with retro-viruses (in particular HIV virus), one can understand how this step occurred. Reverse RNA transcriptase allowed to transform ordinary RNA sequences to DNA sequences inside newly emerged pre-nuclei. The reverse transcriptase catalyzes also the transcription of DNA back to RNA so that DNA began to produce new RNA.

Reverse transcriptase requires amino-acids sequences. Amino-acids appeared as catalysts in $tRNA_2$ already during RNA era but the spontaneous emergence of reverse transcriptase before RNA$\rightarrow$ amino-acids translation look improbable. After the fusion of $tRNA_1$ and $tRNA_2$ RNA_2 could replicate only if $tRNA_1$, $tRNA_2$ and $tRNA_3$ continued to live in symbiosis for some time. This could have led naturally to the generation of reverse transcriptase and DNA. After that DNA could have taken care of the production of RNA and $tRNA_1$ and $tRNA_2$ might have lost in the fight for molecular survival or at least their importance could have diminished. The emergence of DNA could have been associated with the replacement of RNA_1 membrane with ordinary cell membrane. For instance, it might be that DNA was able to form only magnetic flux tubes only with lipid bilayer membrane.

The reverse transcription is not reliable (one error per about 1000 nucleotides), and this led to a rapid evolution of DNA analogous to that of HIV virus. This meant an escape from the fixed point situation, and a genuine DNA $\rightarrow$ RNA predecessor of the genetic code emerged. Together with the emergence of membrane bounded structures this meant genuine evolution at DNA level. Reverse transcription is possible only for the ordinary RNA and explains why exotic doublet RNA has disappeared from cell.

What were the first self replicators?

The TGD inspired model of pre-biotic evolution suggests a reasonable guess for the first self-replicating molecular entities. Both $tRNA_1$ and $tRNA_2$ molecules must have resulted as more or less copies of corresponding RNA_2 sequences (amino-acid was added after transcription to $tRNA_2$) and the minimal self-reproducing system could have consisted of $tRNA_1$, $tRNA_2$ and corresponding RNA_2 molecules. Since $tRNA_1$ and $tRNA_2$ are hairpins in the usual configuration and the mechanism making possible biochemical reaction series suggests that these hairpin molecules catalyzed the opening of the corresponding RNA_2 pieces and their coding to $tRNA_1$ or $tRNA_2$.

Note that double strands in the sense they occur for DNA are not necessary since the double strand part of hairpin is analogous to DNA double strand and the opening of hairpin structure is analogous to the opening of DNA double strand during transcription and replication. The non-determinism of 1-code could have rapidly led to a genuine evolution and one can also imagine a spontaneous generation of RNA_2 sequences as oligonucleotides consisting of copies of pieces of RNA_2 coding for $tRNA_2$.

Also more general hairpin might be used to construct a self-catalyzing system. Since exotic and normal RNA do not differ too much, a reasonable amount of guess work might allow to identify $tRNA_1$ and $tRNA_2$, and perhaps even create simple pre-biotic life-forms in the laboratory.

5.5.5 Is RNA Era Continuing Inside Cell Nuclei?

The last issue of [I59] contains an article about the discovery that only roughly one half of DNA expresses itself as amino-acid sequences. A detailed summary of the results has been published in Nature [I20]. The Encyclopedia of DNA Elements (ENCODE) project has quantified RNA transcription patterns and found that while the "standard" RNA copy of a gene gets translated into a protein as expected, for each copy of a gene cells also make RNA copies of many other sections of DNA. In particular, intron portions ("junk DNA", the portion of which increases as one climbs up in evolutionary hierarchy) are transcribed to RNA in large amounts. What is also interesting that the RNA fragments correspond to pieces from several genes which raises the question whether there is some fundamental unit smaller than gene.

None of the extra RNA fragments gets translated into proteins, so the race is on to discover just what their function is. TGD proposal is that the RNA gets braided and performs a lot of topological quantum computation [**?**]. Topologically quantum computing RNA fits nicely with replicating number theoretic braids associated with light-like orbits of partonic 2-surfaces and with their spatial "printed text" representations as linked and knotted partonic 2-surfaces giving braids. An interesting question is how printing and reading could take place. Is it something comparable to what occurs when we read consciously? Is the biological portion of our conscious life identifiable with this reading process accompanied by copying by cell replication and as secondary printing using amino-acid sequences?

This picture conforms with TGD view about pre-biotic evolution. Plasmoids [I119], which are known to share many basic characteristics assigned with life, came first: high temperatures are not a problem in TGD Universe since given frequency corresponds to energy above thermal energy for large enough value of $\hbar$ [K18]. Plasmoids were followed by RNA, and DNA and amino-acid sequences emerged only after the fusion of 1- and 2-letter codes fusing to the recent 3-letter code. The cross like structure of tRNA molecules carries clear signatures supporting this vision. RNA would be still responsible for roughly half of intracellular life and perhaps for the core of "intelligent life".

I have also proposed that this expression uses memetic code which would correspond to Mersenne $M_{127} = 2^{127} - 1$ with 2^{126} codons whereas ordinary genetic code would correspond to $M_7 = 2^7 - 1$ with 2^6 codons. Memetic codons in DNA representations would consist of sequences of 21 ordinary codons. Also representations in terms of field patterns with duration of.1 seconds (secondary p-adic time scale associated with M_{127} defining a fundamental bio-rhythm) can be considered.

A hypothesis worth of killing would be that the DNA coding for RNA has memetic codons scattered around genome as basic units. It is interesting to see whether the structure of DNA could give any hints that memetic codon appears as a basic unit.

1. In a "relaxed" double-helical segment of DNA, the two strands twist [I44] around the helical

axis once every 10.4 base pairs of sequence. 21 genetic codons correspond 63 base pairs whereas 6 full twists would correspond to 62.4 base pairs.

2. Nucleosomes [I32] are fundamental repeating units in eukaryotic chromatin [I11] possessing what is known as 10 nm beads-on-string structure. They repeat roughly every 200 base pairs: integer number of genetic codons would suggest 201 base pairs. 3 memetic codons makes 189 base pairs. Could this mean that only a fraction $p \sim 12/201$, which happens to be of the same order of magnitude as the portion of introns in human genome, consists of ordinary codons? Inside nucleosomes the distance between neighboring contacts between histone and DNA is about 10 nm, the electron Compton scale $L_e(151)$ associated with the Gaussian Mersenne $(1+i)^{151}-1$ characterizing also cell membrane thickness and the size of nucleosomes. This length corresponds to 10 codons so that there would be two contacts per single memetic codon in a reasonable approximation. In the example of Wikipedia [I32] nucleosome corresponds to about 146=126+20 base pairs: 147 base pairs would make 2 memetic codons and 7 genetic codons. The remaining 54 base pairs between histone units + 3 ordinary codons from histone unit would make single memetic codon. That only single memetic codon is between histone units and part of the memetic codon overlaps with histone containing unit conforms with the finding that chromatin accessibility and histone modification patterns are highly predictive of both the presence and activity of transcription start sites. This would leave 4 genetic codons and 201 base pairs could decompose as memetic codon+2 genetic codons+memetic codon+2 genetic codons. The simplest possibility is however that memetic codons are between histone units and histone units consist of genetic codons. Note that memetic codons could be transcribed without the straightening of histone unit occurring during the transcription leading to protein coding.

5.5.6 Could Nanno-Bacteria Correspond To Predecessors Of TheTriplet Life-Forms?

The experiments of Leslie Orgel (at 1980) imitating the primordial ocean demonstrate the emergence of the exotic RNA for which doublet effectively replaces the triplet. The so called nanno-bacteria represent a mystery at the borderline between living and non-living matter. The web article of Robert L. Folk [I130], who is one of the pioneers in the field besides Y. Morita [I132] and E. O. Kajander [I93], provides a brief summary about nanno-bacteria and contains also references. A priori one cannot exclude the possibility that nanno-bacteria might represent a predecessor of the triplet code, perhaps even singlet or doublet life-form or their symbiosis.

Basic facts about nanno-bacteria

Nanno-bacteria (often called also nanobacteria) are considerably smaller than ordinary bacteria. The sizes of the nanno-bacteria vary from about 20 nm to.2 micro-meters. Thus the smallest nanno-bacteria have size scale not much above $L_e(151)$ so that optical microscope does not allow to study them. Indeed, geologists discovered nanno-bacteria by using scanning electron microscope.

Nanno-bacteria can originate a precipitation in calcite and argonite crystals by providing the seed of the crystal. Nanno-bacteria act also as catalysts by attracting cations to their negatively charged cell walls. They appear as dense clumps in various minerals and rocks such as limestones, dolomites, native sulphur crystals, and metallic sulfide minerals [I130]. Nanno-bacteria produce complex silicates such as clays, where their sizes can be as small as 30 nanometers. They are involved even with the construction of bird's eggs! Nanno-bacteria of size about.1 micro-meters were found in the Martian meteorite ALH84001 [E6], and there is evidence that carbonaceous chondrite meteorite Allende [I130] contains them. According to Folk, the nanno-bacteria might the biological counterpart of the dark matter perhaps dominating over the ordinary bio-matter in the entire universe. An interesting question is how deep in the rock nanno-bacteria based life forms can survive. The hypothesis about intra-terrestrial life suggests that there is no limit here!

Although nanno-bacteria have been demonstrated to replicate [I130], the prevailing belief has been that nanno-bacteria cannot be real life forms since by their small size they cannot contain the usual genetic apparatus. A Finnish biologist Kajander and his collaborators have done a lot of self-funded pioneering work in the study of the nanno-bacteria [I93]. It has not been demonstrated

that nanno-bacteria possess DNA-mRNA-amino-acid translation machinery, the existence of which is often taken almost as a definition for what it is to be a living system (a size larger than.2 micro-meters has been the second prevailing definition of a living system!). This failure could be understood if nanno-bacteria contain only replicating DNA or if only the RNA-to-RNA translation machinery exists possibly accompanied by RNA-DNA transcriptase transforming the code to DNA-RNA code. Due to the hard cell wall of nanno-bacteria, the study of DNA/RNA is very difficult but according to the Kajander's private communication to Folk [I130], the nanno-bacterial DNA exists and consists of very short strands.

Nanno-bacteria as RNA life?

Nanno-bacteria could correspond to some predecessor of the recent genetic code. One can consider several options.

1. Nanno-bacteria represent an RNA life form involving two kinds of RNA sequences and closed inside RNA_1 membrane. This does not require DNA.

2. If the claim of Kajander about about nanno-bacterial DNA is correct, then two options remain.

   i) Nanno-bacteria are able to just replicate DNA and do not possess genetic code. Thus nanno-bacteria would be at a higher level than viruses.

   ii) RNA-DNA reverse transcription is utilized so that nanno-bacteria could realize DNA-RNA code and would probably be at a higher developmental level than RNA life-forms but had not yet realized DNA-amino-acid code. The objection against this is that the reverse transcriptase enzyme probably requires RNA-amino-acid translational machinery.

   One can ask what what RNA life-forms (option 1) would look if they still exist.

1. Singlet RNA would express itself as RNA sequences containing only U (or C) and A (or G) nucleotides. The tRNAs used by these life-forms should appear as fossil remnants in the ordinary tRNA.

2. In the case of a singlet life-form the layer could correspond to the length scale $L_e(2,73)\backslash = "L_e(146)$ and be formed by doublet atomic layer corresponding to the twin pair of p-adic length scales formed by $L_e(16,9)\backslash = "L_e(144)$ and $L_e(2,73)\backslash = "L_e(146)$.

3. In the case of doublet life-forms the length scale $L_e(2,29)\backslash = "L_e(145)$ and the tertiary p-adic length scale $L_e(3,7^2)\backslash = "L_e(147)$ form a twin pair and could define a double-layered structure. The reported hard cell wall could correspond to this double layered structure. A cell wall consisting of minerals (also nanno-bacteria induce also the precipitation of mineral crystals) might however be most appropriate for life-forms living in the pores of rock, and possibly utilizing tectonic energy in some form to satisfy their metabolic needs.

The generation of the triplet code would have been accompanied by the generation of double lipid layers and possibly a transition to water environment. The most natural location for the primitive RNA-RNA translation machinery is at the inner surface of a lipid membrane if present inside nanno-bacteria.

The singlet or doublet RNA life-forms and their fusions could correspond to what I have christened plasmoids. Intelligent looking plasma balls occur repeatedly in UFO reports and they are also reported to occur around crop formations. There is even a report about a plasma ball in the act of constructing the crop formation. The plasmoid like life forms serving as couriers of ITs could be also seen as multi-cellulars consisting of nanno-bacterial cells or, more probably, of their predecessors. The immune response against nanno-bacteria and their predecessors generated during very early evolution would make possible encounters with crops and even humans (abduction experiences) without fatal consequences. The reported immune response against exotic doublet RNA suggests that plasmoids contain exotic doublet RNA. The visible light from plasmoids suggests that the metabolism indeed involves also the hot $k = 131$ space-time sheet so that ITs or IPs might be in question.

Was the encounter of nanno-bacteria and plasmoids the moment of Gaian fertilization?

Earth consists mostly of ancient meteorites known as chondrites. Carbonaceous chondrites are shown to contain not only basic bio-monomers but even nanno-bacteria. The meteoritic material can end up to the interior of Earth along magnetic flux tubes even today. Recall that this mechanism actually explains the magnetized iron from meteors found in crop circles [K12]).

Thus IT life might have developed nanno-bacteria contained by meteorites in the womb of Mother Gaia. The bio-molecules/nanno-bacteria contained by the meteorites from outer space would thus take the role of the sperm as in panspermia theory.

There is a temptation to develop the fertilization metaphor to a more concrete level in order to understand what happened when the symbiosis of pre-nucleus containing DNAandpre-cell containing RNA was established and led to the development of the genetic code and established a genuine evolution.

1. The simple nanno-bacteria in the meteorites having only replicating DNA or perhaps only the ability to produce DNA nucleotides would have been the sperm. Cell nucleus is much smaller than cell and might itself be regarded as having originated from ancient nanno-bacteria. The much more complex pre-cells containing RNA, amino-acids, and reverse transcriptase as well as the potentiality for the realization of the genetic code plus the needed metabolic machinery, were located in the interior of Earth and played the role of the egg. Since the hot $k = 131$ space-time sheets essential for the metabolic machinery were also involved, primitive plasmoid is an excellent candidate for the egg.

2. The encounter of nanno-bacteria and plasmoids led to the fertilization of Mother Gaia. What is fascinating that balls of light reported to appear near the crop circles and reported to even fabricate them migh be there in order to get fertilized by nanno-bacteria contained by meteors! Alternatively, the simultaneous appearance of pre-biotic egg and sperm might be interpreted as a symbolic hint about what happened in the key event of the pre-biotic evolution.

5.6 Did Life Evolve In The Womb Of Mother Gaia?

The idea that Earth interior, even the hot regions at the boundary of core and mantle, could serve as a seat for life, sounds totally outlandish in the standard physics framework. The many-sheeted space-time and hierarchy of Planck constants however allow to consider at least half seriously this idea although I hasten to admit that during these years I have very often had the feeling that this is one of those painfully stubborn fix idees that like to tease imaginative theoretician. This idea has variants characterized by a varying degree of craziness. It is a fact that rocks contain simple life forms down to surprising depths. A crazier idea is that underground lakes could have served as seats for evolving life. The really crazy variant of the idea is that the boundary between mantle and Earth's core as a regions containing strong gradients has been a seat of self organization leading to the emergence of life in some form.

Recently however completely unexpected support for this idea came as I learned that the geological evolution of Earth involves an anomaly. The continents would fit nicely to form a single super continent (Wegener's theory does not predict complete fit) if the radius of Earth would have been at the time of Cambrian explosion by factor of 1/2 smaller than now. The fact that Cambrian explosion is one of the biggies mysteries of biology puts bells ringing. For long time ago this anomaly has inspired what have been called Expanding Earth Theory but the physical mechanism giving rise to expansion has been lacking.

Quantum TGD provides this mechanism. TGD predicts that cosmic expansion does not take place smoothly but via quantum jumps induces by the growth of the Planck constant by a factor of 2 for space-time sheet considered. This holds true also in planetary scales and TGD variant of Expanding Earth theory predicts relatively fast expansion of Earth's radius with a factor 2. The sudden appearance of completely new life forms in Cambrian explosion could be understood as a burst of various multicellular life forms which have developed in the womb of Mother Gaia sheltered from UV light and meteoric bombardment. What remains open is how deep in Earth's interior life is possible. This of course depends also on the definition of life: probably biological

life would not be possible at core mantle boundary but one can consider much more general forms of molecular life.

In the following I will proceed in stepwise manner from not totally crazy (I hope so) to really crazy and discuss first the quantum version of Expanding Earth theory and its possible connection with Cambrian explosion and only after consider the really crazy possibilities.

5.6.1 Quantum Version Of Expanding Earth Theory And Cambrian Explosion

TGD predicts that cosmic expansion at the level of individual astrophysical systems does not take place continuously as in classical gravitation but through discrete quantum phase transitions increasing gravitational Planck constant and thus various quantum length and time scales. The reason would be that stationary quantum states for dark matter in astrophysical length scales cannot expand. One would have the analog of atomic physics in cosmic scales. Increases of $\hbar$ by a power of two are favored in these transitions but also other scalings are possible.

This has quite far reaching implications.

1. These periods have a highly unique description in terms of a critical cosmology for the expanding space-time sheet. The expansion is accelerating. The accelerating cosmic expansion can be assigned to this kind of phase transition in some length scale (TGD Universe is fractal). There is no need to introduce cosmological constant and dark energy would be actually dark matter.

2. The recently observed void which has same size of about 10^8 light years as large voids having galaxies near their boundaries but having an age which is much higher than that of the large voids, would represent one example of jerk-wise expansion.

3. This picture applies also to solar system and planets might be perhaps seen as having once been parts of a more or less connected system, the primordial Sun. The Bohr orbits for inner and outer planets correspond to gravitational Planck constant which is 5 times larger for outer planets. This suggests that the space-time sheet of outer planets has suffered a phase transition increasing the size scale by a factor of 5. Earth can be regarded either as n=1 orbit for Planck constant associated with outer planets or n= 5 orbit for inner planetary system. This might have something to do with the very special position of Earth in planetary system. One could even consider the possibility that both orbits are present as dark matter structures. The phase transition would also explain why n=1 and n=2 Bohr orbits are absent and one only n=3, 4, and 5 are present.

4. Also planets should have experienced this kind of phase transitions increasing the radius: the increase by a factor two would be the simplest situation.

The obvious question - that I did not ask - is whether this kind of phase transition might have occurred for Earth and led from a completely granite covered Earth - Pangeia without seas - to the recent Earth. Neither it did not occur to me to check whether there is any support for a rapid expansion of Earth during some period of its history.

Situation changed when my son visited me and told me about a Youtube video [F51] by Neal Adams, an American comic book and commercial artist who has also produced animations for geologists. We looked the amazing video a couple of times and I looked it again yesterday. The video is very impressive artwork but in the lack of references skeptic probably cannot avoid the feeling that Neal Adams might use his highly developed animation skills to cheat you. I found also a polemic article [F1] of Adams but again the references were lacking. Perhaps the reason of polemic tone was that the concrete animation models make the expanding Earth hypothesis very convincing but geologists refuse to consider seriously arguments by a layman without a formal academic background.

The claims of Adams

The basic claims of Adams were following.

1. The radius of Earth has increased during last 185 million years (dinosaurs [I13] appeared for about 230 million years ago) by about factor 2. If this is assumed all continents have formed at that time a single super-continent, Pangeia, filling the entire Earth surface rather than only 1/4 of it since the total area would have grown by a factor of 4. The basic argument was that it is very difficult to imagine Earth with 1/4 of surface containing granite and 3/4 covered by basalt. If the initial situation was covering by mere granite -as would look natural- it is very difficult for a believer in thermodynamics to imagine how the granite would have gathered to a single connected continent.

2. Adams claims that Earth has grown by keeping its density constant, rather than expanded, so that the mass of Earth has grown linearly with radius. Gravitational acceleration would have thus doubled and could provide a partial explanation for the disappearance of dinosaurs: it is difficult to cope in evolving environment when you get slower all the time.

3. Most of the sea floor is very young and the areas covered by the youngest basalt are the largest ones. This Adams interprets this by saying that the expansion of Earth is accelerating. The alternative interpretation is that the flow rate of the magma slows down as it recedes from the ridge where it erupts. The upper bound of 185 million years for the age of sea floor requires that the expansion period - if it is already over - lasted about 185 million years after which the flow increasing the area of the sea floor transformed to a convective flow with subduction so that the area is not increasing anymore.

4. The fact that the continents fit together - not only at the Atlantic side - but also at the Pacific side gives strong support for the idea that the entire planet was once covered by the super-continent. After the emergence of subduction theory this evidence as been dismissed.

5. I am not sure whether Adams mentions the following objections [F6]. Subduction only occurs on the other side of the subduction zone so that the other side should show evidence of being much older in the case that oceanic subduction zones are in question. This is definitely not the case. This is explained in plate tectonics as a change of the subduction direction. My explanation would be that by the symmetry of the situation both oceanic plates bend down so that this would represent new type of boundary not assumed in the tectonic plate theory.

6. As a master visualizer Adams notices that Africa and South-America do not actually fit together in absence of expansion unless one assumes that these continents have suffered a deformation. Continents are not easily deformable stuff. The assumption of expansion implies a perfect fit of *all* continents without deformation.

Knowing that the devil is in the details, I must admit that these arguments look rather convincing to me and what I learned from Wikipedia articles supports this picture.

The critic of Adams of the subduction mechanism

The prevailing tectonic plate theory [F27] has been compared to the Copernican revolution in geology. The theory explains the young age of the seafloor in terms of the decomposition of the litosphere to tectonic plates and the convective flow of magma to which oceanic tectonic plates participate. The magma emerges from the crests of the mid ocean ridges representing a boundary of two plates and leads to the expansion of sea floor. The variations of the polarity of Earth's magnetic field coded in sea floor provide a strong support for the hypothesis that magma emerges from the crests.

The flow back to would take place at so called oceanic trenches [F20] near continents which represent the deepest parts of ocean. This process is known as subduction. In subduction oceanic tectonic plate bends and penetrates below the continental tectonic plate, the material in the oceanic plate gets denser and sinks into the magma. In this manner the oceanic tectonic plate suffers a metamorphosis returning back to the magma: everything which comes from Earth's interior returns back. Subduction mechanism explains elegantly formation of mountains [F21] (orogeny), earth quake zones, and associated zones of volcanic activity [F37] .

Adams is very polemic about the notion of subduction, in particular about the assumption that it generates steady convective cycle. The basic objections of Adams against subduction are following.

1. There are not enough subduction zones to allow a steady situation. According to Adams, the situation resembles that for a flow in a tube which becomes narrower. In a steady situation the flow should accelerate as it approaches subduction zones rather than slow down. Subduction zones should be surrounded by large areas of sea floor with constant age. Just the opposite is suggested by the fact that the youngest portion of sea-floor near the ridges is largest. The presence of zones at which both ocean plates bend down could improve the situation. Also jamming of the flow could occur so that the thickness of oceanic plate increases with the distance from the eruption ridge. Jamming could increase also the density of the oceanic plate and thus the effectiveness of subduction.

2. There is no clear evidence that subduction has occurred at other planets. The usual defense is that the presence of sea is essential for the subduction mechanism.

3. One can also wonder what is the mechanism that led to the formation of single super continent Pangeia covering 1/4 of Earth's surface. How probable the gathering of all separate continents to form single cluster is? The later events would suggest that just the opposite should have occurred from the beginning.

Expanding Earth theories are not new

After I had decided to check the claims of Adams, the first thing that I learned is that Expanding Earth theory [F6], whose existence Adams actually mentions, is by no means new. There are actually many of them.

The general reason why these theories were rejected by the main stream community was the absence of a convincing physical mechanism of expansion or of growth in which the density of Earth remains constant.

1. 1888 Yarkovski postulated some sort of aether absorbed by Earth and transforming to chemical elements (TGD version of aether could be dark matter). 1909 Mantovani postulated thermal expansion but no growth of the Earth's mass.

2. Paul Dirac's idea about changing Planck constant led Pascual Jordan in 1964 to a modification of general relativity predicting slow expansion of planets. The recent measurement of the gravitational constant imply that the upper bound for the relative change of gravitational constant is 10 time too small to produce large enough rate of expansion. Also many other theories have been proposed but they are in general conflict with modern physics.

3. The most modern version of Expanding Earth theory is by Australian geologist Samuel W. Carey. He calculated that in Cambrian period (about 500 million years ago) all continents were stuck together and covered the entire Earth. Deep seas began to evolve then.

Summary of TGD based theory of Expanding Earth

TGD based model differs from the tectonic plate model but allows subduction which cannot imply considerable back-flow of magma. Let us sum up the basic assumptions and implications.

1. The expansion is or was due to a quantum phase transition increasing the value of gravitational Planck constant and forced by the cosmic expansion in the average sense.

2. Tectonic plates do not participate to the expansion and therefore new plate must be formed and the flow of magma from the crests of mid ocean ridges is needed. The decomposition of a single plate covering the entire planet to plates to create the mid ocean ridges is necessary for the generation of new tectonic plate. The decomposition into tectonic plates is thus prediction rather than assumption.

3. The expansion forced the decomposition of Pangeia super-continent covering entire Earth for about 530 million years ago to split into tectonic plates which began to recede as new non-expanding tectonic plate was generated at the ridges creating expanding sea floor. The initiation of the phase transition generated formation of deep seas.

4. The eruption of plasma from the crests of ocean ridges generated oceanic tectonic plates which did not participate to the expansion by density reduction but by growing in size. This led to a reduction of density in the interior of the Earth roughly by a factor 1/8. From the upper bound for the age of the seafloor one can conclude that the period lasted for about 185 million years after which it transformed to convective flow in which the material returned back to the Earth interior. Subduction at continent-ocean floor boundaries and downwards double bending of tectonic plates at the boundaries between two ocean floors were the mechanisms. Thus tectonic plate theory would be more or less the correct description for the recent situation.

5. One can consider the possibility that the subducted tectonic plate does not transform to magma but is fused to the tectonic layer below continent so that it grows to an iceberg like structure. This need not lead to a loss of the successful predictions of plate tectonics explaining the generation of mountains, earthquake zones, zones of volcanic activity, etc...

6. From the video of Adams it becomes clear that the tectonic flow is East-West asymmetric in the sense that the western side is more irregular at large distances from the ocean ridge at the western side. If the magma rotates with slightly lower velocity than the surface of Earth (like liquid in a rotating vessel), the erupting magma would rotate slightly slower than the tectonic plate and asymmetry would be generated.

7. If the planet has not experienced a phase transition increasing the value of Planck constant, there is no need for the decomposition to tectonic plates and one can understand why there is no clear evidence for tectonic plates and subduction in other planets. The conductive flow of magma could occur below this plate and remain invisible.

The biological implications might provide a possibility to test the hypothesis.

1. Great steps of progress in biological evolution are associated with catastrophic geological events generating new evolutionary pressures forcing new solutions to cope in the new situation. Cambrian explosion indeed occurred about 530 years ago (the book "Wonderful Life" of Stephen Gould [I136] explains this revolution in detail) and led to the emergence of multicellular creatures, and generated huge number of new life forms living in seas. Later most of them suffered extinction: large number of phylae and groups emerged which are not present nowadays.

   Thus Cambrian explosion is completely exceptional as compared to all other dramatic events in the evolution in the sense that it created something totally new rather than only making more complex something which already existed. Gould also emphasizes the failure to identify any great change in the environment as a fundamental puzzle of Cambrian explosion. Cambrian explosion is also regarded in many quantum theories of consciousness (including TGD) as a revolution in the evolution of consciousness: for instance, micro-tubuli emerged at this time. The periods of expansion might be necessary for the emergence of multicellular life forms on planets and the fact that they unavoidably occur sooner or later suggests that also life develops unavoidably.

2. TGD predicts a decrease of the surface gravity by a factor 1/4 during this period. The reduction of the surface gravity would have naturally led to the emergence of dinosaurs 230 million years ago as a response coming 45 million years after the accelerated expansion ceased. Other reasons led then to the decline and eventual catastrophic disappearance of the dinosaurs. The reduction of gravity might have had some gradually increasing effects on the shape of organisms also at microscopic level and manifest itself in the evolution of genome during expansion period.

3. A possibly testable prediction following from angular momentum conservation ($\omega R^2 = constant$) is that the duration of day has increased gradually and was four times shorter during the Cambrian era. For instance, genetically coded bio-clocks of simple organisms during the expansion period could have followed the increase of the length of day with certain lag or failed to follow it completely. The simplest known circadian clock is that of the prokaryotic cyanobacteria. Recent research has demonstrated that the circadian clock of Synechococcus

elongatus can be reconstituted in vitro with just the three proteins of their central oscillator. This clock has been shown to sustain a 22 hour rhythm over several days upon the addition of ATP: the rhythm is indeed faster than the circadian rhythm. For humans the average innate circadian rhythm is however 24 hours 11 minutes and thus conforms with the fact that human genome has evolved much later than the expansion ceased.

4. Scientists have found a fossil of a sea scorpion with size of 2.5 meters [I62], which has lived for about 10 million years for 400 million years ago in Germany. The gigantic size would conform nicely with the much smaller value of surface gravity at that time. The finding would conform nicely with the much smaller value of surface gravity at that time. Also the emergence of trees could be understood in terms of a gradual growth of the maximum plant size as the surface gravity was reduced. The fact that the oldest known tree fossil is 385 million years old [I115] conforms with this picture.

Did intra-terrestrial life burst to the surface of Earth during Cambrian expansion?

Intra-terrestrial hypothesis is one of the craziest TGD inspired ideas about the evolution of life and it is quite possible that in its strongest form the hypothesis is unrealistic. One can however try to find what one obtains from the combination of the IT hypothesis with the idea of pre-Cambrian granite Earth. Could the harsh pre-Cambrian conditions have allowed only intra-terrestrial multicellular life? Could the Cambrian explosion correspond to the moment of birth for this life in the very concrete sense that the magma flow brought it into the day-light?

1. Gould emphasizes the mysterious fact that very many life forms of Cambrian explosion looked like final products of a long evolutionary process. Could the eruption of magma from the Earth interior have induced a burst of intra-terrestrial life forms to the Earth's surface? This might make sense: the life forms living at the bottom of sea do not need direct solar light so that they could have had intra-terrestrial origin. It is quite possible that Earth's mantle contained low temperature water pockets, where the complex life forms might have evolved in an environment shielded from meteoric bombardment and UV radiation.

2. Sea water is salty. It is often claimed that the average salt concentration inside cell is that of the primordial sea: I do not know whether this claim can be really justified. If the claim is true, the cellular salt concentration should reflect the salt concentration of the water inside the pockets. The water inside water pockets could have been salty due to the diffusion of the salt from ground but need not have been same as that for the ocean water (higher than for cell interior and for obvious reasons). Indeed, the water in the underground reservoirs in arid regions such as Sahara is salty, which is the reason for why agriculture is absent in these regions. Note also that the cells of marine invertebrates are osmoconformers able to cope with the changing salinity of the environment so that the Cambrian revolutionaries could have survived the change in the salt concentration of environment.

3. What applies to Earth should apply also to other similar planets and Mars [E2] is very similar to Earth. The radius is .533 times that for Earth so that after quantum leap doubling the radius and thus Schumann frequency scale (7.8 Hz would be the lowest Schumann frequency) would be essentially same as for Earth now. Mass is.131 times that for Earth so that surface gravity would be.532 of that for Earth now and would be reduced to.131 meaning quite big dinosaurs! have learned that Mars probably contains large water reservoirs in it's interior and that there is an un-identified source of methane gas usually assigned with the presence of life. Could it be that Mother Mars is pregnant and just waiting for the great quantum leap when it starts to expand and gives rise to a birth of multicellular life forms. Or expressing freely how Bible describes the moment of birth: in the beginning there was only darkness and water and then God saidLet the light come!

To sum up, TGD would provide only the long sought mechanism of expansion and a possible connection with the biological evolution. It would be indeed fascinating if Planck constant changing quantum phase transitions in planetary scale would have profoundly affected the biosphere.

5.6.2 Did Pre-Biotic Life Evolve In Mantle-Core Boundary?

In the sequel this question is taken to mean simple prebiotic life forms preceding the life that possibly developed in underground seas near to the surface of Earth. One can imagine that prebiotic life moved from high temperature environment in the Earth's interior to the underground seas and charged molecules polymerized in this process and generated gel like phase around them.

Some arguments supporting IT life

The following arguments favor IT hypothesis.

1. Life would have originated already in interstellar space via evolution of primitive metabolic cycles involving temporary chemical storage of metabolic energy. The decay of molecules would have been induced by incoming radiation in UV and visible range and fusion would have occurred spontaneously liberating energy quantum. As stars and planetary systems formed these primordial predecessors of life would have naturally ended into the planetary and even interiors and received their metabolic energy from the hot environment.

   The dropping of particles, in particular protons and electrons, to large space-time sheets could have provided fundamental metabolic energy quanta, and the anomalies lines in the IR, visible, and UV radiation from interstellar space indeed contains this kind of lines with energies which can be understood in terms of the spectrum of these quanta [**?**].

   In many-sheeted space-time particles topologically condense at all space-time sheets having projection to given region of space-time so that this option makes sense only near the boundaries of space-time sheet of a given system. Also p-adic phase transition increasing the size of the space-time sheet could take place and the liberated energy would correspond to the reduction of zero point kinetic energy. Particles could be transferred from a portion of magnetic flux tube portion to another one with different value of magnetic field and possibly also of Planck constant h_{eff} so that cyclotron energy would be liberated. In the following only the "dropping" option is discussed.

2. Boundary layers are ideal places for self-organization since they contain gradients which give rise to energy currents feeding self-organization. Liquid state is certainly crucial for life since this makes it possible quantum control the atomic space-time sheets very effectively. Ordinary life relies actually on the liquid crystal property of water which suggests that the same is the case quite generally. Thus those parts of the planetary core which correspond to boundary regions between solid and liquid phases and thus analogous to ordered water, could be ideal places for IT life forms to flourish, and it is actually difficult to imagine any other state of matter making possible life able to control the surrounding world effectively.

3. This picture is consistent with and would realize concretely the general vision about magnetosphere as a living system. In Earth's interior the mantle-core and core-inner core boundaries are especially interesting in this respect since these boundaries represent solid liquid boundaries.

4. Mg, Fe, Al, Si, and O are the dominant elements in mantle. Also Ca is present. These are the basic minerals involved with life. Also the minerals believed to be important for the evolution of polymer structures (like kaolinites consisting of Al, Si, and O) could form both at the hot space-time sheets and atomic space-time sheets. Below mantle-core boundary Fe and S are the prevailing elements. Fe-S centers play a key role in high temperature and pressure models for photosynthesis pathways [I64]. The establishment of the photosynthesis has been proposed to occur first in a sulphur containing environment with S replacing O. Inner core contains mainly Fe at hot space-time sheets.

5. A further possibly important aspect is the transparency of the liquid glass state at mantle-core boundary implying that visible light propagates over long distances without absorption. This might be absolutely essential for the possibility of visible photons to propagate through sufficiently long distances. For dark photons situation changes, and the transparency of liquid glass might be due the fact that some fraction of photons propagate as dark photons through

it. Hence quartz is transparent in liquid state, and thus an optimal candidate for a medium whose behavior is quantum controlled from larger space-time sheets.

6. Magnetic body means the presence of both magnetic nervous system and the analog of blood circulation which could bring in sufficient amounts of elements needed for the synthesis of bio-polymers. The low concentrations of the elements needed to build up bio-monomers need not be a problem anymore since magnetic Mother Gaia could control them.

Structure of the Earth's interior and IT life

Combining the above described general ideas with the knowledge about Earth interior, one ends up with a more detailed picture.

1. Earth's interior decomposes into a relatively thin crust of thickness 30-60 km; a plastic mantle consisting mainly of Si, O, Mg, Fe, and Al mostly in form of silicates FeO-SiO_2 and MgO-SiO_2; a liquid core containing mainly Fe and S; and the inner core consisting mainly of solid Fe. There are thus two solid-liquid boundary regions. The upper boundary region could contain at least glass in liquid crystal form and the lower boundary region Fe in liquid crystal form.

2. Theoretically, the thickness for the mantle-core layer is expected to be of order few meters. The reflection of tectonic waves from mantle-core boundary has given evidence for a rich structure at this boundary and suggests that this expectation is not quite correct [F52]. Structures of thickness about 150 meters and with of several kilometers and between liquid and solid state have been identified at the top of the liquid core. One explanation is that lighter elements in the core-inner core boundary saturate and condense to solid form and being lighter than iron, raise up and form kind of puddles at the highest points of core.

   A more radical explanation is that these structures relate to a highly developed self-organization patterns which have given rise to some kind of life-forms. In the mantle-core layer the velocity of tectonic waves gets ultra-low. The velocity of sound in solid phase is quite generally higher than in liquid phase: this reflects directly the fact that the approximately harmonic forces between atoms are stronger. If liquid crystal phase is present the velocity in transversal liquid directions should be low. What is fascinating that sooner or later the analysis of reflected tectonic waves could give detailed information about mantle-core boundary.

3. Earth contains a previously unidentified core region with size of 300 km [F38]. Assuming that the magnetic field behaves like a dipole field down to the distances of order 300 km, the electronic cyclotron frequency at this distance is 5 GHz which corresponds to the wave length of about 6 cm, the size scale of BOLs for the dark companion $B_{end} = 2B_E/5$ of B_E. If the magnetization density below this distance is constant (so that the core would be like ordinary magnet), the magnetic field would be constant below this length scale.

Also some other experimental findings support this picture. It has been found that the times for of the compressional waves to travel through Earth in magnetic north-south direction and equatorial direction differ by 2-3 seconds [F47]. This suggests a gigantic crystal structure with symmetry axis parallel to magnetic field. If the join along boundaries/flux tube condensate associated with atomic space-time sheets is hollow with a hole of radius 300 km, and if only $k = 151$ space-time sheet consisting of cold and magnetized iron is at this space-time sheet one can understand the crystal structure and how Earth's magnetic field results by magnetization. The estimated velocity of propagation for compressional waves in the crystal is about 3 km/s which is rather near to the 5 km/s for steel at room temperature. The appearance of a relatively small hole at the atomic space-time sheet is not so surprising since typically the field equations of TGD imply hole like singularities at given space-time sheet, and the hole could be analogous to black hole like singularity carrying inertial and gravitational masses at its boundary.

The simplest hypothesis is that the magnetic field associated with the plasmoids is the Earth's magnetic field in the core region of Earth. This would mean that some kind of plasmoid like life forms could reside also at the boundary layer associated with the new core. If the $k = 151$ space-time sheet is not ferromagnet above the radius $r = 300$ km, the boundary region could be

in spin glass type magnetic phase and the bio-control from magnetic flux tubes would operate on the local direction of magnetization of the magnetized regions in the boundary region.

5.6.3 What Conditions Can One Pose On Life At Mantle-Core Boundary?

In the following some conditions on life at high temperatures at pressures are discussed as a mere intellectual exercise certainly not to meant taken deadly seriously. The speculations rely on the ideas which should be already familiar such as presence of strong gradients driving self-organization as indeed found in mantle-core boundary, magnetic bodies as controllers of biological bodies, dark matter as phases with large value of Planck constant able to form macroscopic quantum phases even at high temperatures, and the notion of universal metabolic currencies. Gel-sol phase transitions are also key element in the model of life. The condition that topological quantum computation like information processing based on braids requires existence of some kind of polymers defining braids and consisting of some basic building blocks stable under the conditions in question. The presence of analogs of lipids and cell membranes might be argued to be also necessary.

Plasmoid life as minimum option

The least non-realistic assumption is that IT life corresponds to plasmoid like life forms having magnetic body containing dark matter with large Planck constant controlling visible matter at high temperatures and in plasma phase. Fractality suggests that the high frequency analog of EEG is present and allows magnetic body to use the visible body as a sensory receptor and motor instrument. Frequencies and the values of Planck constant should be such that the energies of dark photons are above thermal energy. General vision about evolution suggests that the values of Planck constant are not very high so that frequency scale should be rather high.

1. Only biologically important ions and relatively simple molecules are expected to be present. Primitive metabolic cycles based on the fusion and decay of molecules induced by the radiation coming from environment can be considered. Cyclotron Bose-Einstein condensates of ions at magnetic flux tubes correspond to energies above thermal threshold only if the magnetic field is strong enough.

2. At temperature of about 4000 K at mantle core interior hydrogen bonds are still stable and metabolic energy quantum of $E_0 = .5$ eV is near thermal energy. There exists of course other metabolic quanta comings as power of two multiples of this quantum. Hence one can assumes that the dropping of protons and possibly of electrons from larger space-time sheets is responsible for metabolic energy quanta also now. One might argue that the typical p-adic length scale associated with the space-time sheets corresponds to the de-Broglie wave length a $\lambda_{dB} = \sqrt{3}\hbar/\sqrt{2mT}$ associated with electron. For electron this wavelength is around 35 slightly below $L(149) = 50$ A defining the thickness of the lipid layer of ordinary cell membrane. This scale increases with increasing $\hbar$.

3. Dark micro-waves amplified by quartz crystals might be crucial for the metabolism of plasmoid life-forms and replace visible light serving as the "food" of the terrestrial life forms. Tectonic activity might be as important for these life-forms as solar radiation is for us. The crust and mantle could serve as amplifiers of em waves is a wide wave length range and make possible communications between IT and us.

Could topological quantum computation like activities be considered?

Could even more advanced life forms have evolved in the environment provided by mantle-core boundary? The presence of magnetic body makes possible braidings and simple versions for the mechanisms of memory, of topological quantum computation like information processing, and of catalysis. The presence of braids could be taken almost as a basic prerequisite of life. The presence of polymers of some basic molecules seems necessary if one wants something resembling DNA as TQC.

1. The presence of polymers consisting of some thermally stable basic units is the basic requirement. Hydrocarbons, lipids, amino-acids, and nucleotide polymers are not chemically stable at temperatures considered and mantle contains carbon only in trace amounts. The dominating elements in mantle are O, Si, and Mg whereas C is present only in trace amounts. S is present in core and thus also in mantle-core boundary. P is so called siderophilic element meaning that it tends to avoid Si. It is theorized that during the formation of Earth from magma ocean siderophilic elements including P separated from the mantle and went to core. In [F39] ratio of concentrations of P in core and mantle was estimated to be $D(P) = 30$ but the article does not report the concentration of P on mantle. In [F40] the phosphorus content of upper mantle is reported to be in the range 130-220 ppm which would give 3-7 percent in core. One can also imagine a formation of phosphate deposits in mantle core boundary: in absence of oxygen these kind of deposits are formed at sea floor. This kind of deposits might have formed at the top of the solid structures reported to exist at mantle core boundary [F52]. These structures could themselves have formed as light elements from inner core has gradually diffused to the mantle core boundary and could include phosphate deposits. If so then mantle-core boundary could contain considerable amounts of P and the replacement C, N, O with Si, P, O or Si, P, S might make sense.

2. Water flow is not the only flow which could generate the self-organization patterns defining braidings as the analogs of TQC programs. Since O dominates in mantle water is however the first guess. It is known that lower mantle can contain water at least up to.2 weight per cent [F42]. Water molecules are stable at the temperatures considered. The phase diagram of water [D2] shows that water is in overcritical phase in the temperatures and pressures considered4000 K and 1.4 million atm and at the bottom of the mantle.

3. The replacement of O with S might be considered in the mantle-core boundary since S is present in liquid core. Water would be replaced with hydrogen sulfide H_2S (responsible for the smell of rotten eggs!) if it appears in liquid form H_2S at temperatures and pressures considered. H_2S could be also used as food. H_2S is used by some bacteria living in deep ocean volcanic vents as a nutrient and also in our own gut: chemically this means that H_2S acts as electron donor in primitive photosynthesis like process to give ATP. That sulphur is essential for growth and physical functioning of plants might be due to the fact that it preceded oxygen based life [F2]. For instance, Cys and met containing sulphur are very important amino-acids.

4. The polymers should contain atoms acting as plugs for flux tubes acceptors flux tubes ($O =$ or $S =$) and terminal points of flux tubes identifiable as donors of hydrogen bonds. $S - H$ shows only very weak tendency for hydrogen bonding so that Si, P, O option looks more promising and is of course especially natural if IT life forms are considered. For instance, silicic acids [F30] satisfying the formula $[SiO_x(OH)_{4-2x}]_n$ are candidates for polymers containing both $O =$: s and OH: s. The presence of PO_4 could have made possible the formation simple analogs of nucleotides and AMP, ADP, and ATP molecules. It might be possible to abstract nucleotides with a polymer consisting of four different simple molecules which are phosphorylized and attached to the backbone made of sugars.

5. One can continue the analogy with carbon life even further. The backbone could consist of the variants of riboses with carbon cycles replaced with Si cycles, the variants of aromatic rings with C and N replaced with P, and base pairing between $N - H$ and $O =$ replaced with $P - H$ and $O =$. In the case of amino-acids one can also consider the replacement of $C, N \to Si, P$. It is of course far from obvious that the possibly existing silicon analogs of organic polymers are stable enough against rapid burning to SiO_2 and water. One might hope that the higher mass of Si stabilizes them chemically at temperatures involved. Professional chemist could probably kill this kind of ideas without big effort.

Could one consider analogs of cell membrane and gel phase crucial for cellular life?

1. The first guess would be that gel like phase might have emerged only after these plasmoid like life-forms came in contact with water and induced the generation of structure water in presence of metabolic energy feed. On the other hand, it could well be that structured dater

might form around charged polymers also at high temperatures and pressures as in the case of ordinary cell. Also silica (SiO_2) is known to form a gel. Also glass consists of SiO_2: the transparency of glass to visible light might be also relevant. A group of algae polymerize silicic acid to so called biogenic silica used to construct their cell walls.

2. Lipids forming cell membrane would be replaced with structures consisting of hydrosilicons with the silicon analog of carbon residue as its hydrophilic head and silicon analog of the hydrophobic fat forming the tail of the lipid. The formation of these double layers would be an outcome of self-organization. The analogs of phospholipids having PO_4 at their hydrophilic tail would be needed for TQC.

3. Super-conductivity plays an essential role in the TGD based model for cell membrane. Large enough values of Planck constant in principle allow to have super-conductivity at magnetic flux tubes.

4. The requirement that the energy $E = ZeV$ associated with Josephson junctions over the cell membrane like structure is above thermal energy requires very strong electric field over the membrane unless the membrane is thick. In the case of ordinary cell membrane the energy is rather near to thermal energy at room temperature. Now the energy would be roughly ten times higher and correspond to about.5 eV. Whether this kind of strong electric field is realizable is not clear. One might hope that the densities of ions could be high enough in the dense environment.

Do metabolism and photosynthesis possess signatures telling about intra-terrestrial evolution?

Also the intra-terrestrial metabolism should rely on atomic/molecular "Karma's cycles". Assume that the protons and electrons can be modeled as free particles in box. This assumption might not be correct as the model for ATP- ADP involving Coulomb binding energy of proton with negatively charge ATP molecule reducing the size of metabolic energy quantum already demonstrated. In this case the wavelength would be roughly by a factor 1/2 longer than predicted meaning Coulombic binding energy of order.25 eV.

In any case, with this assumption the quanta saturating to $E_{max}(k) = [.5, 1, 2, 4, 8, 16]$ eV and wavelengths $\lambda_{min} = [1240, 620, 310, 155]$ nm could have been important. The maximal quanta $E_0(k)$ correspond to the dropping from space-time sheet labeled by $k = 137 - \Delta k$ (in the case of proton) to a very large space-time sheet. The size of the space-time sheets would be given by $L(k) = r \times 2^{(k-151)/2} \times L(151)$, $L(151) = 10$ nm and $r = \hbar/\hbar_0$ the ratio of the Planck constant in question to its standard value. Actually and entire spectrum of quanta given by the formula $E_n = (1 - 2^{-}n)E_0(k)$ saturating to $E_0(k)$ for large values of n. In [**?**] the presence of unidentified lines in the spectrum of UV, visible, and IR radiation from interstellar space has been shown to have a satisfactory explanation in terms of universal metabolic energy quanta.

The spectrum of diffuse interstellar medium exhibits three poorly understood structures [I22]: Unidentified Infrared Bands (UIBs), Diffuse Interstellar Bands (DIBs) [I12], and Extended Red Emission (ERE) [I141] allowing an interpretation in terms of dropping of protons or electrons (or their Cooper pairs) to larger space-time sheets. The model also suggests the interpretation of bio-photons in terms of generalizes EREs.

1. Unidentified infrared bands (UIBs) contain strong bands at $\lambda = 3300, 6200, 11, 300$ nm. Th

2. There are diffuse interstellar bands (DIBs) at wavelengths 578.0 and 579.7 nanometers and also at 628.4, 661.4 and 443.0 nm. The 443.0 nm DIB is particularly broad at about 1.2 nm across - typical intrinsic stellar absorption features are 0.1 nm [I22].

3. The Extended Red Emission (ERE) [I22, I141] is a broad unstructured emission band with width about 80 nm and located between 540 and 900 nm. The large variety of peak wavelength of the band is its characteristic feature. In majority of cases the peak is observed in the range 650-750 nm but also the range 610-750 nm appears. This general vision can be compared with experimental facts.

The generalization ontogeny recapitulates phylogeny principle would suggest that the recent metabolism should have some features serving as telltale signatures of the IT past. The IT past could in turn reflect the primordial evolution in interstellar dust. The signatures of this period would be maxima of the action spectrum for wavelengths which correspond to both the universal metabolic energy quanta and transition energies for transitions of simple molecules present in the molecular dust. Visible and UV range are the most promising regions to consider.

1. There are two wave lengths of maximal effectiveness in the photosynthesis of plants and these correspond to what are called photo-system I and II (see p. 287 of [I61]). Photo-system I is maximally activated at $\lambda = 680$ nm, corresponds to the chlorophyll a, and is not involved with the oxygen evolution. $k = 136$ corresponds to wavelength saturating to $\lambda_{min} = 620$ nm (1 eV). The model of ATP- ADP process suggests that Coulombic binding energy is increases the wavelength.

2. Photo-system II is activated by shorter wave lengths and maximum effectiveness is between 500-600 nm. Photo-system II utilizes second type of chlorophyll (b, c or d) plus some accessory pigments. All photosynthetic cells producing oxygen possess both photo-systems whereas bacteria which do not produce oxygen have only the photo-system I. Hence at least the photo-system I might derive from a very early intra-terrestrial period. The spectrum of metabolic energy quanta for $k = 135$ corresponds to the wave length range [620, 413, 354, .., 310] nm. Coulombic binding energy could increase the wavelength from the 413 nm for $k = 135$ and $n = 2$.

3. The action and absorption spectra of green alga Ulva Taeniata, see p. 284 of [I61], have besides 680 nm maximum also a broad maximum in the range 400-500 nm peaked around 430 nm. The action spectrum has also a shoulder like structure around 600 nm. For $k = 135$ the first peak could correspond to $n = 1$ (620 nm) and second peak $n = 2$ (412 nm).

4. For some bacteria encountered in hot springs [I38] the effective wave length range is in the near infrared range 700-1000 nm rather than in the range of visible frequencies dominating the sunlight. This looks strange since in general the evolution favors maximal metabolic economy. This leads to ask whether these bacteria might be kind of living fossils evolved in an intra-terrestrial environment. This range of wavelength corresponds in a reasonable approximation to that obtained by scaling the wave length range 400-500 nm in previous case and thus to $k = 136$.

5. DNA bases (A, G, T, C) strongly absorb UV light at around 260 nm. For $k = 16$ the nearest metabolic energy quanta correspond to $n = 2$ and $n = 3$ giving wavelengths 310 nm and 207 nm. For proton the p-adic length scale is below atomic size for $\hbar/\hbar_0 \geq 16$.

5.6.4 What About Analogs Of EEG?

It looks strange to mention EEG if one speaks about primordial life forms. These analogs of EEG have of course nothing to do with brains. The prediction is that the fractally scaled counterparts of EEG (in loose sense of course) provide the fundamental communication and control tool for the magnetic body. This analog of EEG is determined by the cyclotron energy spectrum nE_c of biologically important ions scaling like $\hbar$ and by the characteristic energy $E_J = ZeV$ associated with Josephson junctions assignable to membrane like structures and having no dependence on $\hbar$. The energies nE_c and the differences $nE_c \pm E_J$ define the harmonics of bands and their satellites. alpha band corresponds to E_c and beta and theta bands to differences in the case of ordinary EEG.

Conditions from the thermal stability of the analog of EEG

The analogs of EEG and its scaled up variants are in a fundamental role in the control of biological body by magnetic body and this should hold true also for ITs. According to the model of EEG resulting as a special case of the model for the fractal hierarchy of EEGs and its generalizations [K15], the analog of EEG involves two components.

1. *Cyclotron component*

The first component corresponds to the harmonics of cyclotron frequencies of biologically important ions: many of them belong to the alpha band in the case of ordinary ions.

Since 10 Hz corresponds to a secondary p-adic time scale assignable to electron defining an inherent time scale of elementary particle in zero energy ontology, one can ask whether this frequency means breakdown of the fractality hypothesis and raises the frequency scale of ordinary EEG in special role. One can also wonder whether 10 Hz frequency could define a universal biorhythm.

Dark ions reside at magnetic flux sheets traversing DNA and cyclotron radiation affects directly DNA. Cyclotron frequencies are associated with motor control affecting directly DNA and inducing gene expression among other things. The models leads naturally to the introduction of the notions of super genome and hyper genome [K15].

2. Josephson junction component

Josephson junctions assumed to be associated with cell membrane define second contribution to EEG as frequencies associated with coherent state of photons emitted by Josephson current. This component is present only if Josephson junctions, naturally assignable with a membrane like structure separating the plasmoid from environment, are present.

The frequencies are expressible as $f_{n,\pm} = nf_c \pm f_J$ and in the case of ordinary EEG alpha band and its harmonics split into counterparts of beta and theta band. alpha band has scaled variant also in more general case and corresponds to ions which define alpha band for ordinary ions.

1. The essential condition is that cyclotron energy scale is above the thermal energy $E_{th} = 2.88T$ ($k_B = 1$ in the units used). This fixes the minimal value of the integer k_d characterizing the level of dark matter hierarchy involved. Note that the hypothesis is $h_{eff} = nh$, where n is product of distinct Fermat primes and power 2^{k_d}. For ordinary EEG frequency of order 1 Hz the minimal value of k_d is roughly $k_d = 44$. DNA cyclotron frequencies assuming that the charge of DNA is solely due to the phosphate groups PO_4^{2-} are around 1 Hz and just above the thermal threshold.

2. Second condition is that Josephson energy determined by the membrane voltage defines Josephson energy which is above thermal energy. This gives $Q_{em}eV \geq 2.88T$ for far from vacuum extremals. For almost vacuum extremals the classical Z^0 field proportional to the classical em field contributes to the coupling and one must replace the charge Q_{em} of charge carrier with effect em charge Q_{eff} [K15]: this increases the scale of Josephson energies roughly by a factor 10. For far from vacuum extremals Josephson energies are near thermal energies whereas for almost vacuum extremals they are in visible and UV region, and one can identify bio-photons and EEG photons as decay products of dark Josephson photons.

3. Superconductivity prevails only below some critical temperature whereas vacuum extremal property is expected to be possible only above some critical temperature. This suggests that cell membrane functions properly only in a narrow temperature range. The range 36-37 C is suggested by the fact that the effects of ELF em fields on vertebrate brain are observed only in this range.

Josephson frequency f_J is inversely proportional to $\hbar$ and would scale in the case of EEG would scale as

$$f_J = \frac{T}{T_{room}} \times f_{J,room} \quad ,$$

where $f_{J,room} \simeq 5$ Hz holds true. alpha band and its harmonics and also the widths of theta and beta bands would scale like B. The positions of theta and beta bands would scale like temperature, and one would have the formula

$$f_{n,\pm} = \frac{B}{B_E} nf_c \pm \frac{T}{T_{room}} f_J$$

for the frequencies in the generalized beta and theta bands, when $k_d = 44$ holds true also in the high-T environment.

It is illustrative to consider some examples.

1. *Mantle-core boundary*
   The temperature is $T = 4000$ K $\sim 13T_{room}$ at the mantle-core boundary. This temperature allows simple ordinary molecules like carbon monoxide and water (due to the high pressure). Thermal energy is still eV and below Josephson energy and super-conductivity is possible only if cyclotron energies are high enough. For 5 Hz cyclotron frequency $r = 47$ gives energy of order eV. One could thus consider the possibility that both the super-conductivity and criticality could be possible in scaled up temperature range.

2. *Sunspots*
   The average temperature of the solar photosphere is about 5800 K whereas the minimum temperature is $T_{min} = 4000$ K and same as the temperature at mantle-core boundary. Inside sunspots the temperature varies in the range 3000-4800 K and sunspots, which are analogous to tornadoes, would be good candidates for the seats of solar life forms. Spectral analysis demonstrates the presence of water inside sunspots [E3]. There is also evidence for a solid calcium ferrite surface at photosphere [E9].

   The value of the sunspot magnetic field is between 1600-2500 Gauss and thus cyclotron frequency is about $3200 - 5000$ times higher than at the surface of Earth. Also in this case $k_d = 44$ level would correspond to thermally stable "EEG" photons with frequencies in the range of ordinary EEG.

What could the analog of EEG for IT look like?

In the following estimates for cyclotron frequencies are for the possibly existing dark companion $B_{end} = 2B_E/5$ of the Earth's magnetic field for which the effects of ELF fields on vertebrate brain provide a direct support.

If the sensory representations of IT life-forms are realized at the personal magnetic canvas and at magnetosphere in the same manner as ours, the cyclotron frequency of the representing ion at distance r_1 is must be same as the cyclotron frequency of the represented ion at distance r_0. Assuming that magnetic field strength scales like $1/r^3$, this gives cyclotron transitions at the distance of about

$$r_1(A) = (A/A_1)^{1/3} \times r_0 \ ,$$

giving

$$y(A, A_1) = (A/A_1)^{1/3} \times x \ .$$

Here $r_0 = xR$ is the radius associated with the life-form, and $r_1 = yR$ is the distance at which the sensory representation is realized. R denotes the radius of Earth and A the mass of the ion at r_0 associated with IT cyclotron transition and A_1 the mass of the ion at r_1 defining the cyclotron transitions associated with the sensory representation.

If the most important frequencies of generalized EEG correspond to cyclotron frequencies, if prebiotic live resides at the mantle-core and core-inner core boundaries, and if the magnetic field inside Earth behaves as dipole field in a reasonable approximation, one can deduce the EEG frequency range of aliens by scaling the human frequency range by the ratio

$$x^{-3} = (\frac{R}{r})^3 = \left[\frac{f_S(r)}{f_S(R)}\right]^3 \ ,$$

where r is the distance of the boundary region from the center of the Earth. The constraint that representation is realized in inner magnetosphere gives the bound $y \leq 6$ and the constraint that it is realized in ionosphere gives $y \simeq 1$.

1. Biosphere

In this case the basic equation is obtained by putting $x = 1$ in the general equation so that one has

$$y = (\frac{A}{A_1})^{1/3} \ .$$

For protonic representations with $A_1 = 1$ possible in entire inner magnetosphere the constraint $y \leq 6$ allows all possible values of A.

2. Mantle-core boundary

For mantle-core boundary the ratio is roughly $x^{-3} = 7.1$ so that the EEG frequency range $1.5 - 90$ Hz scales up to $107 - 639$ Hz. Sensory representations can in this case be realized as ionic transitions in atmosphere. The basic equation is

$$y = (\frac{A}{A_1})^{1/3} x \ ,$$

where A is the mass number of the ion in mantle-core boundary and A_1 is the mass number of representative ion. For protonic representation one has

$$y = 1.92 A^{1/3} \ .$$

The condition $y \leq 6$ guarantees that representation is realized in the inner magnetosphere and gives $A \leq 27$. This corresponds in ordinary EEG to frequencies $f \geq 11$ Hz. For $A_1 > 1$ also scaled up variants of alpha and theta frequencies are representable: note however that the densities of these ions are probably much smaller than in ionosphere.

One can consider also ionospheric ion representations satisfying $y \simeq 1$ for mantle-core boundary. Now the mass numbers of the ions involved are related by

$$\frac{A}{A_1} \simeq x^{-3} \simeq 7.1 \ .$$

The biologically most interesting ions have $A > 7$ and are representable. One manner to realize this sensory representation is using cells or brains of various organisms and one might consider the possibility that we actually are life-forms which have developed as magnetospheric sensory representations of the life-forms at the mantle-core boundary.

3. Core-inner core boundary

For core-inner core boundary the ratio is roughly $x^{-3} = 263$ for $f_S(r) = 50$ Hz and $x^{-3} = 135$ for $f_S(r) = 40$ Hz. In this case only electronic sensory representations are possible and one has

$$y = (\frac{Am_p}{m_e})^{1/3} x \ ,$$

1. For $x^{-3} = 263$ this gives

   $$y \simeq 1.98 \times A^{1/3} \ .$$

   The range $[1, 6]$ for y corresponds to the inner magnetosphere and the upper bound $A \leq 27$ and to scaled up variants of cyclotron frequencies above 11 Hz in ordinary EEG. Only beta and gamma bands would be represented.

2. For $x^{-3} = 135$

   $$y \simeq 2.48 \times A^{1/3}$$

   The upper bound for A is $A \leq 14$ and to the scaled up variants of cyclotron frequencies above ~ 20 Hz in ordinary EEG.

4. Inner core-most inner core boundary

The boundary of the most inner core of radius 300 km could also be carrier of life-forms, perhaps plasmoid like life-forms. The simplest hypothesis is that the magnetic field associated with the plasmoids is the Earth's magnetic field in the core region of Earth, which would be constant and of order .2 Tesla below this distance if dipole approximation makes sense.

If important "EEG" frequencies correspond to cyclotron frequencies, part of the "EEG" would be scaled up by a factor $2^{169-157} = 2^{12} \simeq 4000$ so that EEG frequency range $.25 - 90$ Hz would be mapped to $1 - 360$ kHz. Ionic cyclotron frequencies would be in the MHz range with proton cyclotron frequency equal to 1.2 MHz. The cavity resonance frequency analogous to the lowest Schumann frequency for a structure with radius 300 km is 159 Hz.

If the sensory representations of IT life-forms possibly existing at at $r_0 = 300$ kilometers are realized as electronic cyclotron transitions one has

$$y \simeq .59 \times A^{1/3} \quad .$$

Ions with $A \geq 6$ would be represented above Earth's surface. All ionic representations would be realized in Earth's interior.

5.7 Comparison Of Mcfadden's Views With TGD

In his book Quantum Evolution [I114] Johnjoe McFadden discusses the deep problems of molecular biology from quantum point of view and develops very interesting ideas about evolution and consciousness. Because of deep insights about what is not understood in biology, this discussion should provide new insights for any quantum consciousness theorist attempting to build a bridge between theory and biological reality. In the sequel McFadden's vision is compared with TGD view and some new ideas inspired by it in TGD framework are proposed.

5.7.1 General Ideas

Before dwelling into concrete examples, it is good to compare McFadden's general starting points with those of TGD.

1. In accordance with most interpretations of quantum mechanics, McFadden assumes that the initial situation involved no de-coherence and that the biological evolution means basically the emergence of de-coherence, essentially the appearance of conscious observers performing quantum measurements.

   In TGD framework the situation is just the opposite: evolution means the emergence of effective macro–temporal quantum coherence meaning that the duration of sharp mental images (sub-selves) increased. During the primordial stage typical lifetime of self was of order 10^4 Planck times and defined minimal de-coherence time. Dark matter hierarchy provides and hierarchy of Planck constants a concrete realization for a hierarchy of moments of consciousness with increasing geometric duration and quantum parallel dissipation which is second new element of TGD picture.

   The number theoretic generalization of Shannon entropy having negative values for rational and even algebraic entanglement is a further mathematical concept. Quantum computers are basic examples of systems possessing positive number theoretic negentropy, and this certainly conforms with the genuine information content of multi-verse states. It is not clear whether Negentropy Maximization is really consistent with the Second Law of thermodynamics and one must keep mind open for the possibility that Second Law is illusion created by the neglect of dark matter hierarchy meaning at the same time neglect of living life forms.

2. McFadden does not fix his views about quantum measurement theory but assumes that de-coherence is an outcome of quantum measurements performed by environment or some subsystem of it. McFadden sees enzymatic action as a basic example of quantum measurement in which an amplification to a macroscopic phenomenon occurs.

   In TGD framework one can imagine two basic elements.

   (a) The emergence of symbolic representations as names of molecules made possible lock and key mechanism and "molecular sex". Once it is possible to name molecules, it becomes possible to regard bio-chemical pathways as analogs of computer programs proceeding rather deterministically. As already found, this idea has very concrete implications for understanding of bio-catalysis.

(b) The most important bio-molecules could be seen as selves with especially long wake-up periods in a highly negentropic state of macro–temporal quantum coherence, and able to perform intentional actions applying the time mirror mechanism (see **Fig. ??** in the appendix of this book) (`http://tgdtheory.fi/appfigures/.jpg`), which is also The magnetic bodies of bio-structures are at the top of the intentional hierarchy.

3. McFadden sees quantum Zeno effect and its inverse as basic quantum control tools used by enzymes to increase reaction rates or induce mutations. Although the Zeno effect has also TGD counterpart, the intentional action of molecular magnetic bodies based on time mirror mechanism seems a more plausible option. Long ranged dark weak forces, in particular charge entanglement by W MEs, exotic ionization, and the control of the strength of the screening of the classical Z^0 force provides an additional mechanisms of enzyme control explaining chiral selection. Sol-gel transition inducing polymerization and its reverse allows to control the stability of bio-polymers. The leakage of particles between space-time sheets is a further control mechanism and involved with the time mirror mechanism.

4. McFadden assumes that the superpositions of peptide-environment product states involving different peptides with different neutron and proton numbers are possible so that the measurement involves also measurement of proton and neutron numbers. This option looks implausible because it is very difficult to think that states with different fermion numbers, masses, and charges would quantum superpose.

   In fact, it has become clear quite recently that TGD could in well-defined sense allow also quantum superpositions of different DNA molecules. This kind of superpositions are routinely assumed for coherent states of Cooper pairs in super-conductivity although they break conservation of charge, fermion number, and energy. The point is that in zero energy ontology (ZEO) [K8] the total quantum numbers of physical states always vanish and the states decompose into positive energy part such that negative energy part located in its geometry future. Therefore it is possible to have quantum superpositions which in positive energy ontology, which is excellent approximation, would look like quantum superpositions of different DNA molecules. This possibility is not discussed in this chapter but it is needless to say that it could mean a revolution in the understanding of living matter. Even thermodynamics could be interpreted in a completely new manner since thermodynamical states which are "superpositions" of states with different values of conserved charged could have genuine quantal counterparts.

McFadden's view about biochemistry

McFadden represents a very general view about the essentials of bio-chemistry.

1. Protons associated with hydrogen bonds and electronic Cooper pairs serve as basic tools of quantum bio-control.

2. The localization of proton induces what McFadden interprets as a quantum measurement of proton's position.

In TGD framework the mechanism of catalytic action based on the temporary dropping of proton from the H_N-atom associated with catalyst or reactant, replaces this mechanism. Catalytic action could be seen as a short lasting period of "group sex" between catalyst and reacting molecules. Liberation of standard metabolic energy quantum is automatically involved with the process.

In many-sheeted space-time particles topologically condense at all space-time sheets having projection to given region of space-time so that this option makes sense only near the boundaries of space-time sheet of a given system. Also p-adic phase transition increasing the size of the space-time sheet could take place and the liberated energy would correspond to the reduction of zero point kinetic energy. Particles could be transferred from a portion of magnetic flux tube portion to another one with different value of magnetic field and possibly also of Planck constant h_{eff} so that cyclotron energy would be liberated. In the following only the "dropping" option is discussed.

Important problems of quantum biology

The following list provides examples of problems that McFadden wants to understand in terms of quantum physics.

1. The extreme effectiveness of enzyme action.

2. The mechanism of mutations, in particular that of adaptive mutations and multiple mutations.

3. Evolution.
   i) The loss of complexity in computational models of evolution contra the increase of complexity in real evolution.
   ii) The emergence of the first self replicators.
   iii) The evolution of extremely complex reaction pathways, such as the one leading to the buildup of the ATP ase enzyme.

5.7.2 Enzyme Action

Enzymes as quantum mouse traps is the metaphor introduced by McFadden. Typically enzyme catches the reactant molecules to a fixed conformation and fires a proton to the substrate molecule inducing in this manner a re-organization of some chemical bonds. The enzyme gains the lost proton later from a water molecule.

Mouse trap metaphor conforms completely with the TGD described view about catalytic action and also with the idea about enzyme as a quantum critical system.

1. Production of lactic acid from pyruvate

McFadden represents the production of the lactic acid from pyruvate, which is one of the last steps of catabolism, as a typical example of enzyme action. The process involves LDH, lactate dehydrogenase, catalyzing the transformation of the pyruvate to lactic acid, and NADH providing a proton and an electron pair. LDH donates the proton involved with the transformation of C=0 to C-O-H. NADH in turn provides proton and electron pair so that C=O is replaced with H-C-OH. NAD^+ receives proton and a compensating electron pair from water and LDH_- receives a proton from a water molecule.

2. Catabolism of lactose

Second example used my McFadden relates to the catabolism of lactose induced by the enzyme beta galactose. The rate of the process is trillion times higher than one might expect. McFadden proposes that the process involves a localization of proton in certain amino-acid of the beta galactose to a particular hydrogen bond. If the localization occurs to a correct hydrogen bond, the proton is injected to the lactose molecule and induces hydration. The suggestion is that a repeated quantum measurement of proton's position in beta galactose keeps the proton in the correct position so that the decay occurs with a much higher rate than it would occur otherwise.

It is not necessary to repeat how the catalysis could be understood in TGD framework. The decay of the lactose involves hydrolysis in which lactose molecule receives water H_N-O-H molecule from the environment and the loss of proton de-stabilizes the negatively charged molecule.

Hydrolysis could involve local gel-sol type transition transforming ordered water to ordinary water, which is able to provide the needed water molecule. The gel-sol transition could closely correlate with the non-standard localization of the proton inside enzyme. The process could involve an intentional action of a magnetic body of some system involved and thus negative energy topological light rays and charge entanglement by W MEs.

5.7.3 Quantum Evolution

McFadden considers evolution from a quantum point of view. After the criticism of the RNA world paradigm McFadden poses several questions. How complexity could have emerged during the evolution? What was the first self-replicator? How the complex metabolic pathways could have evolved? What might be the quantum mechanisms of adapted and multiple mutations?

How evolution can create complexity?

McFadden pays attention to the fact that in the computational models of evolution final states tend to be less complex than the initial ones. This can be seen as a consequence of dissipation which leads to asymptotic self-organization patterns which are very simple. This is just the opposite of what is observed in Nature (note however the fact that the rapid extinction of new species after Cambrian explosion might be interpreted in terms of a loss of complexity).

In TGD framework the ability of living systems to circumvent the loss of complexity is due the facts that TGD Universe is quantum critical and p-adic cognition implies p-adic evolution predicting the emergence of systems characterized by increasing values of the p-adic prime and the integer characterizing the levels of dark matter hierarchy serving as their "intelligence quotients".

At the molecular level TGD allows to resolve this puzzle elegantly. During the pre-biotic exotic RNA period the predecessor of the genetic code is realized as many-to-one replication of exotic RNAs meaning a loss of information. This occurred for both singlet and doublet exotic RNA and for their composite forming a double helix with the size of the singlet helix being scaled up by a factor two. This however led to a dead alley involving only the RNAs representing the maximal invariant set of the RNA→RNA mapping as an asymptotic state. Final state was indeed simpler than the initial state.

At some stage the product code transformed to a code coding for RNA triplets, and amino-acids which originally catalyzed the mapping of RNA to RNA, took the role of the coded molecules. RNAs were mapped to DNAs by reverse transcriptase and the high error rate of the reverse transcription implied a rapid mutational rate. The many-to-one character of RNA→RNA replication implying the dead alley thus transformed from a curse to a blessing since it represented implicitly the protein-DNA genetic code.

Criticism of RNA world

McFadden represents severe critics against RNA world paradigm which is the dominating vision about pre-biotic evolution [I113]. The basic objections are following.

1. In water environment bio-polymers become un-stable against de-polymerization by hydration. This makes the idea of primordial sea implausible. The presence of the ordered water could resolve this problem even in the standard physics based models. In many-sheeted space-time the hypothesis that pre-biotic evolution occurred intra-terrestrially in the womb of the magnetic Mother Gaia makes sense and could resolve basic objections against the notion primordial sea.

2. Enzymatic action requires chiral selection. In TGD framework this can be interpreted as a strong indication for the necessity of the classical long ranged weak forces in the enzymatic control (say charge entanglement by W MEs).

3. McFadden lists several reasons for why RNA is implausible as a pre-biotic chemical. RNA consists of three components: RNA base, ribose, and phosphate. RNA bases and phosphate have been generated in the experiments trying to simulate pre-biotic evolution but the spontaneous emergence of ribose looks implausible. The problem is that a plethora of other sugars are produced.

   Some property of ribose should distinguish it from the other sugars. In TGD framework one might argue that for the ribose self "wake-up" periods or even periods of macro-temporal quantum coherence meaning sharp and non-entropic mental images are longer than for the other sugars. Quite generally, important bio-molecules could be identified as maximally autonomous systems able to "stay awake" and realize intentions.

   A more concrete explanation is based on stability.

   i) Both RNA, DNA and amino-acids are negatively charged and thus inherently unstable. The assignment of "names" to generalized hydrogen bonds represented by quark and antiquark at the ends of the magnetic flux tube to the basic building bricks of these polymers could make them stable and lead automatically to highly selective catalytic actions.

   ii) Suppose that the OH groups associated with the sugars have tendency to form a hydrogen bond with water molecules leading to ionization of the water molecule and liberation of proton

dropping to a larger space-time sheet so that the polymer generates negative charge. If the number of O-H groups is too large the resulting negative charge can de-stabilize polymers formed by ribose, phosphate, and RNA nucleotides. Note that also the formation of double strand a liberates one proton per hydrogen bond which has a further de-stabilizing effect. This could explain why RNA with 4 O-H groups forms only short double strands whereas DNA having only 3 O-H groups forms very long double strands.

4. One can also wonder why just phosphate, ribose and RNA bases find each other and why the large number of other combinations are not realized. The naming based on flux tubes would restrict dramatically the possible combinations able to form spatially and temporally coherent systems bound together by flux tubes and automatically lead to a final state in which molecules having no braids with environment disappear from the system. Phosphate, ribose and RNA base could also find each other by tuning to common wave length by sending negative energy MEs entangling them with each other.

5. The presence of RNA bases, phosphate and ribose is not enough. McFadden finds it difficult to understand why only RNA molecules amongst many other reaction products of its three basic components are selected. In laboratory the activation of the RNA base allows to select RNA as a dominant reaction product. One possibility is that the liberation of activation energy helps to overcome the potential wall hindering the formation of RNA. This is could also due to the fact that the bound states of the activated RNA base with other two components are short-lived or decay to RNA in accordance with the idea RNA selves have especially long wake-up periods and is winner in the fight for survival. Magnetic body could be able to intentionally activate the RNA bases using universal metabolism present even without ATP ase machinery.

6. In the laboratory isolation, purification, and channeling of the reactants to the reaction volume are crucial parts of the process producing RNA and ribozymes, and almost-self-replicators. In the conventional chemistry framework it is very difficult to imagine how these processes could have occurred during pre-biotic evolution.

   The notion of magnetic body might come in rescue. Magnetic flux quanta could make possible highly controlled reaction network. A possible concrete toy model goes as follows. Suppose that quantum-classical correspondence holds true in the sense that the shape of the magnetic flux tube containing charged particles reacts to the presence of the charged particles so that it can be regarded as a classical orbit of a charged particle in the average magnetic field inducing Lorentz force. This makes sense only if a given magnetic flux tube contains particles with a fixed charge-to-mass ratio, and means that magnetic body indeed isolates and purifies the reactants to the magnetic flux tubes and allows them to react at the nodes of the magnetic web.

Evolution of metabolism

McFadden describes basic aspects of catabolism in an enjoyable manner. Catabolism can be seen as a process in which electrons from the orbitals of complex bio-molecules (in particular glucose) are gradually transferred to the orbitals of oxygen atoms. This process releases energy used as a metabolic energy in the form of ATP molecules.

In the standard chemistry framework the mechanisms behind $ADP \to ATP$ transformation seem miracle like. It is not easy to understand how an evolution based on mere chance and necessity could have led to the recent form of this machinery: intermediate steps seem to be simply absent. For instance, according to McFadden the reaction pathways generating the ATP ase enzyme catalyzing the generation of ATP involves 13 steps and all these steps are necessary. The probability that this pathway could have been generated by a random change is infinitesimally small and comparable to that for a monkey playing with a typewriter to compose Shakespeare's sonnets by accident.

1. Universal metabolic currencies

In TGD framework the predicted universal metabolic currencies remove partially the veil of mysteries surrounding the evolution of metabolism.

The dropping of a proton from atomic space-time sheet to a larger one generates a universal metabolic energy quantum. Thus metabolism would have been present already before the chemical storage of the metabolic energy. At the pre-biotic period the generation of negative energy topological light rays with photon energy $\sim .5$ eV could have induced the dropping of protons and remote utilization of the liberated energy. Indeed, the model for intra-terrestrial life led to the hypothesis that the infrared radiation corresponding to a temperature of about 4000 K near the mantle-core boundary could have provided the energy quanta of about.4 eV driving protons back to the atomic space-time sheets. The evolution of photosynthesis led later to the chemical storage of the metabolic energy.

The mitochondrial battery is kept at the potential of.15 eV by the metabolic energy feed. This process involves oxidation process in which electrons from the orbitals of molecules like glucose end down to the orbitals of oxygen atoms. The electron pairs are provided by NADH molecules in mitochondrial metabolism occurring in the water filled space between mitochondrial membranes. The energy liberated in this manner drives protons from the interior of the mitochondria to the space between the membranes. NAD^+ ion then receives the compensating electronic Cooper pair from water later.

The molecular battery provides the energy to generate ATP molecules serving as universal energy currencies. Three protons leaking back along the channel inside ATP ase molecule, which is analogous to the wire connecting the plus and minus poles of a battery, gain a net energy of $3 \times .15 = .45$ eV. This energy they donate to a proton, which uses it to get back to the atomic space-time sheet of the ATP molecule.

2. Does metabolism generate cell level qualia?

In a philosophical mood one could wonder the purpose of the endless ATP Karma's cycle: why not just the primitive metabolism involving only.5 eV photons? A partial explanation is the possibility to store metabolic energy chemically so that system becomes less dependent on environment. A connection with the TGD based model of sensory receptor as a quantum capacitor suggests a deeper interpretation. The dielectric breakdown of the quantum capacitor gives rise to qualia which correspond to the increments of the total quantum numbers at either electrode when the dielectric breakdown occurs. ATPase could be seen as generating local di-electrical breakdown inducing primitive protonic qualia as a side product.

3. Molecular intentionality

The basic challenge of the bio-chemistry based approach to evolution is to understand how simple reaction steps coherently integrate to long multi-step reaction pathways. The assumption of molecular intentionality simplifies dramatically this task. Indeed, the best manner to understand and plan a complex electronic instrument is to know its purpose. The manual provides explanation of the purpose and magnetic body serves as the manual of the bio-logical body. For instance, it is much easier to understand how the reaction pathway leading to ATP ase has developed if one knows that the function of this pathway is to liberate universal metabolic energy quanta from mitochondrial battery besides possibly producing protonic qualia.

The fact the number of steps is 13 suggests 13-adicity and it would be interesting to see whether various reaction pathways tend to have a prime number of steps. It deserves to be noticed that $k = 169 = 13^2$ defines the p-adic prime associated with the magnetic flux tubes of the Earth's magnetic field and its possible dark companion $B_{end} = 2B_E/5$, and that the micro-tubular surface defines naturally cognitive code with $k = 13^2$ bits consisting of 13 13-bit sequences defined by tubuline conformations for a full 2π twist around micro-tubule.

Biological evolution could be seen as being induced by the evolution of cognition and of intentional actions. By the properties of the p-adic topology it proceeds from long time and length scales to shorter ones (p-adically short corresponds to something long in the real sense since rational space-time points are common to real and p-adic sectors of the imbedding space). This would suggest that the evolution of bio-logical functions is induced by the evolution of the intentional actions of the magnetic bodies, which were initially like rough sketches and gradually became more and more refined. Also motor skills develop in the same manner.

4. The emergence of molecular pathways

The emergence of names attached to molecules makes possible generation of computer pro-

gram like dynamics in which programs call corresponds to association of molecules with names conjugate to some name of catalyst molecule to clusters so that catalytic action leading to a particular final state becomes possible.

The names of molecules could dictate the dynamics to a high degree. Situation could be like in the human society: knowing that person carries the label "physics teacher" allows to make amazingly precise long term predictions about the daily behavior of the person whereas the knowledge of all imaginable chemical and physical data about the person would not allow to predict anything interesting about the activities of the person in time scales longer than few seconds.

Quantum mechanism of mutations

McFadden suggests the reduction of the superposition of normal and enol configurations of T nucleotide to a tautomeric enol configuration as a quantum mechanism of mutation. The position measurement of the proton can locate it to the second nitrogenic hydrogen bond and thus transform T nucleotide to the isomeric but short-lived enol configuration having only two hydrogen bonds connecting it to the complementary base. In the enol state DNA replication assigns G instead of A with T.

Zeno effect could allow to effectively freeze T to this configuration and thus increase the rate of mutations. The same mechanism could work also at the level DNA→ mRNA transcription and protein translation and assign lys instead of glu to the enol configuration.

The mechanism poses an additional condition to the proposal that DNA nucleotides correspond to quarks and antiquarks. The question is what determines which quark or antiquark corresponds to a given nucleotide and the mechanism of mutation based on disappearance of hydrogen bond suggests that the number of hydrogen bonds (2 or 3) determines this so that one would have correlation with with the weak isospin of quark (u or d) and number of hydrogen bonds (3 or 2).

1. Adaptive mutations of E. coli

In adaptive mutations the bacterium E. coli unable to catabolize lactose to get metabolic energy develops a mutation allowing it to generate beta galactose inducing the decay of the lactose. This mutation occurs with a probability which is higher than predicted by randomness. McFadden poses the question how the information about the presence of the lactose is communicated from the environment to the DNA level.

If life would be mere quantum chemistry, the only possibility would be that the information transfer sequence DNA→mRNA→ proteins of Central Dogma is somehow reversed. What McFadden suggests is DNA-mRNA-betagalactoce-lactose entanglement such that DNA appears as a superposition of ordinary and enol configurations. Lactose would take the role of quantum measurer of the proton's position inside T nucleotide, and Zeno effect would increase the rate of the mutation.

In TGD Universe the bacterial magnetic body receives information about the presence of lactose and its intention to "eat" lactose is transformed to a desire represented by a negative energy ME entangling directly with DNA. The intention of the magnetic body of E. coli would be to push the DNA to enol configuration by kicking the proton to the abnormal position. Negative W ME could induce long lasting entanglement with normal and enol configurations of T nucleotide so that the enol configuration would appear with a higher probability than in the absence of quantum entanglement and mutated DNA results more often in the replication. The alternative option is that magnetic body induces the gel-sol transition inducing mutation in the manner already described.

Quite generally, feeding of dark protons to atomic space-time sheets and gel-sol transition would serve as switches used by the cellular magnetic body to realize its desires. This mechanism could be seen as a refined form of remote metabolism providing metabolic energy for the starving bacterium.

2. Multiple mutations of TB bacteria

TB (tubercle bacillus) bacteria are able to develop a simultaneous resistance against several drugs [I114]. This occurs for bacteria which have only brief growth periods followed by long dormant periods. McFadden interprets dormant periods in terms of entanglement with the environment.

When this period ends even multiple mutations could result in the quantum measurement at DNA level.

In the TGD framework the magnetic body of TB population would receive information about the fates of various members of the population in the multi-drug environment and would have a strong desire to develop multi-drug resistance. The long dormant periods of bacteria allowing them to survive bring in mind the sleeping periods of higher life forms, and suggests the entanglement of the bacteria with the other members of the population, also those living in the geometric past and already deceased as victims of the drugs. This kind of entanglement would allow the magnetic body to manipulate the genomes of the still-living bacteria so that they have better changes to survive in the multi-drug environment. McFadden does not discuss whether the simple mechanism of mutations working in the case of E. coli might be enough in the case of TB bacteria.

Note that the notion of hyper-genome allows to understand bacterial colonies as systems analogous to multi-cellulars controlled by genes expressed collectively.

3. Mutations and intronic DNA

The TGD based view about pre-biotic evolution allows to imagine more effective mechanisms of mutations replacing the simple mechanism utilized by E. coli and working in case of eukaryotes.

In the TGD Universe reverse transcriptase plays a key role in the pre-biotic evolution as a generator of the genetic variation. The variation is due to the high error rate of the reverse transcription. For instance, the amazing ability of the HIV virus (retro-virus) to adapt is based on the reverse transcription of HIV RNA to DNA. It would be strange if this ability would have been lost during the sub-sequent evolution. Perhaps fragments of DNA are transformed to mRNA also during dormant, "inwards directed" periods. mRNA fragments are however not translated to proteins now but transformed back to DNA fragments by reverse transcriptase replacing the previous DNA fragment in DNA with a new one. This mechanism might work at least in case of eukaryotes having cell nucleus and mean that mRNA is not transferred outside the nucleus. The replacement of DNA fragment need not occur immediately. mRNA fragments would thus act like retro-viruses to produce the needed genetic variation. In this framework ordinary retro-viruses such as HIV might be seen as kind of fallen angels.

This kind of activity in which collective selves of populations modify the genomes of their members might be present in all eukaryotes during sleeping (or more generally, dormant) periods. The generation of mutations might be one of the fundamental purposes of sleep and explain why sleep is so important for healing.

This mechanism of mutations might be still too primitive for eukaryotes. In TGD framework the intronic portion of DNA expresses itself as temporal field patterns using p-adic cognitive codes, in particular memetic code. Introns play the role of the computer software whereas genes take the role of the hardware. In this picture introns would be naturally involved with the control of the adaptive mutations of higher organisms. In the modern home computers hardware is becoming more and more dynamical, and computer metaphor suggest that the passive DNA could contain segments representing kind of computer store containing variants of various genes taken in use if required. Transposons might represent these new pieces of the hardware.

This replacement need not involve the removal of the old gene fragment and could be only functional. Computer metaphor inspires the idea that the intronic portion of DNA represents a given gene as a dynamical list of addresses, kind of links or program calls, specifying which portions of DNA contribute to the gene, and that this list characterizes how the splicing of mRNA occurs. Therefore the mutation could occur at the intronic software level as a mere updating of the list representing the gene.

The challenge is to understand how this addressing might be realized physically. For instance, addressing might involve simply common fragments of DNA in meme and corresponding portions of gene serving as addresses making possible a "tuning to a common wave length". Alternatively, magnetic flux tubes might serve as space-time correlates of the links. They could be generated intentionally as wormhole magnetic fields consisting of pairs of positive and negative energy magnetic flux tubes parallel to DNA strand. The generation of wormhole magnetic fields identified as the basic motor activity of the magnetic body could also explain the appearance and disappearance of EEG bands. By the p-adic fractality similar mechanism could be at work also in DNA length scale.

4. Could zero energy ontology be relevant for living matter?

Zero energy ontology [K60] emerged originally from the observation that Robertson-Walker cosmologies correspond in TGD framework to vacuum extremals for which all conserved classical charges vanish (the non-conserved gravitational mass density does is non-vanishing). The construction of S-matrix led to a precise formulation of zero energy ontology.

Zero energy ontology states that physical states have vanishing net quantum numbers and consist of positive energy states at boundaries of future directed light-cones in the geometric past ("not so big bang") and negative energy states at the boundaries of past directed light cones in the geometric future ("not so big crunch") assignable to arguments of N-point function.

Due to the fact that conformal weights are complex it is possible to distinguish between positive energy particles propagating to the geometric future and negative energy particle propagating to geometric past. Phase conjugate laser photons contra ordinary laser photons represent basic empirical example about this distinction.

In the construction of S-matrix identified as entanglement coefficients between these tow kinds of states (this notion makes sense for hyper-finite factors of type II_1 since trace of unit matrix is now equal to unit) these states represent incoming and outgoing states of particle reaction so that measurement of reaction rates is basically quantum measurement in which time-like entanglement is reduced instead of space-like entanglement [K8].

A rather strong argument in favor of zero energy ontology comes from superconductivity [K6]. The models super-conductivity utilize formally the notion of coherent state of Cooper pairs involving quantum superposition of arbitrary numbers of Cooper pairs. This is in conflict with various conservation laws in standard ontology but in zero ontology it is quite possible to consider quantum superposition of zero energy states with various values of quantum numbers for positive energy states.

This opens the gates for rather fascinating speculations. Time-like charge entanglement would allow to imagine a time-like variant of the capacitor model of sensory receptor. For instance, sensory qualia could result in the reduction of coherent state of Cooper pairs to a state with a well defined charge.

Also different DNA sequences with different masses and charges might appear in quantum superpositions for time like entanglement and this might be relevant for evolution of genetic code. In particular, the model of McFadden for mutations might generalize dramatically. As a matter fact, the proposed identification of S-matrix (or rather its generalization M-matrix which need not be unitary) as time-like entanglement coefficients assumes the presence of all pairs of initial and final states appearing in the S-matrix in the superposition so that this possibility could be seen as a prediction.

5.8 Great Vision About Biological Evolution And Evolution Of Brain

The following great vision about evolution and is not perhaps strictly about hierarchy of EEGs. The hierarchy of dark matter and EEGs however leads to this vision naturally. The first part of vision relates to biological evolution. Second part is about the evolution of brain. Here the key thread is evolution of two kinds of intelligences, the ordinary fast intelligence evolving via the emergence of fast computation type activities and emotional slow intelligence developing via the emergence of higher levels of dark matter hierarchy. The latter intelligence is what distinguishes us from animals.

5.8.1 Basic Assumptions

The great vision about evolution and brain relies on two several new notions and ideas.

1. Life as something in the intersection of real and p-adic worlds making possible negentropic entanglement- both space-like and time-like. This makes possible to understand what conscious intelligence is and NMP reduces evolution to a generation of negentropic entanglement (see **Fig.** `http://tgdtheory.fi/appfigures/cat.jpg` or **Fig. ??** in the appendix of this book). DNA as topological quantum computer hypothesis [K17] finds also a justification.

2. The notion of many-sheeted space-time (see **Fig.** `http://tgdtheory.fi/appfigures/manysheeted.jpg` or **Fig.** 9 in the appendix of this book) suggesting a universal hierarchy of metabolic energy quanta, and the notion of magnetic body.

3. Communication and control based on Josephson radiation and cyclotron transitions crucial for understanding bio-photons and EEG and its fractal generalization as a key element of bio-communications.

4. Zero energy ontology and the closely related notion of causal diamond (CD) assigning a hierarchy of macroscopic time scales to elementary particles coming as octaves of the basic time scale and justifying p-adic length scale hypothesis. Zero energy energy ontology also justifies the vision about memory and intentional action and the idea that motor action can be seen as time reversal of sensory perception.

5. The hierarchy of Planck constants and the identification of the fundamental evolutionary step as an increase of Planck constant. Evolutionary steps mean migration to the pages of the Big Book labeled by larger values of Planck constant and living system can be regarded as a collection of pages of the Big Book such that a transfer of matter and energy between the pages is taking place all the time. The change of the Planck constant implies either reduction or increase of the quantum scales-this leads to a model for biocatalysis and a model of cognitive representations as scaled down or scaled up "stories" mimicking the real time evolution.

6. A resonant like interaction between hierarchy of Planck constants and p-adic length scale hierarchy favoring the values of Planck constant proportional to powers of two, and idea that weak and color interactions are especially important in the length scales which correspond to Mersenne primes and Gaussian Mersennes. The simplest option is that weak bosons have their standard masses but appear as massless below their Compton length which scales up like $\hbar$ and preferred p-adic length scales correspond to Mersenne primes. Also copies of weak bosons and gluons with ordinary value of Planck constant and reduced mass scale can (and will) be considered.

How to identify the preferred values of Planck constant?

The basic problem is to identify the preferred values of Planck constant and here one can only make theoretical experimentation and all what follows must be taken in this spirit. One can consider assumptions which become increasingly stronger.

1. If only singular coverings of CD and CP_2 are possible Planck constant is a product of integers. Algebraic simplicity of algebraic extensions of rationals favors ruler and compass integers (Appendix).

2. A resonant interaction between the dark length scales and p-adic length scales with ordinary value of Planck constant favors Planck constants coming as powers of two.

3. An even stronger assumption would be that p-adic length scales coming as Mersennes and Gaussian Mersennes are especially interesting.

   (a) If weak bosons can appear with the ordinary value of Planck constant only in the p-adic length scale $k = 89$, one obtains the condition

   $$k_d = k - 89 \quad , \quad k \in \{89, 107, 113, 127, 151, 157, 163, 167\} \tag{5.8.1}$$

   for the values of of $r = 2^{k_d}$ allowing dark weak bosons in p-adic length scales assignable to Mersennes. These values of k_d assign to electrons and quarks dark p-adic length scales $L(k_{eff}) = \sqrt{r}L(k)$, $r \equiv \hbar/\hbar_0 = 2^{k_d}$. The scales could correspond to size scales of basic units of living systems.

(b) If weak bosons and possibily also gluons with ordinary value of Planck constant are possible in all p-adic length scales $L(k)$, $k \in \{89, 107, 113, 127, 151, 157, 163, 167\}$, one obtains much richer structure. This hierarchy defines defines secondary dark matter hierarchies from the condition that the scaling the p-adic length scale $L(k_1)$ in this set by $\sqrt{r}$, $r \equiv \hbar/\hbar_0 = 2^{k_d}$, gives a p-adic length scale equal to another p-adic length scale $L(k_2)$ in this set. This requires $k_d + k_1 = k_2$ so that the values

$$k_d = k_2 - k_1 \tag{5.8.2}$$

are favored for the scaling of $\hbar$. In this case the hierarchy of dark scales assignable to quarks and leptons is much richer. The tables below demonstrate that electron appears as its dark variant for all Mersennes and also in atomic length scales $k = 137, 139$ so that this option puts electron in a completely unique position.

4. Also other scales are possible. For instance, $r = 2^{47}$ required by 5 Hz Josephson frequency gives dark weak scale which corresponds $k = 136$ as a p-adic scale. The stages of sleep can be understood in terms of scaling of $\hbar$ by factor 2 and 4 so that also the atomic length scale $k = 137$ and the scale $k = 138$ are involved.

Since the experimental input is rather meager, one is forced to do theoretical experimentation with various hypothesis. The quantitative experimental tests are rather primitive but basically quantal.

1. The time scales assignable to CDs of leptons and quarks and their scaled up counterparts for the preferred values of Planck constant should define biologically important time scales. One might even speak about evolutionary level of electron. These time scales could define fundamental biorhythms and also time scales of long term memory and planned action.

2. Josephson frequencies and cyclotron frequencies scaling like $1/\hbar$ (if magnetic field scales down like $1/\hbar$) charactering biologically important ions and elementary particles. In accordance with the quantum criticality of living matter it is assumed that cell membrane corresponds to almost vacuum extremal so that classical Z^0 force is an essential element of the model. Also these frequencies should define fundamental bio-rhythms and characterize the evolutionary level of cell. Experimentally of special importance are the cyclotron frequencies assignable to Ca^{++} ions.

3. The amplitude windows for electric field scaling like $\hbar$ for a particular cyclotron frequency define a basic prediction.

Tables about predicted time and length scales

The following tables summarize various predictions for time scales and length scales. They correspond to the most general assumption that exotic bosons with the ordinary value of Planck constant are possible in all length scales associated with Mersennes and Gaussian Mersennes.

Note that **Table 5.5** includes only the dark length scales associated with $k = 89$ gauge bosons.

Electron and u quark are different

Before continuing an important observation is in order. Electron is exceptional when compared to quarks. It appears as a dark particle in all p-adic length scales defined by biologically important Gaussian Mersennes and also in atomic length scales $k = 137$ and $k = 139$. The reason is trivial: by the basic assumptions electron must appear at same length scales as weak bosons above $k = 127$ since it corresponds to Mersenne prime. Also for the less general option (exotic intermediate gauge bosons are possible only as the dark variants of the standard ones) it appears at cell membrane length scale $k = 151$, which is due to the fact that one has $113 - 89 = 151 - 127 = 24$. Also u quark can appear with $k_{eff} = 137, 139, 163, 167$ and also this is an accident. The light invariants of intermediate gauge bosons appearing in long p-adic length scales would naturally correspond to

Table 5.5: The integers k_d characterizing the preferred values of $r = \hbar/\hbar_0 = 2^{k_d}$ identified from the condition that the dark variant of p-adic length scale $L(p_1)$ corresponding to some ordinary p-adic length scale defined by Mersenne prime M_p or Gaussian Mersenne $M_{G,p}$, $p \in \{89, 107, 113, 127, 151, 157, 163, 167\}$ corresponds to similar p-adic length scale $L(p_2)$. If one assumes that weak bosons can appear with ordinary value of Planck constant only in the p-adic length scale $k = 89$, only the rows with $p_1 = 89$ of the table are possible: in these cases p_1 is in boldface and the row has double underline. The corresponding values of k_d are in the set $\{18, 24, 38, 62, 68, 74, 78\}$.

k_d	p_1	p_2		k_d	p_1	p_2
4	163	167		38	**89**	127
6	107	113		38	113	151
6	151	157		40	127	167
6	157	163		44	107	151
10	157	167		44	113	157
12	151	163		50	107	157
14	113	127		50	113	163
16	151	167		54	113	167
18	**89**	107		56	107	163
20	107	127		60	107	167
24	**89**	113		62	**89**	151
24	127	151		68	**89**	157
30	127	157		74	**89**	163
36	127	163		78	**89**	167

almost vacuum extremals making possible the criticality as the basic aspect of life. One must of course be very cautious about the masses of exotic counterparts of u and d quark: one can also consider the possibility that masses are identical.

5.8.2 Dark Matter Hierarchy And Big Leaps In Evolution

Dark matter hierarchy leads to an amazingly concrete picture about evolutionary hierarchy allowing to identify the counterparts for concepts like mineral, plant, and animal kingdom that we learned during schooldays and ceased to take seriously as students of theoretical physics as we learned that other sciences are just taxonomy. Even more, a view about what distinguishes between prokaryotes, eukaryotes, animal cells, neurons, EEG, and even about what makes cultural evolution, becomes possible. This view is also very useful when one tries to understand the role of microtubules.

The appearance of CDs scaled up in size by $r = \hbar/\hbar_0$ and space-time sheets scaled up in size by $\sqrt{r}$ means the emergence of new levels of structure and it is natural to identify big leaps in evolution in terms of emergence of new larger matter carrying space-time sheet magnetic flux sheets and corresponding magnetic bodies. If magnetic flux quanta are scaled by r magnetic flux quantization conditions remain unaffected if magnetic field strengths scale down by $1/r$ so that the energies of cyclotron photons are not affected. The thickness of flux tubes can remain unchanged if the currents running at the boundaries of the flux quantum cancel the magnetic flux. As already found, this mechanism must be at work inside living organisms wheras in far away region flux quanta are scaled up in size.

The attractive hypothesis is that the leaps in evolution correspond to the emergence of dark variants of weak and possibly also color interactions in dark p-adic length scales which correspond to ordinary p-adic length scales characterized by Mersenne primes. These leaps would be quantum leaps but in different sense as thought usually. The emergence of higher dark matter levels would basically mean the integration of existing structures to larger structures. A good metaphor are text lines at the pages of book formed by magnetic flux sheets whose width is scaled up by r as the new level of dark matter hierarchy emerges. The big leaps can occur both at the level of organism and population and organisms with rather low individual dark matter level can form societies with

Table 5.6: The dark p-adic length scales $\sqrt{r}L(k) = L(k_{eff})$, $k_{eff} = k + k_d$, of intermediate gauge bosons Z, W, d and u quarks, and electron for the values $r = 2^{k_d}$ of Planck constant defined in **Table 5.5**. The uppermost row gives the integers characterizing the p-adic length scales of the particles for the standard value of Planck constant. k_{eff} characterizes also the CD times scale through the formula $T(CD, k_{eff}) = 2^{k_{eff}-127} \times .1$ seconds. The rows which correspond to the less general option for which only M_{89} corresponds to weak bosons with ordinary value of Planck constants have double underline and the corresponding values of k_d are in boldface.

Z, W	d	u	e	k_d
89	120	124	127	**0**
93	124	127	131	4
95	126	129	133	6
99	130	133	137	10
101	132	135	139	12
103	134	137	141	14
105	136	139	143	16
107	138	141	145	**18**
109	140	143	147	20
113	144	147	151	**24**
119	150	153	157	30
125	156	159	163	36
127	158	161	165	**38**
129	160	163	167	40
133	164	167	171	44
139	170	173	177	50
143	174	177	181	54
145	176	179	183	56
149	180	183	187	60
151	182	185	189	**62**
157	188	191	195	**68**
163	194	197	201	**74**
167	198	201	205	**78**

Table 5.7: Table gives all weak boson length scales -both non-dark and dark implied by the assumption that all Mersennes primes and their Gaussian counterparts and their dark counterparts defined $k_d = k_i - k_j$ them are possible.

k_1	k_M		k_1	k_M		k_1	k_M		k_1	k_M
113	89		113	107		163	127		163	157
127	89		119	107		167	127		169	157
151	89		123	107		133	127		173	157
157	89		113	107		139	127		163	157
163	89		117	107		143	127		167	157
167	89		111	107		133	127		161	157
95	89		175	113		137	127		169	163
109	89		181	113		131	127		183	163
133	89		187	113		225	151		207	163
139	89		191	113		229	151		213	163
145	89		119	113		157	151		219	163
149	89		133	113		171	151		223	163
103	89		157	113		195	151		177	163
127	89		163	113		201	151		201	163
133	89		169	113		207	151		207	163
139	89		173	113		211	151		213	163
143	89		127	113		165	151		217	163
113	89		151	113		189	151		187	163
119	89		157	113		195	151		193	163
125	89		163	113		201	151		199	163
129	89		167	113		205	151		203	163
95	89		137	113		175	151		169	163
101	89		143	113		181	151		175	163
105	89		149	113		187	151		179	163
95	89		153	113		191	151		169	163
99	89		119	113		157	151		173	163
93	89		125	113		163	151		167	163
145	107		129	113		167	151		187	167
169	107		119	113		157	151		211	167
175	107		123	113		161	151		217	167
181	107		117	113		155	151		223	167
185	107		195	127		235	157		227	167
113	107		201	127		163	157		181	167
127	107		205	127		177	157		205	167
151	107		133	127		201	157		211	167
157	107		147	127		207	157		217	167
163	107		171	127		213	157		221	167
167	107		177	127		217	157		191	167
121	107		183	127		171	157		197	167
145	107		187	127		195	157		203	167
151	107		141	127		201	157		207	167
157	107		165	127		207	157		173	167
161	107		171	127		211	157		179	167
131	107		177	127		181	157		183	167
137	107		181	127		187	157		173	167
143	107		151	127		193	157		177	167
147	107		157	127		197	157		171	167

Table 5.8: The fundamental frequencies associated with the CDs of intermediate gauge bosons Z, W, d and u quarks, and electron. Note that for intermediate gauge bosons the frequency of CDs corresponds to energy $E = 1.13 \times 10^{-2}$ eV and wavelength $\lambda = 1.01 \times 10^{-4}$ m (size of a large neuron).

particle	Z, W	d	u	e
k	89	120	123	127
f(CD)/Hz	2.7488×10^{12}	1280	160	10

Table 5.9: The $\hbar$-scaled fundamental time scales $T(CD, k_{eff}) = 2^{k_{eff}-127} \times .1$ seconds associated with the CDs of intermediate gauge bosons Z, W, d and u quarks, and electron for the values $\hbar/\hbar_0 = 2^{k_d}$ of Planck constant defined in **Table 5.5**. The scales are expressed in seconds. The uppermost row gives the time scales of CDs for the standard value of Planck constant. The rows which correspond to the less general option for which only M_{89} corresponds to weak bosons with ordinary value of Planck constants have double underline and the corresponding values of k_d are in boldface.

Z, W	d	u	e	k_d
3.64e-13	7.81e-04	6.25e-03	1.00e-01	**0**
5.821e-12	1.25e-02	1.00e-01	1.60e+00	4
2.31e-11	5.00e-02	4.00e-01	6.40e+00	6
3.73e-10	8.00e-01	6.40e+00	1.02e+02	10
1.49e-09	3.20e+00	2.56e+01	4.10e+02	12
5.97e-09	1.28e+01	1.02e+02	1.65e+03	14
2.38e-08	5.12e+01	4.10e+02	6.55e+03	16
9.54e-08	2.05e+02	1.64e+03	2.62e+04	**18**
3.81e-07	8.19e+02	6.55e+03	1.05e+05	20
6.10e-06	1.31e+04	1.05e+05	1.68e+06	**24**
3.91e-04	8.39e+05	6.71e+06	1.07e+08	30
2.50e-02	5.37e+07	4.30e+08	6.87e+09	36
1.00e-01	2.15e+08	1.72e+09	2.75e+10	**38**
4.00e-01	8.59e+08	6.87e+09	1.10e+11	40
6.40e+00	1.37e+10	1.10e+11	1.76e+12	44
4.10e+02	8.80e+11	7.04e+12	1.12e+14	50
6.55e+03	1.41e+13	1.13e+14	1.80e+15	54
2.62e+04	5.63e+13	4.50e+14	7.21e+15	56
4.19e+05	9.01e+14	7.21e+15	1.15e+17	60
1.68e+06	3.60e+15	2.88e+16	4.61e+17	**62**
1.07e+08	2.31e+17	1.84e+18	2.95e+19	**64**
6.87e+09	1.48e+19	1.18e+20	1.89e+21	**74**
1.10e+11	2.36e+20	1.89e+21	3.02e+22	**78**

high dark matter levels and high collective intelligence (honeybees and ants are good example in this respect).

Certainly also other scalings of Planck constant than those summarized in tables are possible but these scalings are of primary interest. This intuition is supported by the observation that electron is completely exceptional in this framework. Electron's dark p-adic length scales corresponds to p-adic length scales $L(k)$, $k = 167, 169$, assignable to atomic and molecular physics and to the Gaussian Mersennes $M_{G,k} = (1+i)^k - 1$, $k \in \{151, 157, 163, 167\}$, assignable to the length scale range between cell membrane thickness 10 nm and nucleus size 2.58 μm. The corresponding p-adic length scales or corresponding electronic Compton lengths, the number of which is 23, are excellent candidates for the scales of basic building brickes of living matter and vary from electron's p-adic length scale up to 1.25 m ($k = 167$ defining the largest Gaussian Mersenne in cell length scale range) and defining the size scale of human body. The corresponding p-adic time scales are also highly interesting and vary from.1 seconds for electron defining the fundamental biorhythm to 9.6×10^{14} years which is by 4-5 orders longer than the age of the observed Universe. For $k = 167$ the time scale is 1.1×10^{11} years and is by one order of magnitude longer than the age of the observed Universe estimated to be 1.37×10^{10} years [E1].

This conceptual framework gives rather strong guidelines for the identification of the levels of evolutionary hierarchy in terms of dark matter hierarchy. The outcome is a more detailed vision about big evolutionary leaps. Note that in the sequel only the general option is considered: the justification for this is that for this option electron appears as a dark particle for all length scales defined by Gaussian Mersennes as well as in atomic length scales. The basic vision in nutshell is that evolution means the emergence of dark weak and gluonic physics in both dark and ordinary length scales and that the size scales of the basic biostructures correspond to Mersenne primes and their Gaussian variants.

A sketch about basic steps in evolution

The vision about evolution depends on what one assumes about the initial state.

1. If one assumes that weak bosons with ordinary value of Planck constant were present in the begining, evolution would mean a steady growth of k_d. The problem is that small values of $k_d = k_1 - k_2$ correspond to the Gaussian Mersennes defining cellular length scales. If these exotic weak physics were present from the beginning, large parity breaking in cellular length scales would have been present all the time.

2. An alternative and perhaps more realistic view is that the evolution means the emergence of exotic weak physics corresponding almost vacuum extremals in increasingly longer length scales. A possible mechanism could have been the induction of exotic $\hbar_0$ variant of weak physics at the nearest Mersenne length scale k_{next} by the dark variant of weak physics at level k so that one would have $k_d = k_{next} - k$. The simplest induction sequence would have been $89 \to 107 \to 113 \to 127 \to 151 \to 157 \to 163 \to 167$ corresponding to $k_d \in \{18, 6, 14, 24, 6, 6, 4\}$. A possible interpretation of exotic $\hbar_0$ physics is in terms of almost vacuum extremals and non-standard value of Weinberg angle: also weak bosons of this physics would be light. This sequence defines the minimal values for k_d but also larger values of k_d are possible and would correspond to steps between neighbours which are not nearest ones.

   The following sketch about the basic steps of evolution relies on the latter option.

   1. Elementary particle level

Magnetic bodies with size scale defined by the sizes of CDs assignable to quarks and leptons and possibly also weak bosons (already now the size of big neuron emerges) corresponds to the lowest level of hierarchy with the sizes of the basic material structures corresponding to the Compton lengths of elementary particles. The fundamental bio-rhythms corresponding to frequencies 10, 160, and 1280 Hz appear already at this level in zero energy ontology which suggests that elementary particles play a central and hitherto unknown role in the functioning of living matter.

2. $89 \to 107$ *step with* $k_d = 18$

The first step would have been the emergence of $k_{eff} = 107$ weak bosons inducing $\hbar_0$ weak physics in $k = 107$ length scale characterizing also ordinary hadrons. This in turn would have

led to the emergence of exotic nucleons possibly corresponding to almost vacuum extremals. The reduction of the model for the vertebrate genetic code to dark hadron physics [K53] is one of the most unexpected predictions of quantum TGD and assumes the existence of exotic- possibly dark- nucleons whose states with a given charge correspond to DNA, RNA, mRNA, and tRNA. The $\hbar_0$ variants of these nucleons would interact via weak bosons with hadronic mass scale. The exotic variants of the ordinary $k = 113$ nuclei would correspond to the nuclear strings consisting of exotic nucleons [K10, K53] and define nuclear counterparts for DNA sequences. Their dark counterparts could define counterparts of DNA sequences in atomic physics length scales. Therefore a justification for the previous observation that genetic code could be realized at the level of hadron physics and that chemical realization would be higher level realization finds justification. The anomalous properties of water could be also partly due to the presence of dark nucleons and the proposal was that the presence of exotic nuclei is involved with water memory [K24]. The possible existence of the analog of DNA-RNA transcription between ordinary DNA and its nuclear counterpart would have dramatic implications. For instance, one can imagine a mechanism of homeopathy based on this kind of transription process which would also allow a modification of genome by using dark nuclei to communicate the DNA sequences through the cell membrane to the target nuclei.

3. $107 \to 113$ *step with* $k_d = 6$

The next step would have been the emergence of $k_{eff} = 113$ weak bosons inducing $\hbar_0$ weak physics in $k = 113$ length scale characterizing also ordinary hadrons. Exotic variants of the ordinary nuclei possibly corresponding to almost vacuum extremals could have emerged interacting weakly (or actually relatively strongly!) via the exchange of weak bosons with mass scale of order 100 MeV. Also dark variants of the exotic $k = 107$ nucleons could have have emerged and formed exotic nuclei of size scale $k = 119$.

4. $113 \to 127$ *step with* $k_d = 14$

At this step weak bosons in electron mass scale would have emerged. Whether these weak bosons could have induced large parity breakings in atomic and molecular length scales is not clear. Viruses, which do not yet possess cell membrane could correspond to this level of hierarchy.

5. $127 \to 151$ *step with* $k_d = 24$

This step would have been fundamental since weak bosons in cell membrane length scale would have appeared. Note that by $113 - 89 = 24$ this step also leads from $k = 89$ weak bosons to $k = 113$ weak bosons. The weak bosons assignal to $k = 151$ could correspond to the weak interactions associated with almost vacuum extremals and $sin^2(\theta_W) = .0295$ could correspond to the weak physics in question.

$k_d = 24$ step for $k = 113$ $\hbar_0$ weak bosons would have produced them in $k_{eff} = 137$ atomic length scale with $L(137) \simeq .78$ Angstrom This could have naturally led to large parity breaking effects and chiral selection.

Dark $k_{eff} = 151$ electrons appearing in the TGD inspired model of high T_c super-conductivity would have been a by-product of this step. Whether dark electrons could have transformed to light $\hbar_0$ electrons (of mass.25 keV) with a common mass scale of order 10^2 eV with exotic weak bosons is an interesting question. The model of high T_c super-conductivity predicts the presence of structures analogous to cell membrane. This would suggest that cell membranes emerged and chiral selection emerged at this step so that one could not distinguish the emergence of molecular life as a predecessor for the emergence of cell membrane like structures. This would conform with the fact that DNA molecules are stable only inside cell nucleus. Note that for $k_{eff} = 151$ electron's CD has time scale $2^{24} \times .1$ seconds -that is 19.419 days (day=24 hours).

The smallest nanobes [I29] appearing in rocks have size 20 nm and could have emerged at this step. The size of the viruses [I52] is between 10-300 nm covers the entire range of length scales assignable to Gaussian Mersennes, which suggests that smallest viruses could have emerged at this step. Also the smallest [I28] [I28], which by definition have size smaller than 300 nm could have appeared at this stage.

6. The remaining steps

The remaining steps $k = 151 \to 157 \to 163 \to 167$ could relate to the emergence of coiling structure DNA and other structures inside cell nucleus. $k = 167$ would correspond to $k_d = 167 - 89 = 68$ to be compared with the value $k_d = 47$ required by 5 Hz Josephson frequency for the neuronal membrane for -70 mV resting potential. Note that $k_d = 48$ (state 1-2 of deep sleep) corresponds to $k = 163$.

By their smallness also double and triple steps defined by $k_d = k_{i+n} - k_i$, $n > 1$, are expected to be probable. As a consequence, electrons can appear as dark electrons at all the Gaussian Mersenne levels. At these steps the dark electrons corresponding to primes $k_{eff} = 137, 139$ would appear. For $k = 137$ dark electron appears with CD time scale equal to 128 seconds- rather precisely two minutes. The model for EEG suggests that the exotic weak bosons appear in the scales $k_{eff} = 136, 137, 138$.

Further multisteps from the lower levels of hierarchy would give structures with size scales above the size of cell nucleus possibly assignable to organs and structural units of brain. The dark levels assignable to electron are expected to be of special interest. It is encouraging that the longest scale assignable to electron in this manner corresponds to $k = 205$ and length scale of 1.28 m defining body size. As a consequence dark electrons are predicted at levels $k = 137, 139, 141, 143, 145, 147$ coming as octaves.

Prokaryotic cells (bacteria, archea) without cell nucleus for which cell membrane is responsible for metabolic functions and genome is scattered around the cell could have emerged at this step. This would mean that the emergence of the cell membrane thickness as a fundamental scale is not enough: also the size scale of membrane must appear as p-adic length scale. The sizes of most prokaryotes vary between 1 μm and 10 μm: the lower bound would require $k = 163$. There also prokaryotes with sizes between.2 μm ($k = 157$ corresponds to.08 μm) and 750 μm. Cell nuclei, mitochondria, and other membrane bounded cell nuclei would have evolved from prokaryotes in this framework. The sizes of eukaryote cells are above 10 μm and the fact that multicellular organisms are in question strongly suggests that the higher multisteps giving rise to weak bosons and dark electrons in length scales above $L(167)$ are responsible for multi-cellular structures.

This scenario leaves a lot of questions unanswered. In particular, one should understand in more detail the weak physics at various length scales as well as various exotic nuclear physics defined by dark nucleons and dark variants of nuclei.

Division of the evolution to that of biological body and magnetic body

Electron's Mersenne prime M_{127} is the highest Mersenne prime, which does not correspond to a completely super-astrophysical p-adic length scale. In the case of Gaussian Mersennes $M_{G,k}$ one has besides those defined by k in $\{113, 151, 157, 163, 167, \}$ also the ones defined by k in $\{239, 241, 283, 353, 367, 379, \ 457, 997\}$ [A1]. The appropriately extended model for evolution allows to distinguish between three kinds of values of k_{eff}.

1. The values of k_{eff} for which electron can appear as dark particle and thus satisfying $k_{eff} \leq 205$ (Table 5). These levels would correspond to structures with size below 1.25 m defined roughly by human body size and it is natural to assign the evolution of super-nuclear structures to the levels $167 < k_{eff} \leq 205$.

2. The values of of k_{eff} for which dark gauge bosons are possible in the model. This gives the condition $k_{eff} \leq 235$. These levels correspond to structures in the range 1.25 m-40 km. The identification as parts of the magnetic body can be considered.

3. The values of k_{eff} obtained by adding to the system also the Gaussian Mersenne pair $k \in \{239, 241\}$ allowing also the dark electrons. The lower size scale for these structures is 640 km.

4. The higher levels corresponding to k_{eff} in $\{283, 353, 367, ...\}$. The lower size scale for these structures is 3 AU (AU is the distance from Earth to Sun).

$k_{eff} > 205$ levels would correspond to the emergence of structures having typically size larger than that of the biological body and not directly visible as biological evolution. This evolution could be hidden neuronal evolution meaning the emergence of extremely low Josephson frequencies of the neurons modulating higher frequency patterns and being also responsible for the communication of long term memories.

Biological evolution

In principle the proposed model allowing multisteps between hierarchy levels defined by Mersenne primes and their Gaussian counterparts could explain the size scales of the basic structures below the size scale 1.25 m identified in terms of the $k_{eff} \leq 205$ levels of the hierarchy.

1. The emergence of cells having organelles

The appearance of the structures with $k_{eff} > 167$ (possibly idetifiable as magnetic body parts) should correlate with the emergence of simple eukaryotic cells and organisms, in particular plant cells for which size is larger than 10 μm, which could correspond to $k_{eff} = 171$ for electron and dark variants of weak gauge bosons. $k_{eff} = 177$ is the next dark electron level and corresponds to 80 μm scale. It seems natural to assume that these dark weak bosons do not transform to their $\hbar_0$ counterparts at these space-time sheets.

Cell nucleus would be the brain of the cell, mitochondria would be the energy plant, and centrioles generating microtubules would define the logistic system. Also other organelles such as Golgi apparatus, ribosomes, lysosomes, endoplasmic reticulum, and vacuoles would be present. These organelles would live in symbiosis by topologically condensing to $k_{eff} \geq 171$ magnetic body controlling their collective behavior. Centrosomes associated with animal cells would not be present yet but microtubule organizing centers would already be there.

The recent observations show that centrioles are not always in the characteristic T shaped conformation. Daughter centrioles resulting during the replication of mother centriole use first ours of their lifetime to roam around the cell before becoming mature to replicate. A possible interpretation is that they are also life forms and that magnetic body utilizes daughter centrioles to perform some control functions crucial for the future development of the cell. For instance, centrioles visit the place where axonal growth in neurons starts.

Cytoskeleton would act as a counterpart of a central nervous system besides being responsible for various logistic functions such as transfer of proteins along microtobuli. Centrioles give also rise to basal bodies and corresponding cilia/flagella used by simple cells to move or control movement of air or liquid past them. Centriole pair would be also used by the magnetic body to control cell division.

The logistic functions are the most obvious functions of microtubules. Magnetic body would control cell membrane via signals sent through the cell nucleus and communicated to the cell membrane along microtubuli. Basal bodies below the cell membrane and corresponding cilia/flagella would serve as motor organs making possible cell motion. Tubulin conformations representing bits would allow microtubule surface to represent the instructions of the magnetic body communicated via via cell nucleus to various proteins moving along the microtubular surface so that they could perform their functions.

TGD based view about long memory recall as communication with geometric past allows also the realization of cellular declarative memories in terms of the conformational patterns. Memory recall corresponds to a communication with geometric past using phase conjugate bosons with negative energies reflected back as positive energy bosons and thus representing an "image" of microtubular conformation just like ordinary reflected light represents ordinary physical object. There would be no need for a static memory storage which in TGD framework would mean taking again and again a new copy of the same file.

Receptor proteins would communicate cell level sensory input to the magnetic body via MEs parallel to magnetic flux tubes connecting them to the magnetic body. We ourselves would be in an abstract sense fractally scaled up counterparts of receptor proteins and associated with dark matter iono-lito Josephson junction connecting the parts of magnetosphere below litosphere and above magnetosphere. The communication would be based on Josephson radiation consisting of photons, weak bosons, and gluons defining the counterpart of EEG associated with the level of the dark matter hierarchy in question.

3. The emergence of organs and animals

The emergence of magnetic bodies with k_{eff} in the range $(177, 181, 183, 187, 189, 195, 201, 205)$ allowing both dark electron and weak bosons could accompany the emergence of multicellular animals. Magnetic body at this level could give rise to super-genome making possible genetic coding of organs not yet possessed by plant cells separated by walls from each other. The super structures

formed from centrosomes and corresponding microtubuli make possible complex patterns of motion requiring quantum coherence in the scale of organs as well as memories about them at the level of organs.

4. The emergence of nervous system

k_{eff} in the range $(187, 189, 195, 201, 205)$ allowing dark electrons and weak bosons gives size scales $(.25, .5, 4, 32, 128)$ cm, which could correspond to the scales of basic units of central nervous system. What would be of special interest would be the possibility of charged entanglement based on classical W fields in macroscopic length scales. The emergence of the new level means also the integration of axonal microtobuli to "text lines" at the magnetic flux sheets making possible logistic control at the multineuronal level. The conformational patterns of the microtubular surface would code nerve pulse patterns to bit patterns representing declarative long term memories. An interesting question is whether the reverse coding occurs during memory recall.

The evolution of magnetic body

For mammals with body size below 1.25 m the levels $k_{eff} > 205$ cannot correspond to biological body and the identification in terms of magnetic body is suggestive. The identification of EEG in terms of Josephson frequencies suggests the assignment of EEG with these levels.

1. The emergence of EEG

EEG in the standard sense of the word is possessed only by vertebrates and one should understand why this is the case. The value of Josephson frequency equal to 5 Hz requires only $k_d = 47$ so that something else must be involved. A possible explanation in the framework of the proposed model comes from the following observations.

1. Besides the maximal p-adic scale $k = 205$ for which electron and weak bosons appears as dark variants the model allows also levels at which only gauge bosons appear as dark particles. From **Table 5.9**one finds that levels $k \in \{207, 211, 213, 217, 219, 221, 223, 225, 229, 235\}$ are allowed. Could it be that these levels and possibly some highest levels containing both electrons and gauge bosons as dark particles are a prerequisite for EEG as we define it. Its variants at higher frequency scales would be present also for invertebrates. The lowest Josephson frequency coded by the largest value of $\hbar$ in the cell membrane system determines the Josephson frequency.

2. The membrane potentials -55 mV (criticality against firing) correspond to ionic Josephson energies somewhat above 2 eV energy ((2.20, 2.74, 3.07, 2.31) eV, see Table 1). For 2 eV the wavelength 620 nm is near to $L(163) = 640$ nm. Therefore the Josephson energies of ions can correspond to the $L_e(k = 163)$ if one assumes that a given p-adic mass scale corresponds to masses half octave above the p-adic mass scale so that the opposite would hold true at space-time level by Uncertainty Principle. Josephson frequencies $f_J \in \{5, 10, 20, 40, 80, 160\}$ Hz correspond to $k_d \in \{47, 46, 45, 44, 43, 42\}$ giving $k_{eff} \in \{210, 209, 208, 207, 206, 205\}$.

   (a) Cerebellar resonance frequency 160 Hz would correspond to $k = 205$ -the highest level for for which model allows dark electrons (also 200 Hz resonance frequency can be understood since several ions are involved and membrane potential can vary).

   (b) The 80 Hz resonance frequency of retina would correspond to $k_{eff} = 206$ -for this level dark electrons would not be present anymore.

   (c) 40 Hz thalamocortical frequency would correspond to $k_{eff} = 207$.

   (d) For EKG frequencies are EEG frequencies below 20 Hz 12.5 and heart beat corresponds to .6-1.2 second cycle (the average.8 s corresponds to $k_{eff} = 212$).

3. Even values of k_{eff} are not predicted by the model based on Mersenne primes allowing only odd values of k_{eff} so that the model does not seem to be the whole truth. The conclusion which however suggests itself strongly is that EEG and its variants identified as something in the range 1-100 Hz, are associated with the levels in at which only dark weak bosons are possible in the proposed model. Note that the size scales involved with EEG would be

Table 5.10: The Compton frequencies obtained by scaling $2^{k_d/2}$ from the basic triplet $k_{eff} = (239, 240, 241)$. The values of k_d correspond to those predicted by the model based on Mersenne primes.

k_d	f_1/Hz	f_2/Hz	f_3/Hz
0	707	1000	1412
4	177	250	354
6	89	1250	177
10	22.1	31.3	44.2
12	11.1	15.6	22.1
14	5.5	7.8	11.1
16	2.8	3.9	5.5
18	1.4	2.0	2.8
20	0.7	1.0	1.4
24	0.2	0.2	0.3

above the size scale of human body so that we would have some kind of continuation of the biological body to be distinguished from the magnetic body. The time scales assignable to the dark CDs would be huge: for instance, $k = 205$ would correspond to $T = 2^{42} \times .1$s making about 1395 years for electron.

2. Does magnetic body correspond to the space-time sheets carrying dark weak bosons?

The layers of the magnetic body relevant for EEG have have size of order Earth size. Natural time scale for the moment of sensory consciousness is measured as a fraction of second and the basic building blocks of our sensory experience corresponds to a fundamental period of.1 seconds. This scale appears already at $\hbar_0$ level for electron CD. The natural question concerns the relationship of the magnetic body to the $k > 205$ space-time sheets carrying only gauge bosons in the model and having size scale larger than that of biological body. Do they correspond to an extension of biological body or should they be regarded as parts of the magnetic body? The following observations suggest that they could correspond to layers of the magnetic body responsible for the fractal variant of EEG.

1. The primary p-adic time scales (Compton times) $T(239)$ and $T(241)$ correspond to frequencies, which are $2^{\pm 1/2}$ kHz. The geometric average $k = 240$ corresponds to kHz frequency. Is the appearance of kHz scale a mere accident or do the frequencies assignable to the quark CDs correspond to Compton times $\propto \sqrt{2^{k_{eff}/2}}$?

2. One can apply scalings by 2^{k_d} to the triplet $(239, 240, 241)$ to get a triplet $(239 + k_d, 240 + k_d, 241 + k_d)$. The results are summarized in **Table 5.10**. Clearly the frequencies in question cover also the EEG range. Note that these frequencies scale as $\sqrt{1/r}$ whereas Josephson frequencies scale as $1/r$.

Also ZEG and WEG would appear but in much shorter scales dictated by k_{eff} and might accompany EEG. Somehow it seems that the effective masslessness of weak bosons below given scale is highly relevant for life. One can of course ask whether some larger Gaussian Mersenne could change the situation. There is a large gap in the distribution of Gaussian Mersennes after $k = 167$ and the next ones correspond to $M_{G,k}$, with k in $(239, 241, 283, 353, 367, 379, 457, 997)$ [A1]. The twin pair $k = (239, 241)$ corresponds to a length scales $(1.6, 3.2) \times 10^2$ km and the minimum value for k_d are (72, 74) ($167 \to (239, 241)$ transition).

3. Long term memory and ultralow Josephson frequencies

What determines the time scale associated with long term memory is a crucial question if one really wants to understand the basic aspects of consciousness.

1. Does the time scale correspond to the size scale of CD assignable to electron scaled by $r = \hbar/\hbar_0$? In this case relatively small values of r would be enough and $r = 2^{47}$ would give time scale of 10^{13} s for for electron's CD, which is about 3×10^5 years. This does not make sense.

2. Does Josephson frequency define the relevant time scale? In this case the long term memory would require the analog of EEG in the time scale of memory span. $k_{eff} = 205$ would give 6 ms time scale for memory from the assignment of $k_{eff} = 163$ to the Josephson photons at V=-50 mV implying $k_d = 42$. Minute scale would require $k_{eff} = 217$. The highest level $k_{eff} = 235$ allowed by the model involving only Gaussian Mersennes with $k \leq 167$ would correspond to a time scale of 77.67 days (day is 24 hours). For Gaussian Mersennes defined by $k_{eff} = (239, 241)$ the time scales become about (41.4, 82.8) months (3.4 and 6.8 years). These scales should also define important biorhythms. The claimed 7 years rhythm of human life could relate to the latter rhythm: note that the precise value of the period depends on the membrane potential and thus varies. The presence of the scaled up variants of the by $k_d \leq 78$ allows longer time spans of long term memory and the scaling defined by $k_d = 167 - 163 = 4$ scales up the span of long term memories to (54.4, 108.8) years.

4. Cultural evolution

Higher levels in the hierarchy would correspond mostly to the evolution of hyper-genome coding for culture and social structures. Introns are good candidate for the nucleotides involved. The development of speech faculty is certainly a necessary prerequisite for this breakthrough. Already EEG seems to correspond to dark layers of biological body larger than biological body so that one can cask whether the weak bosons and dark electrons in the length scales $k = 239, 241, 283, 353, 367, ...$ could be relevant for the collective aspect of consciousness and cultural evolution. Maybe the size scales $(175, 330)$ km and their scaled up variants by $k_d \leq 78$ might have something to do with the spatial scale of some typical social structure (not city: the area of New York is only 790 km^2).

5.9 Oil Droplets In Water Solution As A Primitive Life Form?

The origin of life is one the most fascinating problems of biology. The classic was carried out almost 60 years ago. In the experiment sparks were shot through primordial atmosphere consisting of methane, ammonia, hydrogen and water and the outcome was many of the amino-acids essential for life. The findings raised the optimism that the key to the understanding of the origins of life. After Miller's death 2007 scientists re-examined sealed test tubes from the experiment using modern methods found that well over 20 amino-acids - more than the 20 occurring in life - were produced in the experiments.

The Urey-Miller experiments have yielded also another surprise: the black tar consisting mostly of hydrogen cyanide polymer produced in the experiments has turned out to be much more interesting than originally thought and suggests a direction where the candidates for precursors of living cells might be found. In the earlier experiments nitrobenzene droplets doped with oleic anhydride exhibited some signatures of life. The droplets were capable to metabolism using oleic anhydride as "fuel" making it possible for the droplet to move. Droplets sensed each other's presence and reacted to it and also demonstrated rudimentary memory.

In the sequel a model for the oil droplets as primitive life form is developed using as a constraint the TGD inspired quantum model for living matter. The key ingredients are the notions of magnetic body, the assignment of dark matter identified a hierarchy of macroscopic quantum phases to a hierarchy of Planck constants, zero energy ontology, the model for DNA-cell membrane system as topological quantum computer, and Negentropy Maximization Principle combined with the notion of number theoretic entropy. This entropy can be negative for rational and even algebraic entanglement probabilities, which inspires the vision about life as something in the intersection of real and p-adic worlds.

The basic objection against the identification of oil droplets as a primitive life form is that droplets have no genetic code and do not replicate. The TGD inspired model for dark nucleons

however predicts that the states of dark nucleon are in one-one correspondence with DNA, RNA, tRNA, and amino-acid molecules and that vertebrate genetic code is naturally realized. The question is whether the realization of the genetic code in terms of dark nucleon strings might provide the system with genetic code and whether the replication could take place at the level of dark nucleon strings rather than droplets. TGD inspired quantum model of biology leads to a model for oil droplets as a primitive life form. In particular, a proposal for how dark genes could couple to chemistry of oil droplets is developed.

5.9.1 Intelligent Oil Droplets

New Scientist (see `http://tinyurl.com/y8qyxymd`) tells about a new twist related to the Urey-Miller experiment (see `http://tinyurl.com/y83eks2s`). Martin Hanczyc (see `http://tinyurl.com/ybvwbvg3`) and his colleagues of University of Southern Denmark in Odense are doing research with a rather ambitious goal: the discovery of the recipe of life. The highly demanding challenge is to find candidates for the protocell that preceded the recent cell. What makes the task so difficult that it is not even clear what one should be searching for. For instance, what basic characteristics distinguishing living matter from inanimate systems protocell is expected to have before one can speak about primitive life form? And if one accepts the dogmas of standard biology, one encounters also the nasty hen-egg question which came first: metabolism or the genetic machinery.

Hanczyc and his colleagues have been experimenting with simple candidates for primitive life forms: oily nitrobenzene [I31] (see `http://tinyurl.com/678a2a`) droplets doped with oleic anhydride [I34] (see `http://tinyurl.com/y7ua8mwq`) immersed in alkaline (see `://tinyurl.com/zelgz`) aqueous solution (alkalinity is by definition an ability to reduce acidicity). They have found that these systems have some attributes generally associated with life. The recent experiments replaced oleic anhydrite with the black tar consisting of complex branched and fractal looking hydrogen cyanide (HCN) polymer [I17] (see `http://tinyurl.com/nehrmu4`) produced by Urey-Miller experiments and found that also now the droplets exhibit lifelike behavior: they sense and respond their neighbors and move towards "food" sources.

The earlier experiments using nitrobenzene droplets doped with oleic anhydridge immersed in alkaline solution began immediately to move along straight lines. What happened that the oleic anhydride at the surface of the droplet reacted with the water splitting to two oleic acid molecules [I33] (see `http://tinyurl.com/yf34q92`) by hydration. This dropped the surface tension of the droplet and by a kind of spontaneous symmetry breaking the reaction rate had maximum at some point of the droplet and a "hot spot" was generated drawing oleic anhydride from the interior of the droplet and generating a convective flow. A pH gradient develops along the surface. The oleic acid in turn moved along the droplet surface from the hot spot to the diametrically opposite side of the droplet [I89] (see (`http://tinyurl.com/yc627j5k`). The net effect was a linear motion. pH gradient is claimed to be essential for the generation of motion but I must admit that I do not quite understand this point. A primitive metabolism liberating energy is obviously in question. By momentum conservation the total momentum for the convective flow and flow of oleic acid was compensated by a center of mass motion of the droplet.

One could claim that this process belongs to the same class of self-organization processes as the generation of convection patterns as one heats liquid from below. Other researchers have however discovered that the oil droplets can also travel along chemical gradients, something known as chemotaxis used by many bacteria to find food and void threats. One oil droplet managed even to (see "solve" (see `http://tinyurl.com/yb7muvg`) a complex maze containing "food" at its other end [I88]. Whether this kind of behavior can be regarded as a mere chemistry is far from obvious to me. To me this a achievement look like a genuinely goal directed intentional behavior.

Hanczyc has also found that when the oil droplets approach each other they change course to avoid collision, or can circle each other-like partners in Viennese waltz! Oil droplets seem to have even memory. By videoing the paths of oil droplets Hanczyc found that the decision to stop or continue was not random but the behavior at any point of orbits was affected by the earlier behavior. This is by the way an elegant experimental manner to show that non-deterministic behavior is not just randomness. The experiments have been also carried using instead of oleic anhydride mineral oil consisting of a mixture of alkanes having as building block polymers from from CH_4 by dropping two hydrogen from each C as also lipids have (methane CH_4 is the simplest alkane). What distinguishes mineral oil molecules from the oleic anhydride molecules are the

oxygen atoms in the middle of the reflection symmetric linear molecule. Also now the droplets move although the process takes place with a slower rate.

The basic objections against the identification of the oil droplets as a life form is that they do not replicate and there is no genetic code. One must be however very cautious with this kind of statements. Maybe the primary life forms are not the droplets and the behavior of droplets reflects the control actions of these life forms on droplets. Perhaps also genetic code could be realized at at totally different level. The recent findings of the group of HIV Nobelist Montagnier [I94] (see `http://tinyurl.com/2co7s6j`) indeed suggest a new realization of genetic code in water closely related to to water memory and TGD suggests a concrete realization of this code [K24].

5.9.2 Some Key Ideas Of TGD Inspired Quantum Biology

Before proposing a model for intelligent oil droplets as a primitive life form its good to list some of the basic ideas of TGD inspired quantum biology.,

1. The basic hypothesis is that the dark matter at the magnetic flux tubes of the magnetic body assignable to any physical system serves as an intentional agent controlling the behavior of the ordinary matter [K14]. Dark matter can correspond to just the ordinary particles- at least electrons and protons- in a phase with non-standard large value of Planck constant forming macroscopic quantum phases. Also biologically important ions could form this kind of phases. TGD inspired nuclear physics [L2] allows also the bosonic counterparts of fermionic with same nuclear charge so that every fermionic ion could be accompanied by exotic bosonic ion so that Bose-Einstein condensates could become possible.

2. The model for dark nucleons [L2, K24] as entangled triplets of three quarks leads to the identification of the counterparts DNA, RNA, tRNA, and amino-acids as three-quark states and one can identify also vertebrate genetic code. DNA sequences correspond to dark nucleon sequences - dark nuclei - in this correspondence. The proposal is that dark proton sequences in water form dark nucleons with so large a Planck constant that nucleon size corresponds to size of singe DNA codon. There is indeed evidence that in atto-second time scale (time scale for corresponding causal diamonds) water obeys effective chemical formula $H_{1.5}O$ as far as scattering of electrons and neutrons is considered [D7, D12, D4]. This would suggest that 1/4 of protons are in dark large Planck constant phase in the experimental situation. This proportion is expected to depend on temperature and pressure and should explain the rich spectrum of anomalies of water [D9] by regarding it as a two phase system [K16]. Perhaps these protons could form dark nucleon sequences realizing genetic code. These sequences could replicate and evolve and could define at least the analog of DNA or RNA. Maybe even DNA-mRNa-amino-acids translation processing could take place. If a translation machinery transforming exotic DNA to ordinary has developed during evolution, this fundamental realization of genetic machinery might make possible kind of Research & Development making possible to experiment with different genomes. Evolution would not be a random process anymore [K24].

3. The proposal is that the ordered water layers associated with polar molecules dissolved in water are attached to the magnetic body of the molecule induced in water environment and that this magnetic body mimicking ithe original molecule is an essential element of this primitive life [K24]. The self-organization processes of these layers induced by external perturbations could be the predecessor of processes like protein folding and de-folding. The mechanism of water memory could be based on "dropping" of the magnetic bodies of molecules as a result of repeated shaking involved with homeopathic procedure inducing a sequence of catastrophes driving the evolution of these primitive life forms. One can also ask whether these magnetic bodies could define the analog of proteins providing one realization of dark matter genetic code.

4. If dark nucleons have been the predecessors of chemical life forms, one can circumvent the hen-egg question about whether the genetic code or metabolism came first. In zero energy ontology negative energy signals propagating in the direction of geometric past would in turn provide fundamental mechanism of intentional action, metabolism, and memory. If this is

the case, evolution would have only led to a refinement of the fundamental mechanisms of life already existing: there would be no need to pull anything out of hat. The mechanisms for chemical storage and utilization of energy are needed and moving oil droplets would provide a primitive realization of these mechanisms.

5. The notion of negentropic entanglement (see **Fig.** `http://tgdtheory.fi/appfigures/cat.jpg` or **Fig. ??** in the appendix of this book) makes sense if one accepts the role of p-adic number fields and the vision about life as something residing in the intersection of real and p-adic worlds [K32]. Entanglement probabilities for negentropic entanglement must be rational or algebraic numbers in the algebraic extension of p-adic numbers involved and there is unique prime for which this entanglement entropy is maximally negative. Negentropic entanglement makes possible new kind of many particle states analogous to bound states but with negative binding energy. The reason is that negentropic entanglement is stable against state function reduction if Negentropy Maximization Principle determines its dynamics also in the case of negentropic entanglement. The proposal is that the mysterious high energy phosphate bond corresponds to negentropic entanglement and carries both metabolic energy and information [**?**]. In this framework ATP-ADP cycle has also information theoretic interpretation as a transfer of conscious information.

The model for DNA as topological quantum computer [K17, K53] led among other things to an identification of magnetic flux tubes connecting bio-molecules as a basic building bricks of living matter.

1. Flux tubes are assumed to connect DNA nucleotides to lipids of the nuclear and cell membranes. Flux tubes could begin from =O in the double bonds R=O or from negatively charged oxygens. In the case of DNA R would correspond to the basic unit in phosphate deoxiribose backbone (see `http://tinyurl.com/69okq`) consisting of aromatic 5-cycle and PO_4 containing one =O and one O^- [I14]. The lipid end would contain =O and -OH and the flux tube could end to either of these or possibly -OH ionized to -O^- by a transformation of proton to dark proton.

2. The braiding of flux tubes makes topological quantum computation like processes possible [K17]. The contractions and expansions of flux tubes induced by phase transitions changing the value of Planck constant would be a basic control mechanism allowing to understand how two biomolecules (say DNA and its conjugate) can find each other in the thick soup of organic molecules. The reconnections of the magnetic flux tubes would be second basic control mechanism and ATP $\rightarrow$ADP process (see `http://tinyurl.com/clnu4`) [I3] involving splitting of phosphate group and liberating metabolic energy and its reverse would represent standardized reconnection process and its reversal.

3. The flux tube ends would contain quark and antiquark (u, d and their antiquarks are involved) coding for the four DNA letters A, T, C, G so that also dark quarks and their antiquarks would provide an elementary particle level realization for the codons. Note that topological quantum computation does not necessitate genetic code and therefore also the repeating DNA sequences regarded as junk could be used for topological quantum computations.

5.9.3 General Ideas About Oil Droplets As A Primitive Life Form

It is interesting to see what one obtains if one takes the dark nucleon realization of genetic code, the mechanism of water memory realized as magnetic bodies attached to the ordered water layers associated with polar molecules, the model for DNA as topological quantum computer, and the ideas about magnetic body with dark matter as fundamental bio-control as basic ingredients of the model of intelligent oil droplets.

1. The formation of hot spot on the oil droplet resembles spontaneous symmetry breaking. The interpretation as a generation of magnetic body of approximately dipolar magnetic field is attractive. The magnetic body would control the droplet. The change of the direction of the motion of the oil droplet would correspond to the change of the orientation of the magnetic body and would thus reduce to a motor action of the magnetic body.

2. The flux tubes of the magnetic body would be most naturally parallel to the direction of the nitrobenzene polymer strands. Oleic anhydride molecules and the hydrogen cyanid polymers would be transferred along the magnetic flux tubes of an approximately dipolar magnetic field entering to the hot spot from interior and the oleic acid molecules could move along the flux tubes continuing along the surface of the droplet to the diametrically opposite point. The migration of birds along magnetic field lines is a direct analogy for this.

3. The dark matter at the magnetic body would give the oil drop its "intelligence". The dark nuclear genome could be realized at the magnetic body and the magnetic bodies might define the replicating life form as in the TGD based model of water memory for which the magnetic bodies represent molecules as far as low frequency electromagnetic fields characterized by cyclotron frequencies are considered. One could see intelligent oil droplets as manifestation of control actions of a life form defined by dark matter at magnetic flux tubes and the first step in the process eventually leading to a complex control and coordination of the behavior of ordinary matter.

4. The ability of droplets to react to the presence of other droplets would be due to the communications between magnetic bodies based on low frequency photons at cyclotron frequencies but having energy above thermal energy if the value of Planck constant is large enough.

At least oleic anhydrite, hydrogen cyanide, and mineral oil can serve as a fuel of oil droplets and this raises the question what might be the common property shared by them. For illustrations of various molecules involved see **Figs.5.3**, **5.4**, **5.5**, **5.6**, **??**, **5.7** in the section containing figures. Certainly this property must relate to metabolism and the model for ordinary metabolism suggests that this property is shared also by the high energy phosphate bond.

1. Oleic anhydrite (see `http://tinyurl.com/y7ua8mwq`) is a lipid formed by as a fusion of two oleic acids consisting of a sequence of CH_2 units and the characteristic (C=O)-(O-H) group at its end. The burning of the molecule splits it to two oleic acids by hydration meaning utilizing one water molecule. The formation of oleic acid in turn involves dehydration so that the burning process is analogous to de-polymerization of DNA or amino-acid sequence by hydration.

2. Mineral oil (see `http://tinyurl.com/eoy5x`) is also a lipid and looks like oleic anhydride locally. In the ideal case however the crucial..(C=O)-O-(C=O)-.. portions are lacking. Oxygenation could however produce this kind of defects to the mineral oil molecules so that the mechanism of burning would remain the same.

3. Hydrogen cyanide (see `http://tinyurl.com/nv8qt8`) HCN involves valence bond of valence 3 between C and N. The polymers are constructed from H-C-N sequences with single valence bond between both C: s and N: s of two subsequent horizontal H-C-N units, which one can think of as being obtained from (H-C)-(H-C)... sequence and ..N-N-N... sequences with each N and C connected by horizontal valence bond. This polymer replaces oleic acid as a "fuel" reacting with water and liberating metabolic energy. These polymers - which would serve as primitive analogs of proteins- would be transferred along the magnetic flux tubes and burned at the hot spot by hydration. HCN has been proposed to have been a primitive precursor of both amino acids and nuclei acids. With motivations coming from the general vision about quantum biology, it will be proposed that also hydrogen cyanide polymers contain in their C-backbone..(C=O)-O-(C=O)-.. portions as local defects due to oxygenation so that the burning would occur via hydration in all three cases.

5.9.4 What Are The Prerequisites For Metabolism And Topological Quantum Computation Like Processes?

The basic question is whether metabolism interpreted in TGD framework as negentropy transfer and thus requiring the analogs of high energy phosphate bond and ATP-ADP cycle is possible. The high energy phosphate bonds make also possible flux tube structures serving as a prerequisite for topological quantum computation like process. Both oleic anhydride, hydrogen cyanide and

mineral oil can serve as a metabolic source and one should identify the common property of them making. This property should be the analog of high energy phosphate bond.

1. High energy phosphate bond carries metabolic energy. This bond is poorly understood and I have proposed that high energy phosphate bond carries negentropic entanglement which identified in TGD framework as the basic characteristic of life [K32]. In the middle of oleic anhydride there (C=O)-O-(C=O) structure and its splitting in hydration liberates energy. This suggests that this structure also now carries the negentropic entanglement and the metabolic energy. The splitting process of oleic anhydrite occurring at the hotspot would be analogous to ATP→ADP process involving splitting of PO_4 molecule from ATP.

2. Oleic acid is a lipid containing at its second end the characteristic (C=O)-OH group assumed to serve as a terminal for the magnetic flux tubes in the model of DNA-cell membrane system as quantum computer. In the presence energy feed one could imagine that the inverse process transforming oleic acid to oleic anhydride takes place and a primitive version of the metabolic cycle involving photosynthesis and cellular breathing can be imagined. Metabolic and quantum information processing would be very intimately related. By DNA as topological quantum computer analogy the magnetic flux tubes connecting oleic anhydride molecules would make be responsible for primitive topological quantum computation if present in the system.

3. Also when the tar from Urey-Miller experiment replaces oleic anhydrite small amount of oleic anhydride was used to build a film around oil droplet to lower surface tension. This suggests that the oleic anhydride has a deeper purpose and defines the analog of cell membrane and make possible for the magnetic flux tubes from the interior of the droplet to attach to the lipids? This could occur at least in the hot spot and at point opposite to it so that magnetic flux tubes would connect the diametrically opposite points of the droplet Oleic anhydride would therefore serve a dual purpose serving both as a metabolic resource and a building brick of the protocell membrane: metabolic energy would be accompanied by information. Also in real life lipids -about which fats are a special case- have this double role.

4. The process occurs also both for hydrogen cyanide and mineral oilandthis raises obvious objections since the energy and information carrying (C=O)-O-(C=O) structures making also possible the flux tube connects are not present in the ideal situation. One must however remember that the situation in real life is far from ideal and the most obvious idea is that the polymers as such are not enough: oxygen is the basic metabolic resource and oxygenation serving as the loading of metabolic batteries might be the crucial element.

   (a) The backbone of both oleic acid (see `http://tinyurl.com/yf34q92`), oleic anhydride, and of mineral oil polymers (see `http://tinyurl.com/eoy5x`) is CH_2 sequence common to all lipids. If some fraction of mineral oil polymers contain (C=O)-O -(C=O): s serving as carriers of metabolic energy and information the situation reduces to that for oleic anhydride apart from effects caused by the fact that the density of metabolic energy per volume is expected to be lower, which would explain why the motion is slower.

   (b) Also in the case of hydrogen cyanide (see `http://tinyurl.com/nv8qt8`) polymers one can imagine the presence of similar defect structures due to oxygenation. A portion of...(H-C)-(H-C)-(H-C).... sequence would be replaced with....(H-C)-(C=O)-O-(C=O)-(H-C)... with three carbons lacking. The nitrogen sequence...N-N-N-N-N.. would split to...N-OH and OH-N... so that three nitrogens would be lacking. The total number of hydrogens would remain the same.

Under these assumptions the model explains all three cases using hydration as the basic mechanism of metabolism as well as the conditions required by DNA as topological quantum computer model. Note that the process consumes oxygen just as the ordinary breathing.

5.9.5 What About Genetic Code And Counterpart Of DNA?

Consider next the possible realization of the genetic code. The first thing to notice is that even in the case that genetic code is not realized the braiding would make possible topological quantum

computation like processes and a realization of memory in terms of braiding patterns. Furthermore, chemical realization of the genetric code is not possible so that dark nucleons remain the only possibility in TGD framework. The challenge is to try imagine whether DNA like structures having flux tube connections with the counterparts of lipids in the cell membrane could exist. The following suggestion is a product of free imagination based on analogies and reflects my amateurish skills in biochemistry.

1. Aromatic rings (see `http://tinyurl.com/ycf3kv24`) [I4] are an essential element of both phosphate deoxiribose backbone of DNA and of DNA letters itself. Nitrobenzene molecule obeys chemical formula (C_6H-5)-NO_2 and contains benzene ring to which NO_2 nitro group is attached. The oily character is due to the benzene ring. Benzene rings could serve as a counterpart for the hydrocarbon 5-cycles appearing in phosphate deoxiribose backbone. Note however that in deoxiribose ring one carbon is replaced with O and two hydrogens with OH. Moreover, single benzene molecule would correspond to the counterpart of DNA triplet rather than single nucleoside. One could however argue that only a backbone is in question so that the differences might not matter.

2. One would naively expect that both nitrogen and phosphorus have same valence equal to three. In PO_4 phosporus has 5 valence bonds as a rule and the interpretation is that phosphorus tends to donate its valence electrons to get empty shell. This kind of states are known as oxidation states and are possible also for nitrogen: hydroxylamine NO_2H is one example of this kind of state. In fact, from the from structural formula of nitrobenzene (see **Fig. 5.3**) one finds that nitrogen gives one electron to second oxygen so that also this state can be regarded as an oxidation state. This inspires the idea that nitrogen takes the role of phosphorus at least partially.

3. If one does not allow oxidation states, the simplest manner to construct the analog of phosphate deoxiribose backbone is as structure ...X-X-X..., with X= R-O- (R_1-N)-O, where R denotes oleic anhydride and R_1 is for benzene residue. The bridges connecting benzene rings would be reflection symmetric. The breaking of reflection symmetry is however essential since it determines the reading direction of DNA.

4. If one accepts oxidation states, the simplest option is that in benzene-NO_2 complex NO_2 is replaced with (N=0)-O and the counterpart of phosphate deoxiribose backbone would have the structure ...X-X-X—, X=R- (R_1-N=0)-O with R denoting oleic anhydride and R_1 benzene. Oleic anhydride has valence bond to N so that N has 5 valence bonds as phosphorus in phosphate. Also the crucial =O is present. The units connecting subsequent benzene rings are not reflection symmetric anymore as indeed required. There is however no charged oxygen as in the case of ordinary DNA. Note that the analogs for AMP, ADP, ATP make sense since one can single replace P by N phosphate PO_4.

5. An interesting question is whether the nitrogen based metabolism could be realized as a primordial metabolism. Nitroglycerin (see `http://tinyurl.com/y9a23qen`) is analogous to tri-phosphate although the nitrates are not arrranged linearly as in ATP and is used as both heart medicine and as an active incredient of explosives. The latter use conforms with the idea about the presence of high energy nitrate bond in NO_4.

6. The two mirror image branches of oleic anhydride molecule consist of 15 carbon atoms and the structure is rather long as compared to the basic unit of phosphate deoxiribose backbone so that the distance between subsequent benzene units would be rather long- of order 10 Angstroms. On the other hand, 10 DNA codons correspond to 10 nm length in a good accuracy so that one codon would take 1 nm length also in this case. If double strand is formed, twisting is possible so that the scales could be the same. The size scale of the dark nucleon representing single DNA codon should correspond to the size scale of single oleic anhydride molecule and the required value of Planck constant would be of order 10^6 as the ratio of this scale and nucleon size of order 10^{-15} meters.

7. The counterparts of DNA nucleotides forming a linear structure should join to the benzene rings. Dark nucleon sequences remain the only possibility if one wants a realization of genetic

code. Each dark codon represented by dark nucleon would be connected by three flux tubes with quark and antiquark at their ends to single unit of the proposed structure. There would be three =O: s per single benzene ring. Since single benzene ring corresponds to single DNA codon three =O: s are indeed expected. Therefore =O: s could indeed correspond to terminals for flux tubes coming from single dark nucleon representing single DNA codon.

8. The division of oil droplet would be the analog of cell replication and would involve at the deeper level the replication of dark nucleon sequences. This requires the analog of DNA double strand and the analogs of DNA codons would be dark nucleons. Genetic codons could be realized in terms of flux tubes connecting dark nucleon sequences to the oleic acids or oleic anhydrides at the surface of the droplet. It remains to be seen whether the division can be achieve in real world.

To sum up, the proposed model is rather direct application of TGD based vision about life and the killer test is whether the mineral oil oil molecules and hydrogen cyanide molecules are not ideal but actually contain the (C=O)-O-(C= O) pieces carrying energy and information and serve as terminals for the magnetic flux tubes.

5.9.6 Another Approach To Protocell

Also the group led by Jack. W. Szostak (see `http://tinyurl.com/y8avsbzd`), who was the 2009 Nobel Prize winner in physiology - has carried out beautiful experiments in which they are able to create a candidate for protocell satisfying many of the basic requirements [I99].

One such condition is the ability of protocell to transfer various nutrient molecules through the protocell membrane. In modern cell pumps and channels consisting of proteins are believed to serve that purpose (for a different view see the remark below). Genetically coded proteins were however absent during the primordial era. Therefore the membrane is constructed of branching lipids believed to exists during prebiotic era allowing sugars which are basic building bricks of DNA to permeate to the protocell. Given the DNA template, the basic building bricks of DNA molecule assemble to a copy of DNA in this protocell.

What is still lacking is the generation of the template strand of DNA itself and also the replication of protocell. If dark DNA in the form of dark nucleon strings is really there, the template could result as the assembly of the basic bricks of DNA around it and above a proposal for the analog of this kind of process is suggested. The replication of the dark genes would have been also present from the beginning and would have preceded the replication of genes and protocell. Biological evolution could be seen as a migration from dark space-time sheets to ordinary ones and somewhat analogous to the migration of life from sea to land.

Remark: There are puzzling experimental findings about quantal currents through cell membrane even in absence of metabolic sources. In many-sheeted space-time [K44] one could interpret these currents as various kinds of Josephson currents running between cell interior and exterior along current carrying space-time shees. Pumps and channels would be more like a diagnostic tool allowing cell to measure the concentrations of various important biomolecules and ions.

At first sight the approaches of Szostak and Martin Hanczyc look very different. These approaches have however a lot of common at deeper level if one accepts TGD based view as DNA-cell membrane system or its more primitive version as a topological quantum computer like system relying on the braiding of magnetic flux tubes connecting the counterpart of DNA nucleotides to the lipids of protocell membrane and on the prebiotic realization of genetic code at the level of dark nuclear physics.

One could also argue that the protocell of Hanczyk represents oil based life as opposed to life as we know it. In TGD framework this is a mis-interpretation. The protocells of Hanczyk live in an aqueous environment. Nitrobenzene oil is an aromatic compound as also sugars and contains nitrogen taking in the proposed scenario same role as phosphorus in ordinary life. Oleic anhydride is lipid and- would provide basic building brick for a particular variant of DNA like structure halfway between dark and completely chemical realization. Oleic anhydride would provide also the building bricks of protocell membrane and serve as a nutrient just like fat molecules- also lipids- serve in "real life".

5.10 Figures

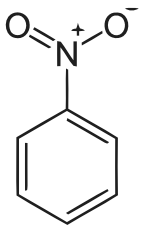

Figure 5.3: Nitrobenzene

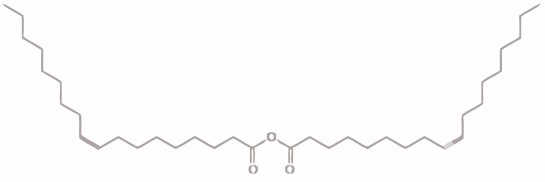

Figure 5.4: Oleic anhydride

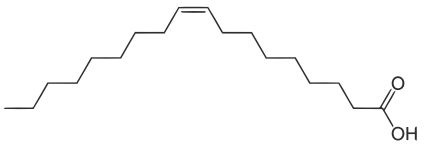

Figure 5.5: Oleic acid

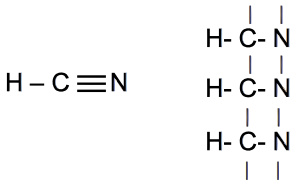

Figure 5.6: Hydrogen cyanide and hydrogen cyanide polymer.

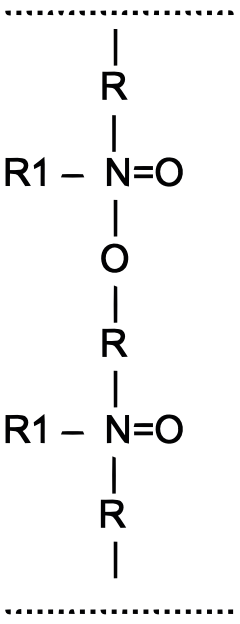

Figure 5.7: The analog of the deoxiribose phosphate backbone. R denotes oleic anhydride containing two =O: s and R1 benzene ring.

Chapter 6

Dark matter, quantum gravity, and prebiotic evolution

6.1 Introduction

The ideas related to prebiotic evolution have developed rather rapidly after the discovery of the hierarchy of Planck constants around 2003 providing a general manner to understand living orgnisms as macroscopic quantum systems.

1. Magnetic body as carrier of dark matter realized as phases with non-standard value $h_{eff} = n \times h$ of Planck constant is the key concept in the developments and brings to the description of the living matter a third level besides organism and environment [K62].

2. EEG and its predicted fractal variants have interpretation in terms of communication from biological body to to magnetic body and as control of biological body by magnetic body [K15]. EEG photons are identified as dark photons and the energy spectrum of dark EEG photons is conjectured to correspond to that for bio-photons. Bio-photons would result in the transformation of dark photons to ordinary ones and their energy spectrum would directly reflect the spectrum of endogenous magnetic fields. If h_{eff} for given ion is proportional to its mass number, the spectrum of energies for bio-photons resulting from dark cyclotron photons is universal and does not depend on charged particle.

3. One can now understand the mechanism making Cooper pairs of bio-superconductors stable, possibly even above room temperatures. Also the understanding of cell membrane as Josephson junction has increased considerably. The recent view [K42, K15] is that generalized Josephson junction is in question. The Josephson energy identified as the Coulombic energy difference at two sides of the membrane is generalized by including also the difference of cyclotron energies. This contribution dominates, and this explains why the value of metabolic energy currency is roughly 5-10 times higher than the value of Josephson energy.

   One ends up with a model of transmembrane proteins as generalized Josephson junctions by taking a "square root" of the thermodynamical model meaning that Boltzman weights are replaced with their complex square roots. The chemical potential difference of thermodynamical model is replaced with the difference of cyclotron energies. Generalized Josephson energies correspond to the differences of cyclotron energies in the first approximation since Coulombic contribution is small. The communications to the magnetic body by dark photons rely on frequency modulation due to variations of membrane voltage, in particular those induce by nerve pulses.

4. The totally unexpected observation was that the states of dark protons forming dark nuclei as string like objects correspond in natural manner to DNA,RNA, aminoacids and even tRNA molecules and that vertebrate genetic code is realized naturally, led to the proposal that prebiotic life relies on dark nuclear physics [L2].

5. Taking seriously the findings related to water memory and homeopathy [I71, I72, I65, I94, I95] as well as the findings of Gariaev et al [I83, I105] has led to a further progress. In this framework water memory and homeopathy provide direct evidence for the role of dark proton sequences at magnetic flux tubes as prebiotic life forms. The preparation of the homeopathic remedy would induce evolutionary process leading to a generation of a population of regions of water mimicking the magnetic body of the invader molecule. The challenge is to identify these regions.

6. The understanding of negentropic entanglement as entanglement described by $n \times n$ unit matrix and by unitary matrix for entanglement coefficient allowed a more precise understanding of Negentropy Maximization Principle and led to the conjecture that n is nothing but the integer characterizing h_{eff}. NMP implies that Universe generates negentropic entanglement, "Akashic records", being analogous to huge library extending quantum jump by quantum jump. It is perhaps not an accident that in quantum computation entanglement matrix is unitary.

7. There was also another thread related to the ideas about hierarchy of Planck constants. The findings of Nottale suggest that planets correspond to Bohr orbits with gigantic gravitational Planck constant. It took quite a time to realize that the same predictions follow if h_{gr} is associated with pairs formed by microscopic systems and Sun and that in this case the values of h_{gr} could be identified with those of h_{eff}.

   Already during first years emerged the idea that the Planck constant characterizes magnetic flux tubes connecting two systems and depends on the quantum numbers of the systems assignable to the interactions in question. Therefore one can speak also about h_{em} assignable to electromagnetic interactions. A vision developed stating that when interaction gets too strong, h_{eff} increases so that the perturbation series in powers of $1/h_{eff}$ converges and perturbation theory works. At space-time level this means non-determinism, which is key feature of the basic varioational principle: the space-time sheets connecting initial and final 3-surface at boundaries of CD are n-sheeted for $h_{eff} = n \times h$ and the sheets co-incide at ends.

8. The findings of Pollack [L15] about exclusion zones and fourth phase of water meant a further breakthrough and led to the proposal that negatively charged exclusion zones (EZs) of water with $H_{1.5}O$ stoichiometry are accompanied by magnetic body carrying dark proton nuclei at the flux tubes. EZs are excellent candidates for primitive life forms and can be identified as the primitive life forms making possible water memory and homeopathy [K62], [L15].

9. The last step of progress relates to the proposal of Tajmar et al that gravimagnetic effect could explain the well-established anomaly relating to the measurement of the mass of Cooper pair in rotating super-conductor. The GRT prediction for the effect is however 28 orders of magnitude too small so that new physics would be needed. The Thomson gravimagnetic field is proportional to h^2 so that large value of Planck constant could explain the effect. The value can be estimated and it is of the order of 10^{14} as required! If it is equal to h_{eff} then the energy spectrum of dark EEG photons is that of bio-photons as conjectured earlier!

The following sections describe in detail the outcome of this progress.

1. In the first section gravimagnetic effect and its biological implications are discussed from TGD point of view.

2. In the second section the model for water memory and homeopathy is discussed and shown to lead to a general model for how immune system and bio-catalysis could have developed from their primordial versions,how dark proteins might have emerged as concrete representations for invader molecules making it possible to make the invader non-dangerous by attaching to its magnetic body, how DNA and genetic code could have emerged as symbolic representations for the magnetic bodies of invader molecules and later as symbolic representation of the magnetic body of the system itself. ZEO implies that actually time evolution of the magnetic body can be coded by DNA and protein folding could provide a concrete representation for this time evolution.

The appendix of the book gives a summary about basic concepts of TGD with illustrations. Pdf representation of same files serving as a kind of glossary can be found at `http://tgdtheory.fi/tgdglossary.pdf` [L11].

6.2 Implications Of Strong Gravimagnetism For TGD Inspired Quantum Biology

Physicists M. Tajmar and C. J. Matos and their collaborators working in ESA (European Satellite Agency) have made an amazing claim of having detected strong gravimagnetism with gravimagnetic field having a magnitude which is about 20 orders of magnitude higher than predicted by General Relativity [E7]. If the findings are replicable they mean a revolution in the science of gravity and, as one might hope, force a long-waited serious reconsideration of the basic assumptions of the dominating super-string approach.

Tajmar et al have proposed [E11] the gravimagnetic effect as an explanation of an anomaly related to the superconductors. The measured value of the mass of the Cooper pair is slightly larger than the sum of masses whereas theory predicts that it should be smaller. The explanation would be that actual London field is larger than it should be because of gravimagnetic contribution to quantization rule used to deduce the value of London field.

TGD explanation of the discrepancy accepting the theory of Tajmar et al comes from the proposal inspired by Nottale's observations [E5] suggesting that Bohr's rules apply in planetary system with Planck constant replaced by $\hbar_{gr} = GMm/v_0$. Here M and m are the masses of Sun and planet. $v_0/c \simeq 2^{-11}$ holds true for the 3 inner planets and $v_0 \to v_0/5$ for the outer planets. The rotation velocities of the planets are related to v_0 by Bohr rules. h_{gr} clearly characterizes the pair Sun-planet rather than being fundamental constant whereas the gravitational Compton length GM/v_0 depends on M only. In TGD framework one assigns gravitational Planck constant to the flux tube connecting the masses and along which the gravitational massless extremals mediating the gravitational interaction are mediated. By Equivalence Principle it is possible to apply the hypothesis only in elementary particle length scales (this does not exclude its application in longer scales) and in these scales $h_{eff} = h_{gr}$ makes sense.

Gravimagnetic London field is proportional to the square of Planck constant and the obvious guess is that the replacement h with h_{gr} could explain the enormous discrepancy with GRT if gravimagnetism is in question. This predicts correctly the magnitude of the effect and one also ends up with the identification of the $h_{gr} = h_{eff}$ in elementary particle scales.

Also a vision about the fundamental role of quantum gravitation in living matter emerges. The earlier hypothesis that dark EEG photons decay to biophotons with energies in visible and ultraviolet range [K66, K65] receives strong quantitative support. This leads also to a simple model for how magnetic bodies control molecular transitions via dark cyclotron radiation with varying frequencies vary but universal energy spectrum since for a given magnetic field all charged particles gives rise to biophotons with same energy. The values of h_{gr}/m and endogenous magnetic field $B_{end} \simeq .2$ Gauss are such that the spectrum of biophotons is in the range of molecular binding energies. This vision would conform with Penrose intuitions about the fundamental role of gravitation in quantum biology.

6.2.1 The Theory fof Tajmar et al for fhe Anomaly ff Cooper Pairs Mass

The starting point of the theory of Tajmar and Matos [E11] is the so called London magnetic moment generated in rotating charged super-conductors adding a constant contribution to the exponentially damped Meissner contribution to the magnetic field. This contribution can be understood as being due to the massivation of photons in super-conductors. The modified Maxwell equations are obtained by just adding scalar potential mass term to Gauss law and vector potential mass term to the equation related the curl of the magnetic field to the em current.

The expression for the London magnetic field is given by

$$B = 2\omega_R n_s \times \lambda_\gamma^2 \ , \tag{6.2.1}$$

where ω_R is the angular velocity of superconductor, n_s is charge density of super-conducting particles and $\lambda_\gamma = \hbar/m_\gamma$ is the wave length of a massive photon at rest. In the case of ordinary superconductor one has $\lambda_\gamma = \sqrt{m^*/q^* n_s}$, where $m^* \simeq 2m_e$ and $q^* = -2e$ are the mass and charge of Cooper pair. Hence one has

$$B = -2\frac{m^*}{2e}\omega_R \ . \tag{6.2.2}$$

Magnetic field extends also outside the super-conductor and by measuring it with a sufficient accuracy outside the super-conductor one can determine the value of the electron mass. Instead of the theoretical value $m^*/2m_e = .999992$ which is smaller than one due to the binding energy of the Cooper pair the value $m^*/2m_e = 1.000084$ was found by Tate [E8]. This inspired the theoretical work generalizing the notion of London field to gravimagnetism and the attempt to explain the anomaly in terms of the effects caused by the gravimagnetic field.

Note that in the case of ordinary matter the equations would lead to an inconsistency at the limit $m_\gamma = 0$ since the value of London magnetic field would become infinite. The resolution of the problem proposed in [E11] is based on the replacement of rotation frequency ω with electron's spin precession frequency $\omega_L = -eB/2m$ so that the consistency equation becomes $B = -B = 0$ for a unique choice $1/\lambda_\gamma^2 = -\frac{q}{m}n$. One could also consider the replacement of ω with electron's cyclotron frequency $\omega_c = 2\omega_L$. To my opinion there is no need to assume that the modified Maxwell's equations hold true in the case of ordinary matter.

Gravimagnetic field

The perturbative approach to the Einstein equations leads to equations which are essentially identical with Maxwell's equations. The g_{tt} component of the metric plays the role of scalar potential and the components g_{ti} define gravitational vector potential. Also the generalization to the superconducting situation in which graviphotons develop a mass is straightforward. Just add the scalar potential mass term to the counterpart of Gauss law and vector potential mass term to the equation relating the curl of the gravimagnetic field to the gravitational mass current.

In the case of a rotating superconductor London magnetic field is replaced with its gravimagnetic counterpart

$$B_{gr} = -2\omega_R \rho_m \lambda_{gr}^2 \ . \tag{6.2.3}$$

Obviously this formula would give rise to huge gravimagnetic fields in ordinary matter approaching infinite values at the limit of vanishing gravitational mass. Needless to say, these kind of fields have not been observed.

Equivalence Principle however suggests that the gravimagnetic field must be assigned with the rotating coordinate frame of the super-conductor. Equivalence principle would state that seing the things in a rotating reference frame is equivalent of being in a gravimagnetic field $B_{gr} = -2\omega_R$ in the rest frame. This fixes the graviphoton mass to

$$\frac{1}{\lambda_{gr}^2} = (\frac{m_{gr}}{\hbar})^2 = G\rho_m \ . \tag{6.2.4}$$

For a typical condensed matter density parameterized as $\rho_m = Nm_p/a^3$, $a = 10^{-10}$ m this gives the order of magnitude estimate $m_{gr} \sim N^{1/2}10^{-21}/a$ so that graviton mass would be extremely small.

If this is all what is involved, gravimagnetic field should have no special effects. In [E11] it is however proposed that in superconductors a small breaking of Equivalence Principle occurs. The basic assumptions are following.

1. Super-conducting phase and the entire system obey separately the gravitational analogs of Maxwell field equations.

2. The ad hoc assumption is that for super-conducting phase the sign of the gravimagnetic field is opposite to that for the ordinary matter. If purely kinematic effect were in question so that graviphotons were pure gauge degrees of freedom, the value of m_{gr}^2 should should be proportional to ρ_m and $\rho_m - \rho_m^*$ respectively.

3. Graviphoton mass is same for both ordinary and super-conducting matter and corresponds to the net density ρ_m of matter. This is essential for obtaining the breaking of Equivalence Principle.

With these assumptions the gravimagnetic field giving rise to acceleration field detected in the rest system would be given by

$$B_{gr}^* = \frac{\rho_m^*}{\rho} \times 2\omega \tag{6.2.5}$$

This is claimed to give rise to a genuine acceleration field

$$g^* = -\frac{\rho_m^*}{\rho} a \tag{6.2.6}$$

where a is the radial acceleration due to the rotational motion.

Explanation for the too high value of measured electron mass in terms of gravimagnetic field

A possible explanation of the anomalous value of the measured electron mass [E8] is in terms of gravimagnetic field affecting the flux Bohr quantization condition for electrons by adding to the electromagnetic vector potential term $q^* A_{em}$ gravitational vector potential $m^* A_{gr}$. By requiring that the quantization condition

$$\oint (m^* v + q^* A_{em} + m^* A_{gr}) dl = 0 \tag{6.2.7}$$

is satisfied for the superconducting ring, one obtains

$$B = -\frac{2m}{e}\omega - \frac{m}{e} B_{gr} \ . \tag{6.2.8}$$

This means that the magnetic field is slightly stronger than predicted and it has been known that this is indeed the case experimentally.

The higher value of the magnetic field could explain the slightly too high value of electron mass as determined from the magnetic field. This gives

$$B_{gr} = \frac{\Delta m_e}{m_e} \times 2\omega = \frac{\Delta m_e}{m_e} \times e m_e \times B \ . \tag{6.2.9}$$

The measurement implies $\Delta m_e/m_e = 9.2 \times 10^{-5}$. The model discussed in [E11] predicts $\Delta m_e/m_e \sim \rho^*/\rho$. The prediction is about 23 times smaller than the experimental result.

6.2.2 Is The Large Gravimagnetic Field Possible In TGD Framework?

TGD allows top consider several alternative solutions for the claimed effect.

Many-sheeted space-time could be an essential part of the effect (if real!).

1. In TGD framework both induced metric and various gauge fields are expressible in terms of CP_2 coordinates and their gradients. Hence the gravimagnetic field would be very probably accompanied by an ordinary magnetic field and could be even proportional to it.

2. The ordinary London magnetic field could be accompanied by analogous magnetic field at different space-time sheet playing the same role as gravimagnetic field in the proposed model. Cooper pair would experience both fields by forming topological sum contacts to both space-time sheets carrying ordinary London magnetic field $B = m_e/e\omega_R$ and much smaller London magnetic field $\Delta B = \Delta m/e\omega_R$? There would be no need to introduce gravitation but one should explain why the value of the parameter $\epsilon = \Delta m_e/m_e$ is what it is.

3. In many-sheeted space the gravimagnetic field and accompanying magnetic field would be associated with the flux tubes mediating gravitational interaction with dark matter fraction of Earth's mass. It would not be surprising if the size of the parameter ϵ might be determined by this fraction. Pioneer and Flyby effects [K45] allow to make a rough estimate for the size of this fraction and the outcome is about 2×10^{-4} which is not far from $\epsilon.9 \times 10^{-4}$.

An alternative explanation is that the experiments probe single space-time sheet and that also other Z^0 magnetic field contributes below weak scale which is scaled up for $h_{eff} = n \times h$ and can be macroscopic.

1. TGD predicts the possibility of classical electro-weak fields at larger space-time sheets. If these couple to Cooper pairs generate exotic weak charge at super-conducting space-time sheets the Bohr quantization conditions modify the value of the magnetic field. Exotic weak charge would however mean also exotic electronic em charge so that this option is excluded. It would also require that the Z^0 charge of test bodies used to measure the acceleration field is proportional to their gravitational mass.

2. According to the simplest recent view about Kähler-Dirac action [K58] the modes of Dirac operator are confined to 2-D string world sheets at which classical W boson fields vanish. This guarantees that em charge is well-defined for the modes. The stronger condition that also classical Z^0 field vanishes makes also sense and should hold at least in the length scales in which weak bosons do not appear. This guarantees the absence of axial couplings and parity breaking effects. In living matter parity breaking effects are large and one could consider the possibility that weak length scale is scaled up for $h_{eff} > h$ and that classical Z^0 fields are present below the weak scale.

3. One cannot exclude the possibility that the classical weak fields vanish for entire space-time surface. In this case spinor modes can still be seen as continuous superpositions of 2-D ones. In principle one can consider also other options - such as vanishing of induced Kähler form or classical em field besides that of W fields.

The conservative option is that classical weak fields vanish in the situation considered so that there is room for the strong gravimagnetic field. The following model starts from the model of Tajmar et al and generalizes it by replacing Planck constant with its gravitational counterpart.

Modification of the model of Tajmar et al by replacing h with h_{gr}

Gravimagnetic London field is proportional to the square of Planck constant and the obvious guess is that the replacement h with h_{gr} could explain the enormous discrepancy with GRT if gravimagnetism is in question. This predicts correctly the magnitude of the effect and one also ends up with the identification of the $h_{gr} = h_{eff}$ in elementary particle scales.

One can of course develop an objection against the gravimagnetic field proportional h_{eff}^2: also ordinary London magnetic field should be scaled in the same manner due to the proportionality to λ_γ^2. The resulting magnetic field would be enormous. One can however argue that the increase of Planck constant cannot affect the value of the ordinary London magnetic field. The scaling up of length scales by h_{eff} and flux conservation suggest that the value of B scales down like $1/h_{eff}^2$. This factor is compensated by the h_{eff}^2 factor in the expression of London magnetic field coming from the expression of magnetic penetration length in terms of mass of photon. One can of course ask why magnetic and gravimagnetic London field are different.

1. The formula used by Tajmar et al [E11] for the gravimagnetic variant of London magnetic field is direct generalization for the London field for ordinary super-conductor. The gravimagnetic field is proportional to the product $B_g = \omega_R r^2$ of the rotation frequency ω_R of

super-conductor and square of the ratio $r = (\lambda_g/\lambda_{g,T})$, where $\lambda_g = \hbar/m_g$ is graviton wave length and $\lambda_{g,T}$ is gravimagnetic penetration length obtained as generalization of the magnetic penetration length for super-conductors by replacing charge with mass. The latter is purely classical quantity whereas graviton wave length depends on Planck constant. Graviton mass can be argued to result in gravitational Meissner effect and can be estimated from the value of cosmological constant Λ being essentially its square root. The resulting value of B_g is too small by 28 orders of magnitude.

2. Tajmar et al [E11] suggests that graviton mass is larger by a factor of order 10^{14} in conflict with the experimental upper bound of order 10^{55} kg for m_g. TGD proposal is that it is Planck constant which should be replaced with effective Planck constant $h_{eff} = nh$ equal to gravitational Planck constant h_{gr} for electron Cooper pair in Earth's gravitational field. The model for planetary orbits as Bohr orbits together with Equivalence Principle implies $\hbar_{gr} = GMm/v_0$ at flux tubes connecting particle with mass m to Sun with mass M. v_0 has dimensions of velocity and has order of magnitude correlating with a typical rotation velocity of planetary orbit by Bohr quantization rules.

3. In the recent case the rotation velocity v_0 is the rotation velocity of Earth at its surface: $v_0(E)/c = 2.16 \times 10^{-6}$ to be compared with $v_0(S)/c \simeq .5 \times 10^{-3}$ for Sun-Earth system. The scaling of λ_g is given by $h_{gr}(E, pair)/h = (h_{gr,S,pair}/h) \times (M_E/M_S) \times v_0(S)/v_0(E)$. This gives

$$r \equiv \frac{h_{gr,S,pair}}{h} = \frac{\lambda(h_{gr,S,pair}}{\lambda(h, pair)} = \frac{\frac{GM}{v_0(S)}}{\lambda_c(pair)} = \frac{\frac{r_S}{v_0(S)}}{\lambda_c(e)} \quad .$$

Using $r_S = 3km$ and $\lambda_e = .243 \times 10^{-12}$ m and $v_0(S) \simeq 2^{-11}$, $M_E/M_S = 3.0 \times 10^{-6}$ one obtains $r \simeq 3.6 \times 10^{14}$. This happens to be correct order of magnitude! Maybe the model might have something to do with reality. Even better, also the value of h_{eff} is consistent with its value spectrum appearing in EEG if one requires that the energy of dark EEG photon with frequency of order 10 Hz is that of biophoton with frequency of about 5×10^14 Hz. If this picture is correct the values of $h_{eff} = h_{gr}$ would comes as proportional to the masses of particles and cyclotron energies proportional to heB/m would not depend on the mass of the particle at all.

4. What is nice that the model unifies the notions of gravitational Planck constant and dark Planck constant. The basic observation is that Equivalence Principle allows to understand the effects of h_{gr} by reducing it to elementary particle level interpreted in terms of flux tubes connecting particle to the bigger system. This allows to avoid gigantic values of h_{gr} and gives connection with TGD inspired quantum biology. The new quantum physics associated with gravitation would also become key part of quantum biology.

Could $h_{gr} = h_{eff}$ hold true?

The obvious question is whether the gravitational Planck constant deduced from the Nottale's considerations and the effective Planck constant $h_{eff} = nh$ deduced from ELF effects on vertebrate brain and explained in terms of non-determinism of Kähler action could be identical. At first this seems to be non-sensical idea since $\hbar_{gr} = GMm/v_0$ has gigantic value.

It is however essential to realize that by Equivalence Principle one describe gravitational interaction by reducing it to elementary particle level. For instance, gravitational Compton lengths do not depend at all on the masses of particles. Also the radii of the planetary orbits are independent of the mass of particle mass in accordance with Equivalence Principle. For elementary particles the values of h_{gr} are in the same range as in quantum biological applications. Typically 10 Hz ELF radiation should correspond to energy $E = h_{eff}f$ of UV photon if one assumes that dark ELF photons have energies of biophotons and transform to them. The order of magnitude for n would be therefore $n \simeq 10^{14}$.

The experiments of M. Tajmar et al [E7, E11] discussed in [K72] provide a support for this picture. The value of gravimagnetic field needed to explain the findings is 28 orders of magnitude higher than theoretical value if one extrapolates the model of Meissner effect to gravimagnetic

context. The amazing finding is that if one replaces Planck constant in the formula of gravimagnetic field with h_{gr} associated with Earth-Cooper pair system and assumes that the velocity parameter v_0 appearing in it corresponds to the Earth's rotation velocity around its axis, one obtains correct order of magnitude for the effect requiring $r \simeq 3.6 \times 10^{14}$.

The most important implications are in quantum biology and Penrose's vision about importance of quantum gravitation in biology might be correct.

1. This result allows by Equivalence Principle the identification $h_{gr} = h_{eff}$ at elementary particle level at least so that the two views about hierarchy of Planck constants would be equivalent. If the identification holds true for larger units it requires that space-time sheet identifiable as quantum correlates for physical systems are macroscopically quantum coherent and gravitation causes this. If the values of Planck constant are really additive, the number of parallel space-time sheets corresponding to non-determinism evolution for the flux tube connecting systems with masses M and m is proportional to the masses M and m using Planck mass as unit. Information theoretic interpretation is suggestive since hierarchy of Planck constants is assumed to relate to negentropic entanglement very closely in turn providing physical correlate for the notions of rule and concept.

2. That gravity would be fundamental for macroscopic quantum coherence would not be surprising since by EP all particles experience same acceleration in constant gravitational field, which therefore has tendency to create coherence unlike other basic interactions. This in principle allows to consider hierarchy in which the integers $h_{gr,i}$ are additive but give rise to the same universal dark Compton length.

3. The model for quantum biology relying on the notions of magnetic body and dark matter as hierarchy of phases with $h_{eff} = n \times h$, and biophotons [K66, K65] identified as decay produces of dark photons. The assumption $h_{gr} \propto m$ becomes highly predictable since cyclotron frequencies would be independent of the mass of the ion.

   (a) If dark photons with cyclotron frequencies decay to biophotons, one can conclude that biophoton spectrum reflects the spectrum of endogenous magnetic field strengths. In the model of EEG [K15] it has been indeed assumed that this kind spectrum is there: the inspiration came from music metaphors suggesting that musical scales are realized in terms of values of magnetic field strength. The new quantum physics associated with gravitation would also become key part of quantum biophysics in TGD Universe.

   (b) For the proposed value of h_{gr} 1 Hz cyclotron frequency associated to DNA sequences would correspond to ordinary photon frequency $f = 3.6 \times 10^{14}$ Hz and energy 1.2 eV just at the lower limit of visible frequencies. For 10 Hz alpha band the energy would be 12 eV in UV. This plus the fact that molecular energies are in eV range suggests very simple realization of biochemical control by magnetic body. Each ion has its own cyclotron frequency but same energy for the corresponding biophoton.

   (c) Biophoton with a given energy would activate transitions in specific bio-molecules or atoms: ionization energies for atoms except hydrogen have lower bound about 5 eV (`http://tinyurl.com/233vcad`). The energies of molecular bonds are in the range 2-10 eV (`http://tinyurl.com/bfsy4ft`). If one replaces v_0 with $2v_0$ in the estimate, DNA corresponds to.62 eV photon with energy of order metabolic energy currency and alpha band corresponds to 6 eV energy in the molecular region and also in the region of ionization energies.

   Each ion at its specific magnetic flux tubes with characteristic palette of magnetic field strengths would resonantly excite some set of biomolecules.This conforms with the earlier vision about dark photon frequencies as passwords.

   It could be also that biologically important ions take care of their ionization self. This would be achieved if the magnetic field strength associated with their flux tubes is such that dark cyclotron energy equals to ionization energy. EEG bands labelled by magnetic field strengths could reflect ionization energies for these ions.

   (d) The hypothesis means that the scale of energy spectrum of biophotons depends on the ratio M/v_0 of the planet and on the strength of the endogenous magnetic field, which

is.2 Gauss for Earth (2/5 of the nominal value of the Earth's magnetic field). Therefore the astrophysical characteristics of planets should be tuned for molecular life. Taking v_0 to be rotational velocity one obtains for the ratio $M(planet)/v_0(planet)$ using the ratio for Earth as unit the following numbers for the planets (Mercury, Venus, Earth, Mars, Jupiter, Saturnus, Uranus, Neptune): $M/v_0 = (8.5, 209, 1, .214223, 1613, 6149, 9359)$. If the energy scale of biophotons is required to be the same, the scale of endogenous magnetic field should be divided by this ratio in order to obtain the same situation as in Earth. For instance, in Mars the magnetic field should be roughly 5 times stronger: in reality the magnetic field of Mars is much weaker. Just for fun one can notice that for Sun the ratio is 1.4×10^6 so that magnetic field should be by the inverse of this factor weaker.

4. An interesting question is how large systems can behave as coherent units with $\hbar_{gr} = GMm/v_0$. In living matter one might consider the possibility that entire organism might be this kind of system. Interestingly, for larger masses the gravitational quantum coherence would be easier. For particle with mass m $h_{gr}/h > 1$ requires larger mass to satisfy $M > M_P^2/m_e$. The first guess that life has evolved from long to shorter scales and reached elementary particle last. Planck mass is the critical mass corresponds to the mass of water blog with volume of size scale of 10^{-4} m (big neuron) is the limit.

5. The Universal gravitational Compton wave length of $GM/v_0 \simeq 864$ meters gives an idea about largest possible living matter system if Earth is the second body. Of course, also other large bodies are possible.In the case of solar system this length is 3×10^3 km. The radius of Earth is 6.37×10^3 km - roughly twice the Compton length. The radii of Mercury, Venus, Earth, Mars, Jupiter, Saturnus, Uranus, Neptunus are (.38, .99, .533, 1, 10.6, 8.6, 4.0, 3.9) using Earth radius as unit the value of h_{gr} is by factor 5 larger than for three inner planets so that the values are reasonably near to gravitational Compton length or twice it. Does this mean that dark matter associated with Earth and maybe also other planets is in macroscopic quantum state at some level of the hierarchy of space-time sheets? Does this mean that Mother Gaia as conscious entity might make sense. One can of course make same question in the case of Sun. The universal gravitational Compton length in Sun would be 18 per cent of the radius of Sun if v_0 is taken to be the rotational velocity at the surface of Sun. The radius of solar core, where fusion takes place, is 20-25 per cent of solar radius.

6. There are further interesting numerical co-incidences. One can for a moment forget the standard hostility of scientist towards horoscopes and ask whether Sun and Moon could have somehow affect our life via astrocopic quantum coherence. The gravitational Compton length for particle-Moon or particle-Sun system multiplied by the natural value of magnetic field is the relevant parameter. For Sun the parameters in question are mass of Sun, and rotational velocity of Earth with respect to Sun, plus magnetic fields of Sun at flux tubes associated with solar magnetic field measured to be about 5 nT at the position of Earth and 100 times stronger than expected from dipole field behavior. This gives that the range of biophoton energies is scaled down with factor of 1/4 in good approximation so that Father Sun might affect terrestrial biology! If one uses for the rotational velocity of particle at surface of Moon as parameter v_0 (particle would be at Moon), biophoton energy scaled scaled up by factor 1.2.

The general proposal discussed above is testable. In particular, a detailed study of molecular energies with those associated with resonances of EEG could be highly rewarding and reveal the speculated spectroscopy of consciousness.

What about $h_{em} = h_{eff}$?

The notion of h_{gr} generalizes to that for other interactions. For instance, in electromagnetic case the formation of strong em fields implying charge separation leads to systems in which $h_{em} = Z_1 Z_2 e^2/v_0$ is large. Pollack's exclusion zone [L15] (`http://tinyurl.com/oyhstc2`) and its complement define this kind of system and TGD inspired identification is as prebiotic life form. I have proposed a TGD inspired model for the fourth phase of water [K61] [L15].

I have proposed that metabolic machinery generates large h_{eff} phase somehow. $h_{eff} = h_{em}$ hypothesis allows to develop this hypothesis in more detail.

1. The rotating shaft of a molecular motor associated with ATP synthase is proposed to play a key role.

2. What comes in mind is that the rotational velocity v_0 of the shaft appears in the formula for h_{em}. The electric field over the mitochondrial membrane generates charge separation and the product of charges of shaft and its complement should appear in the expression for h_{em}.

3. The value of v_0/c is expected to be of order 10^{-14} from the angular rotation rate of ADP synthase about few hundred revolutions per second. The lower bound for the magnitude for h_{em} is same as for h_{gr} associated with Earth-particle system.

Rotating magnetic systems are claimed to exhibit anomalous effects such as spontaneous acceleration and over unity energy production. I have discussed these in [**?**].

1. The proposal is that rotating magnetic systems give rise to dark matter at magnetic flux tubes and sheets associated with the system and that the metabolic energy is needed to rotate the motor to generate the dark matter, which in turn makes possible negentropic entanglement characterized the density matrix proportional to unit matrix. This kind of matrix results if entanglement coefficients form a unitary S-matrix characterizing also quantum computation as unitary process.

2. The parameter v_0 appearing in the general formula for h_{eff} assigned with either em - or gravitational flux tubes is identifiable as the rotation velocity. One has $v_0/c \simeq 3 \times 10^{-8}$.

3. Since these systems are strongly charged, a natural guess is that large h_{em} system is in question.

6.2.3 Gravitational Mother Gaia And Life

Negentropic entanglement (NE) is one of the key notions of TGD inspired quantum biology. For instance, it would seem that NE would look more natural metabolic resource than energy. Nutrients should carry it. NE is however not single particle property but between nutrient and some other system in the recent case. What can one say about this system? Can it be part of nutrient? Could it correspond to oxygen molecules? Or could it be Mother Gaia identified in some sensible manner?

If one believes on the presence of gravimagnetic flux tubes and their role as generator of macroscopic quantum coherence in biology then one is forced to consider seriously also NE between its ends. If this is the case then the view of religions about life might be nearer to truth than that of hard-born materialists.

To make this more concrete, let us first look what the transfer of NE could mean.

1. Suppose that nutrient N has NE with unknown system A which a priori could be part of nutrient. Assume that the transfer of NE of nutrient with A is formed by reconnection of U-shaped flux tubes associated with N (or glucose G produced from it) and A so that two parallel flux tubes connecting N and A are formed.

2. The basic operation allowing transformation of $N - A$ NE to $P - A$ NE is following. The two flux tube portions of U-shaped flux associated with the receiver R are reconnected with the two parallel flux tubes connecting N and A so that two flux tubes connecting R to A are formed. NMP strongly suggests that the entanglement remains negentropic in the process.

3. NE is first transferred to P using this process so that P and A are now NE-connected. After this P attaches to ADP to yield ATP and ATP attaches to B and the transfer process leads to NE between B and A.

   For ATP synthase the h_{em} consisting two elementary charges is of the same order as h_{gr}. This is probably not an accident. Could this mean that this kind of flux tube can reconnect with gravitational flux tube? Could this make possible a reconnection transforming N-Earth NE to P-Earth NE? This looks plausible.

Consider now the identification of A.

1. If one assumes that the negentropic entanglement (see **Fig.** `http://tgdtheory.fi/appfigures/cat.jpg` or **Fig. ??** in the appendix of this book) corresponds to gravitational flux tubes for N-Earth system then A should be gravitational Mother Gaia, whatever its precise definition might be. N (and glucose) molecules would be alive in the sense that they have NE with Mother Gaia.

2. Could oxygen have some deeper role? For instance, could O_2 molecules serve as analogs of cell membrane receptors for Mother Gaia meaning that gravitational flux tubes go through O_2 molecules? This does not look plausible since metabolism is possible also as fermentation involving no oxygen.

3. In this picture the role of breathing and fermentation would be to make possible the transfer of NE from nutrients to the living system.

This picture allows to imagine about what might happen in biological death. Biological death takes first place only at the highest level of self hierarchy assignable to the our biological body. Cells continue for some time their life even after the last breath. The notion of h_{gr} together with Equivalence Principle suggests that the living biological body has negentropic flux tube connections to both electromagnetic magnetic body (personal magnetic body) and to gravitational Mother Gaia (MG) representing collective consciousness in the scale of Earth. Also personal magnetic body has flux tube connections to MG. The latter especially during sleep. Also connections to higher levels in hierarchy are possible. At the moment of biological death the negentropic flux tube pairs connecting the personal magnetic body to biological body are split and only those with MG remain or are generated in this process. This would happen later at lower levels of biological self hierarchy such as organ and organelles and eventually for cells and biopolymers. On the other hand, new life forms using the decay products as nutrients would take the available NE to use during the decay process.

The quantum model for metabolism allows to understand life as a process in which negentropic entanglement of gravitational Mother Gaia with nutrients is transformed to that of molecules of biological body with personal magnetic body and further processed and enriched. At the moment of biological death this information returns to the gravitational Mother Gaia. By NMP information is not lost but increases steadily giving rise to "Akashic records". This view conforms with the core ideas of spiritual and religious teachings.

6.2.4 Could Podkletnov Effect Be Understood Using $H_{Gr} = h_{eff}$ hypothesis?

Podkletnov discovered his effect around 1982. There are funny co-incidences involved. I got my PhD. Podkletnov was kicked out from Tampere University and I was soon to find that it is impossible to find any funding for my work: situation is still the same! God can forgive but not colleagues. I have considered possible models for Pokletnov effect
citebfrPodkletnov, Schnurer, Modanese in TGD framework for years ago assuming that the propagation of gravitons along topological light rays attached to magnetic flux tubes mediate gravitational interaction. A lot of progress has taken since then. Therefore reconsideration is well-motivated.

The effect itself looks rather complex. The experiment involves a levitating disk above a toroidal magnet. Solenoids generating AC fields with frequency in the range $50 - 10^6$ Hz are used to rotate the disk. Above the disk at height of 15 mm is a sample of silicon with weight of 5.47834 g. The claim is that both the rotating disk and sample lose part of their weight: the estimate varies from.3 per cent to few per cent. The effect was resonance like above frequency 10^5 Hz: below this the weight fluctuates. The size of the effect increases with rotation frequency.

Some background

It is best to start by introducing some background.

1. The first thing to notice is that $f = 6 \times 10^5$ Hz is cyclotron frequency of electrons in the magnetic field $B_{end} = .2$ Gauss introduced to explain the quantal effects of ELF em fields on brain which appear at multiples of cyclotron frequencies of biologically important ions. The recent model for bio-photons as decay products of dark protons predicts that their spectrum correspond to a spectrum of B_{end}. Could it be that the magnetic fields at the flux tubes involved has spectrum of B_{end} and resonant transfer of energy in the frequency range containing $f = 6 \times 10^5$ Hz takes place?

2. The hypothesis $h_{eff} = h_{gr} = GM_Dm/v_0$, where M_D is the dark mass assignable with large system (Earth now) and v_0 is velocity parameter [K76] is relatively new piece of TGD inspired quantum biology. One obtains a rough estimate $M_D/M \simeq 2. \times 10^{-4}$ for the fraction of dark matter in the case of Earth and assignable to the dark magnetic body of Earth. One implication of $h_{gr} = h_{eff}$ hypothesis at gravitation mediating flux tubes is that cyclotron frequencies of particles do not depend on the mass of the particle and cyclotron energy spectrum of dark photons is universal and identifiable as that associated with bio-photons. Second implication is that each charged particle corresponds to particular value of Planck constant so that in many-sheeted space-time they populate different flux tubes: this could be very relevant for biology since cell would not be anymore a random soup of molecules. The model for the Pioneer and Flyby anomalies leads to the estimate $M_D/M \simeq 1.3 \times 10^{-4}$ consistent with the above estimate.

3. I have considered recently a model for the fountain effect of superfluidity [K75] considering the possibility that dark phases of matter in TGD sense might be associated with all critical situations - both ordinary critical and quantum critical phase transitions - in which long range fluctuations correlations explained in terms of generation of dark matter are present.

   The superfluid is able to climb from vessel along its walls apparently defying gravitation. The TGD explanation is in terms of large Planck constant $h_{gr} = h_{eff}$ hypothesis. The large value of h_{gr} implies macroscopic quantum gravitational coherence and that the quantum states in gravitational field for dark ^4He atoms have macroscopic size. In particular, the flow along walls is effectively free flow.

The anomaly in the measurement of Cooper pair mass in rotating superconductors

One has discovered an anomalous outcome in the mass measurements of Cooper pairs in the case of rotating superconductors [E8]. The measured mass of Cooper pair in rotating super conductor is slightly larger than the mass of the pair which must be slightly below the sum of the masses. Tajmar et al [E11, E7] try to explain the anomaly is in terms of a gigantic gravimagnetic London effect associated with a rotating superconductor.

1. Recall that in in the ordinary London effect a magnetic field proportional to the negative of rotation frequency is generated inside super-conductor: usually the magnetic field is expelled. London magnetic field corresponds to a magnetic dipole proportional the negative of the rotation frequency (this follows from the negative sign of the charge carriers). The natural expectation is that this gives rise to a dipole field outside the superconductor. The dipole moment would be generated by electron current at the surface of the superconductor.

2. The idea is to to introduce gravitational superconductivity for which all kinds of particles participate in the flow which would be analogous to super-fluidity. One can also speak about gravitational Meissner effect and massivation of graviton as analog of massivation of photons in the ordinary Meissner effect. Also the notion of London magnetic field might generalizes and gives rise to a dipole like gravimagnetic field outside the super-conductor. Now however negative charge is replaced by mass, which is positive so that the sign of the effect changes. The predicted effect is however completely negligible using the existing estimates for the mass of the graviton.

3. The crazy proposal of Tajmar et al is that a gravimagnetic field larger than that predicted by GRT by a factor of order 10^{24} is associated with the rotating super-conductor and combines and produces the slight deviation of the measured mass of the Cooper pair from real when

this since the Cooper pair couples also to gravimagnetic field besides magnetic field. The reason is that the effective magnetic field contains a small contribution of gravimagnetic field so that the measurement gives too large a result for the mass of the Cooper pair.

In standard model plus GRT this kind of effect is impossible. In TGD framework the hierarchy of Planck constants suggests two alternative explanations.

1. The London magnetic field (also gravimagnetic) is a purely quantal effect and proportional to the square h^2 of Planck constant. If h is replaced with say $h_{eff} = h_{gr} \simeq 10^{12}h$ the effect is enormous as compared to that predicted by GRT! There is however an objection: one cannot perform this replacement for ordinary London field! Why?

2. Many-sheeted space-time allows to consider also alternative model in which the change of mass is due to a generation of the analog of dark London magnetic field at dark magnetic flux tubes: electron would couple to the sum of these fields since it would have topological sum contacts to both space-time sheets This magnetic field is proportional to dark matter density and $\rho_D/\rho = M_D/M \simeq 2 \times 10^{-4}$ would give a correct order of magnitude estimate.

3. Since gravimagnetic and magnetic fields are expressible in terms of CP_2 coordinates and their gradients, one can wonder whether the two explanations are actually equivalent.

What about Podkletnov effect?

Also Pokdletknov effect is associated with a rotating superconductor and one can ask whether the above ideas apply also to it.

1. The vision that dark variants of elementary particles are associated with all critical phenomena suggest that a critical phenomenon is in question also now and part of the matter - at least part of Cooper pairs - are in dark phase at magnetic flux tubes satisfying $h_{eff} = h_{gr}$. Could large $h_{eff} = h_{gr}$ be involved also with Podkletnov's effect? Could the reported loss of the weight of the (not necessarily) rotating disk and and of the sample by.3 per cent be due to the transformation of part of Cooper pairs to large $h_{eff} = h_{gr}$ phase de-localized to the magnetic flux tubes along which gravitational force is mediated in a scale considerably larger than that of the sample and disk? Also the air above the rotating superconductor was reported to start to rise. Could this be that also air molecules lost some of their electrons to the dark flux tubes in this manner? Since electron mass is about 2^{-11} fraction of proton mass, also protons and heavier particles should leak to the dark phase to achieve weight loss of order per cent. This effect would be present already for the non-rotating superconductor and would be much like the fountain effect in superfluidity according to TGD [K75].

2. As the frequency of AC fields is increased, the weight of the sample fluctuates but above 10^5 Hz it stabilizes and is resonant like. Levitation is essentially due to the gradient of the magnetic energy associated with AC fields. Could part of AC photons transform to dark photons and could the large energy of dark photons - in visible and UV range - mean much larger excluded magnetic energy in the volume of the gravi-superconducting sample and rotating superconducting disk and in this manner induce stronger levitating effect becoming stronges at cyclotron resonance energies. Resonance absorption would take place when the frequency is in the region of electron cyclotron frequencies for the flux tubes. Also coherence would be achieved thanks to the presence of Bose-Einstein condensates of electronic Cooper pairs.

3. One should explain also the increase of the reported loss of the weight with the rotation velocity of the superconducting disk. Rotation generating the mass current should generate dipolar gravimagnetic field with strength proportional to the rotation frequency (and accompanied by ordinary magnetic fields). The increasing strength of the gravimagnetic field would mean increase in the number of flux quanta or increase of the field strength at the flux tubes. At least in the first case more particles could end up to the dark phase leading to the reduction of effective weight of the sample and rotating disk. This gravimagnetic dipole field would naturally correspond to the gravimagnetic London field continued outside the superconducting rotating disk acting as a magnetic dipole.

6.3 Water Memory And Pre-Biotic Life

Pollack's findings [L15] discussed from TGD view point in [K42, K40] provide new insights to the mechanisms of water memory and homeopathy. Also the attempts to understand the dependence of h_{eff} on parameters of the system involved provide help. This picture also suggests a more detailed vision about prebiotic life forms as analogs of exclusion zones involving charge separation leading to large value of h_{eff}.

6.3.1 Exclusion Zones As Prebiotic Cells

TGD based model model [L15], [**?**] for Pollack's findings [L15] provides further guidelines.

1. Pollack et al discovered what they call exclusion zones and fourth gel like phase of water. The phenomenon occurs when water is bounded by gel and is irradiated with say visible light. Exclusion zones are negatively charged regions of water with positively charged environment. They act like batteries and have rather exotic properties. For instance, various impurities are repelled from exclusion zone.

2. The observed $H_{1.5}O$ stoichiometry implies that every fourth proton or hydrogen atom is dark and is transferred to the region outside the negatively charged exclusion zone. If only protons are transferred, very high negative charge density is generated. The size of the exclusion zone varies up to 100 μm and is in the range of cell sizes.

3. Dark matter corresponds in TGD Universe to phases with nonstandard value of Planck constant: $h_{eff} = n \times h$ phases at the "magnetic body" of the system (negatively charged region now). Magnetic body corresponds in Maxwell's theory to the magnetic fields generated by the system. Magnetic body consists of flux quanta (flux tubes and sheets).

4. If dark protons with say size scale of atomic size reside at flux tubes, one can assume that they form strings giving rise to dark atomic nuclei. Also ordinary nuclei consist of strings of dark protons and strings of neutrons. Various impurities are transferred from exclusion zone to the exterior suggesting that they become dark particles at magnetic flux tubes.

5. The quantum states of dark protons consist of 3 quarks and a simple model involving rotational symmetry around the axis of dark proton string predicts that the states of dark proton can be arranged into groups which correspond to DNA, RNA, amino-acids and possibly also tRNA molecules. Vertebrate genetic code can be realized as a natural correspondence between DNA/ RNA and amino-acids [L2, K24].

6. Negatively charged EZ could define a pre-biotic cell so that water would be a primitive prebiotic life form. The voltage would be the analog of the resting potential. The transformation of dark protons to ordinary ones would liberate metabolic energy so that primitive metabolism and photosynthesis would be realized. One can also consider a more general possibility that cyclotron energies are different at flux tube portions in the interior and exterior of the EZ analogous to cell membrane. This would increase the value of the metabolic energy currency by adding to Josephson energy ZeV the difference of dark cyclotron energies proportional to h_{eff}. One expects that dark counterparts of basic bio-polymers are still present in living matter and play a fundamental role.

6.3.2 TGD View About Homeopathy, Water Memory, And Evolution Of Immune System

The following gives an attempt to build a brief sketch of TGD based model of water memory and homeopathy as it is after the input from Pollack's findings and $h_{eff} = h_{gr} = h_{em}$ hypothesis.

Summary of the basic facts and overall view

A concice summary of the basic qualitative facts about homeopathy [K24] could be following.

1. The manufacture of the homeopathic remedies consists of repeated dilution and agitation of water sample containing the molecules causing the effect which the remedy is intended to heal. This paradoxical looking healing method is based on "Alike likes alike" rule. This rules brings in mind vaccination causing immune system to develop resistance. The procedure seems to somehow store information about the presence of the molecules and this information induces immune response. Usually it is the organisms or molecules causing the disease which induce immune response.

2. The ultra-naive and simplistic objection of skeptic is that the repeated dilution involved with the preparation of homeopathic remedy implies that the density of molecules is so small that the molecules can have absolutely no effect. Despite the fact that we live in information society, this is still the standard reaction of a typical skeptic.

3. A lot of research is done by starting from the natural idea that the electro-magnetic fields associated with the invader molecules (or more complex objects) represent the needed information and that water somehow gets imprinted by these fields. This could for instance mean that water clusters learn to reproduce radiation at frequencies characterizing the invader molecule. Benveniste is one of the most outstanding pioneers in the field [I71]. Benveniste et al [I72] even managed to record the VLF frequency finger print of some bio-active molecules and record them in binary form allowing to to yield the same effect as the real bio-active molecule induced. Benveniste was labelled as a fraud. The procedure used by the journal Nature to decide whether Benveniste is swindler or not brings in mind the times of inquisition. It tells a lot about attitudes of skeptics that magician Randi was one member of the jury!

4. Benveniste's work has been continued and recently HIV Nobelist Montagnier produced what might be regarded as remote replication of DNA using method very similar to that used in manufacturing homeopathic remedy [I94, I95].

The general conclusion is that the em frequencies possibly providing a representation of the molecules are rather low - in VLF region - so that frequencies assignable to molecular transitions are not in question. Cyclotron frequencies assignable to the molecules are the most natural candidates concerning physical interpretation. The corresponding photon energies are extremely low if calculated from $E = hf$ formula of standard quantum mechanics so that quantal effects in the framework of standard quantum theory do not seem to be possible.

My personal interest on water memory was sparked by the work of Cyril Smith [I65]. What I learned was what might be called scaling law of homeopathy [K24]. Somehow low frequency radiation seems to be transformed to high frequency radiation and the ratio $f_h/f_l \simeq 2 \times 10^{11}$ seems to be favored frequency ratio.

These two basic findings suggest what looks now a rather obvious approach to homeopathy in TGD framework. The basic physical objects are the magnetic bodies of the invader molecule and water molecule cluster or whatever it is what mimics the invader molecule. The information about magnetic body is represented by dark cyclotron radiation generated by the invader with frequency f_l. This dark radiation is transformed to to ordinary photons with frequency f_h and energy $h_{eff} f_l = h f_h$, which is above thermal energy, most naturally in the range of bio-photon energies so that the radiation can directly induce transitions of bio-molecules. The analogs for the EZs discovered by Pollack are obvious candidates for "water molecule clusters".

The following summarizes this overall picture in more detail.

Dark photon-bio-photon connection

The idea that bio-photons are decay product of dark photons emerged from the model of EEG [K15] in terms of dark photons with energies above thermal energy. Dark photons in question would be emitted as cyclotron radiation by various particles and molecules, perhaps even macromolecules like DNA sequencies. Also cell membrane would emit dark photons with frequencies, which correspond in good approximation to differences of cyclotron energies for large value of $h_{eff} = nh$ [K42, K15].

1. Bio-photons have spectrum in the visible and UV would decay products of dark cyclotron photons. If the h_{eff} of particle is proportional to its mass then the cyclotron energy spectrum

is universal and does not depend on the mass of the particle at all. The original model of EEG achieved this by assuming that h_{eff} is proportional to the mass number of the atomic nucleus associated with the ion.

2. The ideas about dark matter involve two threads: $h_{eff} = n \times h$ thread motivated by biology and the thread based on the notion of gravitational Planck constant and inspired by the observation that planetary orbits seem to obey Bohr rules. $\hbar_{gr} = GMm/v_0$ is assigned to the pairs of gravimagnetic flux tubes and massless extremals making possible propagation of dark gravitons. The realization was the two threads can be combined to single thread: by Equivalence Principle h_{gr} hypothesis is needed only for microscopic objects and in this case $h_{eff} = h_{gr}$ makes sense and predicts that dark photon energies and dark particle Compton lengths do not depend on particle and that bio-photon energy spectrum is universal and in the desired range if one assumes that h_{gr} is associated with particle Earth par with v_0 the rotational velocity at the surface of Earth. Even $h_{eff} = h_{em} = h_{gr}$ hypothesis makes sense. $h_{em} = h_{gr}$ is also very natural assumption for ATP synthase which can be regarded as a molecular motor whose rotation velocity appears in the formula for h_{em}.

3. The prediction would be that any charged system connected to Earth by flux tubes generates cyclotron dark photons decaying to bio-photons. Bio-photons in turn induce transitions in biomolecules because the energy range is in visible and UV. Magnetic bodies can control biochemistry via resonant coupling with bio-photons.

Molecular recognition mechanism as basic building brick of primitive immune system

The reconnection of U-shaped magnetic flux tubes emanating from a system makes possible a recognition mechanism involving besides reconnection also resonant interaction via cyclotron radiation which can induced also biochemical transitions of $h_{eff} = h_{gr}$ hypothesis holds true.

1. Molecules have U-shaped flux tube loops with fluxes going in opposite directions. This makes possible also super-conductivity with members of Cooper pair at the parallel flux tubes carrying magnetic fluxes in opposite direction since magnetic fields now stabilize Cooper pairs rather than tend to destroy them.

2. The flux loops associated with systems - call them A and B - can reconnect and this leads to the formation of 2 parallel flux tubes connecting A and B. Stable reconnection suggests that magnetic field strengths must be same at the flux tube pairs associated with A and B. This implies same cyclotron frequencies and resonant interaction. This would define molecular mechanism of recognition and sensing the presence of invader molecules - even conscious directed attention might be involved.

3. Systems with magnetic body could be constantly varying the thicknesses of at least some of their flux tubes and in order to reconnect with the magnetic body of a possible invader. This activity could be behind the evolution of the immune system.

The question is how the system or its sub-system could stabilize itself so that it would receive signals only from one kind of molecule specified by its cyclotron frequency spectrum.

1. If the flux tubes carry monopole flux (this is possible in TGD framework and requires the flux tube cross section is closed 2-surface), stabilization of the flux tube thickness stabilizes the magnetic field strength. How the stabilization of the thickness of the flux tubes could have been achieved?

   Pollack's negatively charged EZs with dark protons at magnetic flux tubes giving rise to dark nuclei identifiable as dark proton sequences suggests an answer. Maybe the presence of dark proton sequences could stabilize the flux tube thickness. Dark proton sequences have also interpretation as dark DNA/RNA/amino-acid sequences [L2].

A further question is whether the magnetic body of the prebiotic cell identified as EZ could use the information about invader molecule to represent its magnetic body either concretely and perhaps even symbolically and regenerate the concrete representation when needed.

1. The concrete representation could be in terms of dark proteins whose folding would represent the topology of the invader molecule and symbolic representation in terms of dark DNA transcribed to dark protein. If the dark protein has same topology of knotting it could more easily attach to the invader molecule and make it harmless. Note that the invaders are naturally other dark DNAs and proteins jus as in living matter. The higher purpose behind this cold war would be stimulation of mimicry - emulation in computer science - leading to generation of cognitive representations and negentropic entanglement.

2. Not only the representation of the 3-D magnetic body - its behavior - is possible. In ZEO also the representation of the dynamical evolution of magnetic body becomes possible since basic objects are pairs of 3-surfaces at future and past boundaries of causal diamond. The challenge is to represent the topology time development of magnetic body - 2-braiding, first concretely by mimicking it and then symbolically in terms of DNA coding for proteins doing the mimicry. The obvious representation for the behavior of magnetic body of invader molecule would be in terms of folding and unfolding of protein representing it.

3. The question how the symbolic representation could have emerged leads to a vision about how genetic code emerged. The model for living system as topological quantum computer utilizing 2-braiding for string world sheets at 4-D space-time leads to the idea that 3-D coordinate grids formed by flux tubes are central for TQC: each node of grid is characterized by 6 bits telling about the topology of the node concerning 2-braiding. Could the 6 bits of dark DNA code for the local topology of the invader molecule and an the flux tube complex mimicking it?

4. This raises the possibility that DNA strands - one for each coordinate line in say z-direction could code for the 2-braiding of 3-D coordinate grid and in this manner code for the magnetic template of invader molecule and also that of the biological body. Therefore genetic code would code for both the basic building bricks of the biological body and 4-D magnetic body serving as template for the development of biological body.

   One can imagine how the biochemical evolution after this stage might have taken place.

1. At the next step the chemical representation of genetic code would have emerged. Dark proteins learned to attach to real proteins and real proteins to other proteins and DNA and bio-catalysis became possible.

2. The transformation of the ordinary photons emitted in the transitions of biomolecules to dark photons made possible the recognition of invader molecules using ordinary photons emitted in their molecular transitions.

3. Magnetic bodies learned to control biochemical reactions by using dark cyclotron radiation transformed to bio-photons.

4. Gradually dark and ordinary proteins developed a rich repertoire of functions relying on reconnection, communication by dark photons, and attachment in invader molecule. Proteins began to serve as building bricks, as bio-catalysts, promote the replication of DNA, responding to stimuli, serve as receptors.

Possible mechanism of water memory and homeopathy

The general vision about prebiotic evolution described above suggests that the mechanisms of water memory and homeopathy are basically the same as those underlying the workings of the immune system.

1. Exclusion zones could define primordial life forms with genetic code. They are able to detect the presence of invader molecule from its cyclotron frequency spectrum.

2. Dark proteins can form concrete memory representations of the invader molecules in terms of dark proton sequences defining dark proteins. The folding of these dark proteins mimics the behavior of the magnetic bodies of the invaders. These dark proteins can attach to the

magnetic body of the invader molecule to make it non-dangerous. Even symbolic representations in terms of dark DNA allowing transcription and translation to concrete dark protein representation could be involved. The procedure involved in the manufacture of homeopathic remedy could be seen as a series of "environmental catastrophes" driving the evolution of dark primordial life by feeding in metabolic energy and generating new EZs, which mimic the invader molecules and existing EZs mimicking them.

3. In organism the dark DNA representing the invader molecule would generate ordinary genes coding for ordinary proteins attaching to the invader molecules by the attachment of ordinary DNA nucleotides to them. The attachment would involve h_{eff} reducing phase transition reducing the length of connecting flux tube.

4. Later dark genetic code transformed to chemical genetic code as dark DNA strands were formed around dark double strands and large number of other biological functions emerged besides immune response.

5. The mechanical agitation in the manufacturing of homeopathic remedy generates exclusion zones and new primitive life forms by providing the needed energy. These in turn recognize and memorize invader molecules and their already existing representations as EZs.

6.3.3 Direct Empirical Evidence For Dark DNA?!

Sciencedaily tells about extremely interesting finding related to DNA (`http://tinyurl.com/pbzqx36`. The finding is just what breakthrough discovery should be: it must be something impossible in the existing world view.

What has been found [I98] (`http://tinyurl.com/y9849jkz`) is that knock-out (removing parts of gene to prevent transcription to mRNA) and knock-down of gene (prevent protein translation) seem to have different consequences. Removing parts of gene need not have the expected effect at the level of proteins! Does this mean that somehow DNA as a whole can compensate the effects caused by knock-out but not those by knock-down? This explanation is natural in the standard conceptual framework and is proposed in the article.

Could this be explained by assuming that genome is a hologram as Gariaev et al (`http://tinyurl.com/ycosxzen`) [I81, I6] have first suggested? Also TGD leads to a vision about living system as a conscious hologram [**?**]. Small local changes of genes could be compensated. Somehow the entire genome would react like brain to a local brain damage: other regions of brain take the duties of the damaged region. Could the idea about DNA double strand as nano-brain having left and right strands instead of hemispheres"help here. Does DNA indeed act as a macroscopic quantum unit? The problem is that transcription is local rather than holistic process. Something very simple should lurk behind the compensation mechanism.

Could transcription transform dark DNA to dark mRNA?

Also the TGD based notion of dark DNA comes in mind [K24, L2] (`http://tinyurl.com/ybp338x5`, `http://tinyurl.com/yag67j4p`). Dark DNA consists of dark proton sequences for which states of single DNA proton correspond to those of DNA, mRNA, aminoacids, and tRNA. Dark DNA is one of the speculative ideas of TGD inspired quantum biology getting support from Pollack's findings (`http://tinyurl.com/oyhstc2` [L15], [K76]). Ordinary biomolecules would only make their dark counterparts visible: dark biomolecules would serve as a template around which ordinary biomolecules such as DNA strands are formed in TGD Universe. All basic biomolecules of genetics would be pairs of ordinary biomolecule and its dark proton analog.

Although ordinary DNA is knocked out of ordinary gene, dark gene would still exist! If dark DNA actually serves as template for the transcription to mRNA, everything is still ok after knockout! Could it be that we do not understand even transcription correctly? Could it actually occur at the level of dark DNA and mRNA?! Dark mRNA would attach to dark DNA after which ordinary mRNA would attach to the dark mRNA. One step more!

Damaged DNA could still do its job! DNA transcription would would have very little to do with bio-chemistry! If this view about DNA transcription is correct, it would suggest a totally new manner to fix DNA damages. These damages could be actually at the level of dark DNA,

and the challenge of dark genetic engineering would be to modify dark DNA to achieve a proper functioning.

Could dark genetics help to understand the non-uniqueness of the genetic code?

Also translation could be based on pairing of dark mRNA and dark tRNA. This suggests a fresh perspective to some strange and even ugly looking features of the genetic code. Are DNA and mRNA always paired with their dark variants? Do also amino-acids and anticodons of tRNA pair in this manner with their dark variants? Could the pairings at dark matter level be universal and determined by the pairing of dark amino-acids with the anticodons of dark RNA? Could the anomalies of the code be reduced to the non-uniqueness of the pairing of dark and ordinary variants of basic bio-molecules (pairings RNA–dark RNA, amino-acid– dark amino-acid, and amino-acid–ordinary amino-acid in tRNA).

1. There are several variants of the genetic code differing slightly from each other: correspondence between DNA/mRNA codons and amino-acids is not always the same. Could dark-dark pairings be universal? Could the variations in dark anticodon - anticodon pairing and dark amino-acid-amino-acid pairing in tRNA molecules explain the variations of the genetic code?

2. For some variants of the genetic code a stop codon can code for amino-acid. The explanation at the level of tRNA seems to be the same as in standard framework. For the standard code the stop codons do not have tRNA representatives. If stop codon codes for amino-acids, the stop codon has tRNA representation. But how the mRNA knows that the stop codon is indeed stop codon if the tRNA associated with it is present in the same cell?

   Could it be that stop codon property is determined already at the level of DNA and mRNA? If the dark variant of genuine stop codon is missing in DNA and therefore also in mRNA the translation stops if it is induced from that at the level of dark mRNA. Could also the splicing of mRNA be due to the splitting of dark DNA and dark mRNA? If so genes would be separated from intronic portions of DNA in that they would pair with dark DNA. Could it be that the intronic regions do not pair with their dark counterparts. They would be specialized to topological quantum computations in the TGD inspired proposal [K17].

   Start codon (usually AUG coding met) serves as a Start codon defining the reading frame (there are 3 possible reading frames). Dark DNA would naturally begin from this codon.

3. Also two additional amino-acids Pyl and Sec appear in Nature. Gariaev et al have proposed that the genetic code is context dependent so that the meaning of DNA codon is not always the same. This non-universality could be reduced to the non-uniqueness of dark amino-acid–amino-acid pairing in tRNA if genetic code is universal.

Could dark genetics help to understand wobble base pairing?

Wobble base pairing (`http://tinyurl.com/y73se8vs`) is second not-so-well understood phenomenon. In the standard variant of the code there are 61 mRNAs translated to amino-acids. The number of tRNA anticodons (formed by the pairs of amino-acid and RNA molecules) should be also 61 in order to have 1-1 pairing between tRNA and mRNA. The number of ordinary tRNAs is however smaller than 61 in the sense that the number of RNAs associated with them is smaller than 45. tRNA anticodons must be able to pair with several mRNA codons coding for given amino-acid. This is possible since tRNA anticodons can be chosen to be representative for the mRNA codons coding a given amino-acid in such that all mRNA codons coding for the same amino-acid pair with at least one tRNA anticodon.

1. This looks somewhat confusing but is actually very simple: genetic code can be seen as a composite of two codes: first 64 DNAs/mRNAs to are coded to $N < 45$ anticodons in tRNA, and then these N anticodons are coded to 20 amino-acids. One must select N anticodon representatives for the mRNAs in the 20 sets of mRNA codons coding for a given amino-acid such that each amino-acid has at least one anticodon representative. A large number of choices is possible and the wobble hypothesis of Crick pose reduce the number of options.

2. The wobble hypothesis of Crick states that the nucleotide in the third codon position of RNA codon of tRNA has the needed non-unique base pairing: this is clear from the high symmetries of the third basis. There is exact U-C symmetry and approximate A-G symmetry with respect to the third basis of RNA codon (note that the conjugates of RNA codons are obtained by A↔U and C↔G permutations).

3. The first two basis in the codon pair in 1-1 manner to the second and third basis of anticodon. The third basis of anticodon corresponds to the third letter of mRNA codon. If it is A or C the correspondence is assumed to be 1-to-1: this gives 32 tRNAs. If the first basis of anticodon is G or U the 2 mRNA basis can pair with it: they would be naturally A for G and C for U by symmetry. One would select A from A-G doublet and C from U-C double. This would give 16 anticodons: 48 anticodons altogether, which is however larger than 45. Furthermore, this would not give quite the correct code since A-G symmetry is not exact.

   Smaller number of tRNAs is however enough since the code has almost symmetry also with respect to A and C exchange not yet utilized. The trick is to replace in some cases the first basis of anticodon with Inosine I, which pairs with 3 mRNA basis. This replacement is possible only for those amino-acids for which the number of RNAs coding the amino-acid is 3 or larger (the amino-acids coded by 4 or 6 codons).

4. It can be shown at least 32 different tRNAs are needed to realize genetic code by using wobble base pairing. Full A-C and G-U symmetry for the third basis of codon would give 16+16=32 codons. One can ask whether tRNA somehow realizes this full symmetry?

How dark variants of could help to understand wobble base pairing? Suppose for a moment that the visible genetics be a shadow of the dark one and fails to represent it completely. Suppose the pairing of ordinary and dark variants of tRNA anticodons *resp.* amino-acids and that translation proceeds at the level of dark mRNA, dark anticodons, and dark amino-acids, and is made visible by its bio-chemical shadow. Could this allow to gain insights about wobble base pairing? Could the peculiarities of tRNA serve for some other - essentially bio-chemical - purposes?

The basic idea would be simple: chemistry does not determine the pairing but it occurs at the level of the dark mRNA codons and dark tRNA anticodons. There would be no need to reduce wobble phenomenon to biochemistry and the only assumption needed would be that chemistry does not prevent the natural dark pairing producing standard genetic code apart from the modifications implied by non-standard dark amino-acid–amino-acid pairing explaining for different codes and the possibility that stop codon can in some situation pair with dark mRNA.

One can consider two options.

1. The number of dark tRNAs is 64 and the pairings between dark mRNA and dark anticodons and dark anticodons and dark amino-acids are 1-to-1 and only the pairing between dark RNA codons and anticodons in tRNA is many-to-1.

2. The model of dark genetic code [K24] suggests that there are 40 dark proton states, which could serve as dark analogs of tRNA. This number is larger than 32 needed to realize the genetic code as a composite code. I have cautiously suggested that the proposed universal code could map dark mRNA states of the same total spin (there is breaking of rotational symmetry to that around the axis of dark proton sequences) to dark tRNA/dark amino-acid states with the same total spin projection. The geometric realization would in terms of color flux tubes connecting the dark protons of corresponding dark proton sequences. Also in ordinary nuclei the nucleons are proposed to be connected by color flux tubes so that they form nuclear strings [L2] and dark proton sequences would be essentially dark variants of nuclei.

One should understand the details of the dark mRNA–tRNA anticodon correspondence. One can also ask whether the dark genetic code and the code deduced from the icosahedral model for music harmony [K43] [L12] are mutually consistent. This model implies the decomposition of 60+4 DNA codons to 20+20+20+4 codons, where each "20" corresponds to one particular icosahedral Hamilton's cycle with characteristic icosahedral symmetries. "4" can be assigned to tetrahedron regarded either disjoint from icosahedron or glued to it along one of its faces. This

allows to understand both the standard code and the code with two stop codons in which exotic amino-acids Pyl and Sec appear. One should understand the compositeness $64 \to 40 \to 20$ of the dark genetic code and and whether it relates to the icosatetrahedral realization of the code.

I have proposed [K26] (`http://tinyurl.com/ycm48w54`) that dark variants of transcription, translation, etc.. can occur and make possible kind of R&D laboratory so that organisms can test the consequences of variations of DNA. If ordinary translation and transcription are induced from their dark variants it would not be surprising and if dark biomolecules could also appear as unpaired variants, these processes could occur as purely dark variants. Organisms could indeed do experimentation in the virtual world model of biology and pairing with ordinary bio-molecules would make things real.

There is now evidence for this picture. It has been discovered [J13] (`http://tinyurl.com/oec3mff`) that brain cells have a mosaic like distribution of genomes (`http://tinyurl.com/odwajdq`) . In standard framework this mosaic should be created by random mutations. The mechanism of mutation is reported to involve transcription rather than DNA replication. The mutation would take place for DNA when its is copied to RNA after opening of the DNA double strand. The mutations would have occurred during the period when neurons replicate and the mutation history can be read by studying the distributions of changes in the genome.

This brings in mind the finding that removing a part of gene does not affect transcription. In both cases it is dark DNA, which would serve as a template for transcription rather than ordinary DNA. This suggests that the dark DNA is not changed in these modifications and mRNA is determined by the dark DNA, which would serve as a template for transcription rather than ordinary DNA. If this were the case also for neurons, the mutations of neuronal genes should not affect the gene transcription at all, and there would be no negative (or positive) effects on brain function. This seems too conservative. The mutations should have some more active role.

One can consider also different interpretation. The mutations of DNA could be induced by the dark DNA. As dark DNA changes, ordinary DNA associated with it is forced to change too - sooner or later. Especially so when the genome is in a state in which mutations can take place easily. Neurons during to replication stage could have such quantum critical genomes.

Evolution would not be mere selection by a survival of random mutations by external environment in the time scale much longer than lifetime of individual - but a controlled process, which can occur in time scale shorter than lifetime and differently inside parts of say brain. This is what the idea TGD inspired biology suggests. The modified DNA could be dark DNA and and serve as template for transcription and also induce transformation of ordinary DNA associated with it.

Whether this change can be transferred to the germ cells to be transferred to the offspring remains of course an open question. For instance, one can imagine that dark DNA strands (magnetic flux tubes) can penetrate germ cell membranes and replace the earlier dark DNA sections and induce change of ordinary DNA. Or is a more delicate mechanism involving dark photons in question. With inspiration coming from the findings reported by Peter Gariaev [I81] I have proposed a model of remote DNA replication suggesting that DNA can be replicated remotely if the needed nucleotides are present [K82]: the information about DNA could be transferred as dark photons, which can be transformed to ordinary photons identified as bio-photons. Could Lysenko have been at least partially right despite that he was a swindler basing his views on ideology?

In any case, TGD inspired biology allows to imagine a controlled evolution of DNA in analogy to that what occurs in R&D departments of modern technological organizations. The notion of dark DNA suggests that biological systems indeed have a "R&D department" in which new variants of DNA studied as "dark DNA" sequences realised as dark proton sequences - same about dark RNA, and amino-acids and even tRNA. The possibility to transcribe RNA from dark DNA would mean that the testing can be carried in real life situations.

There indeed exists evidence that traumatic - and thus highly emotional - memories may be passed down through generations in genome [J5] (`http://tinyurl.com/oja8v94`). Could the modifications of brain DNA represent long term memories as the above described experiment suggests? Could the memories be transferred to the germ cells using the mechanism sketched above?

6.3.4 Is Replication Of Magnetic Body Behind Biological Replication?

The vision about exclusion zone (EZ) like regions as primordial life forms and facts about water memory and homeopathy lead to a vision about how primitive immune system might have developed and how the recent genetic code might have emerged.

Magnetic body and dark analogs of bio-polymers should still play key role in living matter. The basic idea is that the time evolution of the magnetic body is the template for the time evolution of the biological body. In [K62] [L13] various pieces of evidence for the role of magnetic body as "morphogenetic field" are discussed. For instance, the replication of DNA and cell would reduce basically to that for corresponding magnetic bodies.

Replication of magnetic body is analogous to what happens in 3-vertex of Feynman diagram. This occurs in several scales. This would make possible dark DNA (dDNA) replication and copying of dDNA to dDNA+dRNA as well as copying of dRNA to dRNA+dark protein.

Replication process should start from the higher levels of dark matter hierarchy and proceed to shorter scales. The basic constraint from ZEO is that the time evolutions of magnetic bodies at various levels of the hierarchy are highly unique as preferred extremals connecting initial and final 3-surfaces. For the maxima of vacuum functional only preferred pairs of 3-surfaces are possible. This gives rise to what might be called "standard behaviors". Also the replication would be this kind of behavioral pattern. In the context of the positive energy ontology it is extremely difficult to understand why the predictability of cell replication or the development of organism from single cell by repeated cell divisions.

Remote gene replication [K82] might be one application: the model described was actually developed before the idea that the replication of the magnetic body could be the fundamental mechanism. Its reversal could be basic mechanism of bio-catalysis and induce the attachement of bio-molecules together. Also ordinary DNA replication could be induced by the same electromagnetic signal as remote replication.

The sketch about replication of DNA would look roughly like following.

1. Assume that the portion of DNA promoting DNA replication is activated by dark radiation at some frequency and that the promoter region emits radiation with same frequency. This activates further promoter regions -also in other cell nuclei. The replication process is amplified exponentially. The negative feedback is necessary in the general case and is provided by attachment of the produced proteins (basically dark proteins) to the genes making them inactive.

2. This might occur during cell division which might involve irradiation by dark analog of white noise exciting all promoter regions. Certainly the coherence of this process is essential and here the higher levels of the dark matter hierarchy would be essential.

3. Remote replication becomes possible if the dark radiation exciting promoter region can leak to other cells or even other organisms. Large h_{eff} might make this possible.

4. Also remote transcription is possible by the same mechanism. Actually remote variants of very many basic processes seem to be possible.

5. The observations of Peter Gariaev's group bout effects of laser light on genes [I83, I105] support this view as also the findings of group of HIV Nobelist Montagnier [I94, I95].

6.3.5 Quantum Model For Metabolism

First it is good to list some basic facts about energy metabolism.

1. ADP$\rightarrow$ ATP meaning the addition of phosphate to ADP is believed to be the fundamental step of metabolism. The process occurs when protons flow through the ATP synthase, which can be regarded as a nano-motor with a rotating shaft. During single turn three ADPs are phosphorylated and 3 protons flow through the "turbine" of the nano-motor and give up their Coulombic and chemical energy parameterized in terms of chemical potential difference. There is clearly a strong analogy with power plant. High energy phosphate bond is believed to receive the metabolic energy transferred from the flow of protons through the mitochondrial membrane.

2. The nominal value of metabolic energy quantum about.5 eV. The Coulomb energy associated with the mitochondrial membrane is 50-80 meV and by almost order of magnitude too small. The large chemical potential difference is believed to explain the large metabolic energy gain. This requires that the process is regarded as purely thermodynamical. This is a questionable assumption even in standard physics context and does not conform with the TGD based idea that transmembrane proteins such as ATP synthase act as large h_{eff} Josephson junctions. The square root of thermodynamics forced by zero energy ontology suggests itself as a proper description of cell membrane as macroscopically quantum coherent system.

3. The notion of high energy phosphate bond is not well understood. The storage of energy dark cyclotron energy at the magnetic body of phosphate suggests itself as TGD based description.

How to understand the value of $heff$?

The basis problem is to understand how h_{eff} depends on the parameters characterizing the situation at the magnetic flux tube connecting two systems. I have considered several mechanisms for the generation of large h_{eff} phase.

1. The model for h_{eff} in systems involving charge separation stimulated by AC current was based on the identification of Josephson frequency with the frequency of AC current: $f_J = E_J/h_{eff} = f_{AC}$ predicting $h_{eff}/h = E_J/hf_{AC}$ [K64].

   The findings of Pollack and the difficulties to understand metabolic energy quantum of nominal value.5 eV in the simplest model for cell membrane as Josephson junction as Josephson energy for Cooper pair equalto to $ZeV = 10-10.6$ mV inspired the assumption that cyclotron energies at flux tubes traversing cell membrane can be different at the two sides of the cell membrane [K15, K42]. This would lead to a generalization of the notion of Josephson junction associated with the transmembrane protein and generalizes $f_J = f_{AC}$ to $\Delta f_c + f_J = f_AC$ predicting $h_{eff}/h = E_J/(h(\Delta f_c - f_{AC})$ so that h_{eff}/h would get arbitrarily large values near resonance $f_{AC} = f_C$. Note that correct sign requires $\Delta f_C - f_{AC} > 0$.

2. The conjecture $\hbar_{eff} = \hbar_{gr} = GMm/v_0$ could make sense at microscopic level for particle-Earth pair and would predict a universal spectrum of bio-photons if identified as resulting from the decays of dark cyclotron photons to bio-photons. The first guess for the parameter v_0 would be as a rotational velocity associated with the two systems such as Earth and electron rotating with it. In case of planetary orbits $v = v_0$ is not consistent with

$$\frac{v}{c} = \frac{\sqrt{\frac{v_0}{c}}}{4\pi n}$$

   following from Bohr rules in $1/r$ potential (n denotes the principal quantum number).

3. $h_{eff} = h_{em} = Z_1 Z_2 e^2/v_0$ hypothesis is a natural looking generalization in systems involve large charge separations, say the exclusion zones discovered by Pollack providing a model for prebiotic life forms. The philosophy would be that when the coupling strength between systems becomes so large that perturbation theory fails, the value of h_{eff} increases and makes perturbation theory is in powers of $1/h_{eff}$) possible again. At space-time level this means emergence of non-determinism so that 3-surfaces at the future and past boundaries of causal diamond are connected by n-branched space-time surface for which branches fuse at the two ends. Dark matter would be Nature's manner to define what non-perturbative phases are. The strong hypothesis $h_{eff} = h_{em} = h_{gr}$ might make possible reconnection between em and gravimagnetic flux tubes and ATP synthase is here a candidate system.

4. Rotating magnetic systems with high negative charge are also good candidates for generating large h_{eff} at the magnetic flux tubes possibly contain dark proton sequences identifiable as dark nuclei. I have also proposed that a system subject to constant torque allowing description in terms of potential function which is multivalued as function of the angle coordinate ϕ leads rather naturally to generation of large h_{eff} [K26] when one requires internal consistency.

How metabolic energy is transferred?

The basic question concerns the mechanism of energy transfer from nutrients. It should be however emphasized that the transfer might not be the really important aspect. The transfer of negentropic entanglement from nutrient to the organism might be of equal importance.

1. Zero energy ontology (ZEO) suggests that magnetic bodies are carriers of the metabolic energy. What does this mean is not quite clear but cyclotron energies or ions or Cooper pairs of them proportional to h_{eff} are obvious candidates concerning energy storage. The value of $h_{eff} \simeq 10^{14}$ guaranteeing the energies of dark EEG photons are in the range of bio-photon energies would mean that storage as cyclotron energies is very effective and the liberated energy quanta can directly induce molecular transitions essential for bio-chemical reactions.

2. The liberation of metabolic energy could take place in a phase transition in which p-adic length scale increases and h_{eff} is reduced in such a manner that the length of flux tubes is not changed. This induces a coherent quantum transition in the sense that large number of particles can liberate cyclotron energy as cyclotron energy scale is reduced in the reduction of magnetic field strength. As protons flow from thinner flux tube with smaller h_{eff} to thicker one, similar reduction of cyclotron energy takes place and the energy is liberated, and would be received by ATP synthase to form ATP from ADP. This mechanism could be universal and at work also in other situations.

3. At quantitative level the identification $h_{eff} = h_{gr}$ of gravitational Planck constant with $h_{eff} = n \times h$ at microscopic level at least is an attractive hypothesis [K72, K42]. Gravitational Planck constant can be expressed as $\hbar_{gr} = GMm/v_0$, where v_0 is taken to be the rotational velocity of Earth. Assuming this for Cooper pairs of rotating super-conductor explains the gravimagnetic anomaly claimed by Tajmar et al [E7, E11]. It also predicts a universal energy spectrum of dark cyclotron photons in the range of bio-photon energies and gives thus support for the hypothesis that dark EEG photons decay to bio-photons. The metabolic energy quantum for proton of order.5 eV is consistent with the identification as cyclotron energy difference for proton over mitochondrial membrane. The hypothesis $h_{em} = h_{eff} = h_{gr}$ makes also sense for the nano-motor defined by ATP synthase transforming ADP to ATP.The interpretation would be that this condition makes possible the reconnection of electromagnetic and gravitational flux tubes.

One can imagine also different scenario involving phase transition changing the value of h_{eff} assignable to atoms. TGD indeed predicts also small values of h_{eff}. $h_{eff} = h_{em}$ would hold true when em interaction becomes non-perturbative. In this case NE would be short ranged and associated with atomic/molecular systems with nonstandard value of h_{eff}.

1. For dark atoms the scale of binding energy behaves like $1/h_{eff}^2$ and is thus reduced for dark atoms [K75]. The creation of dark atoms would require metabolic energy. This metabolic energy could also be liberated as dark atoms transforms to ordinary atom. Metabolic electrons could be associated with dark atoms and also the dark atoms in nutrients could provide metabolic energy driving protons through the mitochondrial membrane against potential gradient and transforming ADP to ATP contains high energy phosphate bond, which would actually correspond to the presence of dark (say hydrogen -) atom. Phosphate containing the dark atom would carry the negentropic entanglement or be accompanied by dark magnetic flux tube.

2. Phosphorylation and de-phosphorylation could be interpreted in terms of reconnection of flux tubes so that the dark proton associated with phosphate is transferred to the acceptor molecule. I have proposed that the deeper meaning of metabolism is transfer of negentropic entanglement (NE). The reconnection of flux tubes would transfer NE between ATP and third party to NE between acceptor molecule and third party. There is a large number of alternative identifications for NE. It could be short range entanglement associated with $h_{eff} = h_{em}$ assignable to electron and nucleus of dark atoms, to pairs of atoms or molecules, or very long range entanglement between molecule and large scale structure with size scale of Earth or even galaxy and associated with $h_{eff} = h_{gr}$. Both forms of NE might be involved and distinguish between two evolutionary levels.

3. Short ranged NE could be associated with dark atoms for which the scale of binding energy behaves like $1/h_{eff}^2$ and is thus reduced for dark atoms [K75]. The creation of dark atoms would require metabolic energy. This metabolic energy could also be liberated as dark atoms transforms to ordinary atom. The dark atoms in nutrients transforming to ordinary atoms could provide the metabolic energy driving protons through the mitochondrial membrane against potential gradient and transforming ADP to ATP contains high energy phosphate bond, which would actually correspond to the presence of dark (say hydrogen -) atom. Phosphate containing the dark atom would carry the NE or be accompanied by dark magnetic flux tube. The transfer of NE would mean its disappearance followed by reappearance and it could happen that $h_{eff}/h = n$ is reduced in the process.

4. The simplest view about photosynthesis would be that the absorption of solar photons excites some atoms to dark states and that nutrients contain these dark atoms as stable enough entities. The contamination of nutrients could mean the decay of these dark atoms to the normal states.

Exclusion zones as prebiotic cells

TGD based model model [L15], [**?**] for Pollack's findings [L15] provides further guidelines.

1. Pollack et al discovered what they call exclusion zones and fourth gel like phase of water. The phenomenon occurs when water is bounded by gel and is irradiated with say visible light. Exclusion zones are negatively charged regions of water with positively charged environment. They act like batteries and have rather exotic properties. For instance, various impurities are repelled from exclusion zone.

2. The observed $H_{1.5}O$ stoichiometry implies that every fourth proton or hydrogen atom is dark and is transferred to the region outside the negatively charged exclusion zone. If only protons are transferred, very high negative charge density is generated. The size of the exclusion zone varies up to 100 μm and is in the range of cell sizes.

3. Dark matter corresponds in TGD Universe to phases with nonstandard value of Planck constant: $h_{eff} = n \times h$ phases at the "magnetic body" of the system (negatively charged region now). Magnetic body corresponds in Maxwell's theory to the magnetic fields generated by the system. Magnetic body consists of flux quanta (flux tubes and sheets).

4. If dark protons with say size scale of atomic size reside at flux tubes, one can assume that they form strings giving rise to dark atomic nuclei. Also ordinary nuclei consist of strings of dark protons and strings of neutrons. Various impurities are transferred from exclusion zone to the exterior suggesting that they become dark particles at magnetic flux tubes.

5. The quantum states of dark protons consist of 3 quarks and a simple model involving rotational symmetry around the axis of dark proton string predicts that the states of dark proton can be arranged into groups which correspond to DNA, RNA, amino-acids and possibly also tRNA molecules. Vertebrate genetic code can be realized as a natural correspondence between DNA/ RNA and amino-acids [L2, K24].

6. Negatively charged EZ could define a pre-biotic cell so that water would be a primitive prebiotic life form. The voltage would be the analog of the resting potential. The transformation of dark protons to ordinary ones would liberate metabolic energy so that primitive metabolism and photosynthesis would be realized. One can also consider a more general possibility that cyclotron energies are different at flux tube portions in the interior and exterior of the EZ analogous to cell membrane. This would increase the value of the metabolic energy currency by adding to Josephson energy ZeV the difference of dark cyclotron energies proportional to h_{eff}. One expects that dark counterparts of basic bio-polymers are still present in living matter and play a fundamental role.

What might happen in ADP→ ATP process?

The identification of the exclusion zone with magnetic body as a basic structure allows to speculate about what might happen in ADP → ATP process and how ATP might store metabolic energy.

1. The strings of dark protons [K24] would be analogous to basic bio-polymers serving as the basic fuel of metabolics hydrolysed in metabolism. Basic biopolymers tend to be negatively charged and could therefore be accompanied by dark proton strings and the liberated metabolic energy might be stored by these strings as cyclotron energy and as Coulomb energy.

2. The simplest guess is that metabolism has developed from the transformation of dark protons to ordinary ones as the analog of EZ transforms back to ordinary water and potential potential difference disappears. One cana also consider generalizations of this picture. A phase transition reducing h_{eff} and increasing p-adic scale such that the size scale of the flux tube remains fixed but cyclotron energy is reduced. This phase transition could also effectively accompany the flow of protons through the boundary of EZ if h_{eff} is smaller and p-adic scale longer at the other side. This mechanism could be stilla at work at the level of mitochondria for dark protons.

3. The notion of high energy phosphate bond is somewhat mysterious. ATP is negatively charged and one can wonder whether it could be accompanied by EZ assignable to the negatively charged phosphates. Also DNA strands and many other biomolecules carry negative charge due to the phosphates. Could the metabolic energy be stored to the magneti body of ATP or of phosphate and eventually liberated by flow of protons to flux tubes with weaker magnetic field?

One can ask why the rotation of ATP synthase motor is necessary. Could the centrifugal acceleration drive dark particles to the magnetic body or keep them there thus stabilizing the dark phase? The dark protons at the magnetic body rotating with the system would remain to magnetic body and would avoid transition to ordinary protons if it is induced by the vicinity of ordinary protons serving as seeds for phase transition. If this interpretation is in the right direction, the rotating magnetic systems might provide a manner to create dark matter [**?**].

Energy metabolism as transfer of negentropic entanglement?

Negentropic entanglement (NE, see **Fig.** `http://tgdtheory.fi/appfigures/cat.jpg` or **Fig. ??** in the appendix of this book) is 2-particle property (or more generally $n > 1$-particle property). One can argue that this is not consistent with the naive idea about systems carrying NE as a resource analogous to metabolic energy. If negentropy transfer is behind metabolism and if one accepts this objection, one must ask whether metabolism actually corresponds to a transfer of NE between nutrient A and some fixed system B so that NE transforms to that between receiver R and same fixed system B? If so, could this could B correspond some higher collective level of consciousness perhaps identifiable as gravitational Mother Gaia (MG) as suggested by the success of $h_{gr} = h_{eff}$ hypothesis at microscopic level?

1. Negentropic entanglement (NE) would be transferred. Nutrients would be negentropically entangled with something very crucial for life. MG is a good candidate in this respect. Even Sun can be considered. Gravitational NE with MG would make possible dark EEG, etc... Basic formula is $\hbar_{gr} = GMm/v_0$, v_0 the rotational velocity at surface at the surface of Earth.

2. Formula generalizes to em case: $h_{em} = Z_1 Z_2 e^2/v_0$ and would apply to ATP synthase being consistent with $h_{gr} = h_{em} = h_{eff}$. Em flux tubes could reconnect with gravitational flux tubes for $h_{gr} = h_{em}$.

3. Nutrient-MG NE can be transformed to molecule-MG NE by the sequence N-MG → P-MG → ATP-MG → R-MG (N for nutrient, R for receiver).

4. The basic mechanism would be the reconnection of magnetic U-shaped loops associated with various molecules serving as kind of tentacles: N/P/ADP/R would have this kind of loops.

One can represent a critical comment. The notion of personal magnetic body (PMB) controlling biological body (BB) is central for TGD inspired theory of consciousness. The above argument does not involve it at all. Can the notion of PMB be therefore consistent with MG hypothesis? Or is PMB in some sense part of the magnetic body of MG - say in the sense that the flux tubes of PMB could be inside flux tubes of MG? Mystics would perhaps equate MG with PMB but this leads to paradoxes.

1. An attractive guess is that $h_{em} = h_{gr}$ holds true for PMB so that it can interact with MG by forming reconnections. Nutrients are dead but have NE with MG so that metabolism allows BB to have NE with MG.

2. How PMB could generate NE with BB? Could it reconnect with the flux tube pairs connecting MG with BB? Do both MG and PMB have NE with BB during life-time. What happens in biological death?: does the NE between PMB and BB transform to that between BB and MG again and only the NE between PMB and MG remains? This would conform with what spiritual teachings say.

3. If the answers to these questions are "yes", the basic purpose of metabolism would be the transformation of gravitational NE between MG and nutrients to that between MG and biomolecules. Magnetic bodies would "steal" part of this NE by reconnecting between MG and BB to that between PMB and BB: note that this process would be something new besides molecular metabolism and could be interpreted as a higher level metabolism. All this would be basically transfer of information from collective level of consciousness to lower levels to be processed and further enriched and to be returned back to MG in biological death: nothing would lost! Biological death itself would be reconnection transforming flux tube bonds to PMB to bonds to MG.

Could electrons serve as nutrients?

The New Scientist article (see `http://tinyurl.com/ybd4g2kl`) about bacteria using electrons as nutrients is very interesting reading since the reported phenomenon might serve as a test for the TGD inspired idea about metabolism as a transfer of negentropic entanglement (NE, see **Fig.** `http://tgdtheory.fi/appfigures/cat.jpg` or **Fig. ??** in the appendix of this book) at fundamental level discussed in [K42] (see `http://tinyurl.com/yat9bx9j`).

1. NE is always between two systems: nutrient and something, call it X. The proposal inspired by a numerical co-incidence was that X could be what I have called Mother Gaia. X could be also something else, say personal magnetic body. The starting point was the claim that the anomalously high mass of electronic Cooper pair in rotating supercounductor (slightly larger than the sum of electron masses!) could be due to a gravimagnetic effects which is however too strong by a factor 10^{28}. This claim was made by a respected group of scientists. Since the effect is proportional to the gravimagnetic Thomson field proportional to the square of Planck constant, the obvious TGD inspired explanation would be $h_{eff} \simeq 10^{14}$ (see `http://tinyurl.com/yb7rsct5` and `http://tinyurl.com/yat9bx9`).

2. Gravitational Planck constant $\hbar_{gr} = GMm/v_0$, v_0 typical velocity in system consisting of masses $M >> m$ and m was introduced originally by Nottale and I proposed that it is genuine Planck constant assignable to flux tubes mediating gravitational interaction between M and m. In the recent case v_0 could be the rotating velocity of Earth around its axis at the surface of Earth.

3. For electron, ions, molecules, .. the value of h_{gr} would of the order of 10^{14} required by the gravimagnetic anomaly and is also of the same order as $h_{eff} = n \times h$ needed by the hypothesis that cyclotron energies for these particles are universal (no mass dependence) and in the visible and UV range assigned to biophotons. Biophotons would result from dark photons via phase transition. This leads to the hypothesis $h_{eff} = h_{gr}$ unifying the two proposals for the hierarchy of Planck constants at least in microscopic scales.

   Thanks to Equivalence Principle implying that gravitational Compton length does not depend on particle's mass, Nottale's findings can be understood if h_{gr} hypothesis holds true only in

microscopic scales. This would mean that gravitation in planetery system is mediated by flux tubes attached to particles. One non-trivial implication is that graviton radiation is dark so that single graviton carries much larger energy than in GRT based theory. The decay of dark gravitons to ordinary gravitons would produce bunches of ordinary gravitons rather than continuous stream: maybe this could serve as an experimental signature. Gravitational radiation from pulsars is just at the verge of detection if it is what GRT predicts. TGD would predict pulsed character and this might prevent its identification if based on GRT based belief system.

4. In the recent case the model would say that the electrons serving as nutrients have this kind of negentropic entanglement with Mother Gaia. $h_{gr} = h_{eff}$ would be of order 10^8. Also in nutrients electrons would be the negentropically entangled entities. If the model is correct, nutrient electrons would be dark and could also form Cooper pairs. This might serve as the eventual test.

This is not the only model that one can imagine. TGD predicts also small values of h_{eff}. $h_{eff} = h_{em}$ would hold true when em interaction becomes non-perturbative. In this case NE would be short ranged and associated with atomic/molecular systems. At this moment one cannot exclude the possibility that only short range NE is involved with living matter.

Short ranged NE could be associated with dark atoms for which the scale of binding energy behaves like $1/h_{eff}^2$ and is thus reduced for dark atoms [K75]. The creation of dark atoms would require metabolic energy. This metabolic energy could also be liberated as dark atoms transforms to ordinary atom. Metabolic electrons could be associated with dark atoms and also the dark atoms in nutrients could provide metabolic energy driving protons through the mitochondrial membrane against potential gradient and transforming ADP to ATP contains high energy phosphate bond, which would actually correspond to the presence of dark (say hydrogen -) atom. Phosphate containing the dark atom would carry the negentropic entanglement or be accompanied by dark magnetic flux tube.

Electrons are certainly fundamental for living matter in TGD Universe.

1. Cell membrane is high T_c electronic super-conductor [K42]. Members of Cooper pairs are at flux tubes carrying opposite magnetic fields so that the magnetic interaction energy produces very large binding energy for the large values of h_{eff} involved: of the order of electron volts! This is also the TGD based general mechanism of high T_c superconductivity: it is now accepted that anti ferromagnetism is crucial and flux tubes carrying fluxes at opposite directions is indeed very antiferromagnetic kind of thing.

2. Josephson energy is proportional to membrane voltage ($E_J = 2eV$) is just above the thermal energy at room temperature meaning minimal metabolic costs.

3. Electron's secondary p-adic time scale is.1 seconds, the fundamental biorhythm which corresponds to 10 Hz alpha resonance.

6.3.6 Humble Origins Of DNA As Nutrient - Really Humble?

I received an interesting link (`http://tinyurl.com/ybv8xu9uDNA_May_Have_Had_Humble_Beginnings_As_Nutrient_Carrier_999.html`) about the indications that DNA may have had rather humble beginnings: it would have served as a nutrient carrier [I100]. Each nucleotide in the phosphate-deoxiribose backbone corresponds to a phosphate and nutrient refers to phosphate assumed to carry metabolic energy in high energy phosphate bond.

In AXP, X=M, D, T the number of phosphates is 1, 2, 3. When ATP transforms to ADP, it gives away one phosphate to the acceptor molecule which receives thus metabolic energy. For DNA there is one phosphate per nucleotide and besides A also T, G, and C are possible.

The attribute "humble" reflects of course the recent view about the role of nutrients and metabolic energy. It is just ordered energy what they are carrying. TGD view about life suggest that "humble" is quite too humble an attribute.

1. The basic notion is potentially conscious information. This is realized as negentropic entanglement for which entanglement probabilities must be rational numbers (or possibly also

algebraic numbers in some algebraic extension of rationals) so that their p-adic norms make sense. The entanglement entropy associated with the density matrix characterizing entanglement is defined by a modification of Shannon formula by replacing the probabilities in the argument of the logarithm with their p-adic norms and finding the prime for which the entropy is smallest. The entanglement entropy defined in this manner can be and is negative unlike the usual Shannon entropy. The interpretation is as information associated with entanglement. Second law is not violated since the information is 2-particle property whereas as Shannon entropy is single particle property characterizing average particle.

The interpretation of negentropic entanglement is as potentially conscious information: the superposition of pairs of states would represent abstraction or rule whose instances would be the pairs of states. The large the number of pairs, the higher the abstraction level.

2. The consistency with standard quantum measurement theory gives strong constraints on the form of the negentropic entanglement. The key notion is that if density matrix is proportional to unit matrix, standard measurement theory says nothing about the outcome of measurement and entanglement can be preserved. Otherwise the reduction occurs to one of the states involved. This situation could correspond to negentropic 2-particle entanglement. For several subsystems each subsystem-complement pair would have similar density matrix. There is also a connection with dark matter identified as phases with non-standard value $h_{eff} = n \times h$ of Planck constant. n defines the dimension of the density matrix. Thus dark matter at magnetic flux quanta would make living matter living.

   In 2-particle case the entanglement coefficients form a unitary matrix typically involved with quantum computing systems. DNA-cell membrane system is indeed assumed to form a topological quantum computer in TGD framework. The braiding of magnetic flux tubes connecting nucleotides with lipids of the cell membrane defines topological quantum computer program and its time evolution is induced by the flow of lipids forming a 2-D liquid crystal. This flow can be induced by nearby events and also by nerve pulses.

   Side-step: Actually pairs of flux tubes are involved to make high temperature superconductivity possible with members of Cooper pairs at flux tubes with same or opposite directions of spins depending on the direction of magnetic field and thus in spin $S = 0$ or $S = 1$ state. For large value of Planck constant $h_{eff} = n \times h$ the spin-spin interaction energy is large and could correspond in living matter to energies of visible light.

3. Negentropy Maximization Principle (NMP, [K32]) is the basic variational principle of TGD inspired theory of consciousness. NMP states that the gain of negentropic entanglement is maximal in state function reduction so that negentropic entanglement can be stable.

4. NMP guarantees that during evolution by quantum jumps recreating the Universe (and sub-Universes assignable to causal diamonds (CDs)) the information resources of Universe increase. Just to irritate skeptics and also to give respect for the ancient thinkers I have spoken about "Akashic records". Akashic records can be said to form books in a universal library and could be read by interaction free quantum measurement preserving entanglement but generating secondary state function reductions providing conscious information about Akashic records defining also a model of self.

   Side-step: Self can be identified as a sequence of state function for which only first quantum is non-trivial at second boundary of CD whereas other quantum jumps induce change of superposition of CDs at the opposite boundary and states at them). Essentially a discretized counterpart of unitary time development would be in question. This allows to understand how the arrow of psychological time emerges and why the contents of sensory experience is about so narrow a time interval. Act of free will corresponds to the first state function reduction at opposite boundary and thus involves change of the arrow of psychological time at some level of self hierarchy: this prediction is consistent with the Libet's findings that conscious decision implies neural activity initiated before the decision ("before" with respect to geometric time, not subjective time).

In this framework the phosphates could be seen as ends of magnetic flux tubes connecting DNA to cell membrane and mediating negentropic entanglement with the cell membrane. DNA as

topological quantum computer vision conforms with the interpretation DNA-cell membrane system as "Akaschic records". This role of DNA-cell membrane system would have emerged already before the metabolic machinery, whose function would be to transfer the entanglement of nutrient molecules with some bigger system X to that between biomolecules and X. Some intriguing numerical co-incidences suggest that X could be gravitational Mother Gaia and flux tubes mediating gravitational interaction with nutrient molecules and gravitational Mother Gaia could be in question [K76]. This brings in mind Penrose's proposal about the role of quantum gravity. TGD is indeed a theory of quantum gravity predicting that gravitation is quantal in astroscopic length scales.

6.4 Jeremy England's Vision About Life And Evolution

I had an intensive discussion with my son-in-law Mikko about the work of Jeremy England [I125] (`http://tinyurl.com/o64rd7o`). The article of the link is probably the most aggressive hyping I have ever seen but this should not lead to think that a mere hype is in question. There is also another, not so heavily hyped popular article at `http://tinyurl.com/m8s2jqt`. The material at the homepageof england lab (`http://tinyurl.com/ycdrdazq`) gives a good view about the work of England for those who cannot tolerate hyping.

England's work is indeed very interesting also from TGD point of view although it is based on standard physics.

In the sequel I will summarize this approach and compare it with TGD vision. The generalization of the thermodynamical approach to TGD framework leads to surprising new insights about the thermodynamical conditions making life and consciousness possible. The new elements relate to zero energy ontology (ZEO), hierarchy of Planck constants labelling levels in a hierarchy dark matters assignable with quantum criticality, the role of macroscopic quantum coherence associated with gravitation, and strong form of holography. The TGD counterparts of Hawking temperature and Hagedorn temperature seem to be crucial for life and correspond to physiological temperature scales. Near Hawking temperature the special features of ZEO become manifest meaning that time reversals of "selves" (mental images) are generated with a considerable rate in heat bath and long term memory and planned action become possible.

6.4.1 Basic Ideas Of England's Theory

I try first to summarize England's vision.

1. Non-equilibrium thermodynamics (NET) is the starting point. NET has been for decades the theoretical framework underlying the attempts to understand living matter using the principles of self-organization theory. Living matter is never an isolated system: dissipation would take it to a totally dead state in this case - nothing would move. Water in the pond when there is no wind, is a good example.

   Self-organization requires an external energy feed - gravitational potential energy liberated in water flow in river or electric power feed to the hot plate below a teapot. This energy feed drives the system to a non-stationary state far from a thermal equilibrium state. Dissipation polishes out all details and leads to an asymptotic spatio-temporal self-organization patterns. The flow in a river and convection in the heated teapot. With high enough energy feed chaos emerges: water fall or boiling of tea pot.

2. The basic hypothesis of England is that evolution means increase in the ability to dissipate. This looks intuitively rather obvious. The evolving system tends to get to a resonance with the energy feed by oscillating with the same frequency so that energy feed becomes maximal and therefore also dissipation. The basic rule is simple: choose the easy option, ride on the wave rather than fighting against it! For instance, the emergence of photosynthesis means that the systems we call plants become very effective in absorbing the energy of sunlight. In this framework essentially all systems are alive to some degree.

   Dissipation means generation of entropy. Evolution of life and conscious intelligence would mean maximal effectivenes in the art of producing disorder. Now I am perhaps exaggerating.

One should speak about "system's maximal ability to transfer entropy out of it": life is not possible without paper baskets. One could argue that the development of civilization durig last decades demonstrates convincingly that evolution indeed generates systems generating disorder with a maximal rate.

One could argue that the definition is too negative. Living matter is conscious and there is genuine conscious information present. The fact is that evolution involves a continual increase of conscious information: the exponential explosion of science is the best proof for this. England's vision says nothing about it. Something is missing.

It is however quite possible to imagine that the principle of maximal entropy generation is true and that the increase of the ability to produce entropy is implied by some deeper principle allowing to speak about living matter as something tending to increase conscious information resources. To formulate this idea one needs a theory of consciousness, thermodynamics is not enough.

3. England has a further idea. The evolution life is not climbing to Mount Everest but coming down from it. Life emerges spontaneously. This is definitely in conflict with the standard wisdom, in particular with the thermodynamical belief on thermal death of the Universe as all gradients disappear. Darwinian evolution would be a special case of a more general phenomenon, which could be called dissipation driven adaptation (DDA). I made a head-on-collision with this principle in totally different framework by starting from quantum criticality of TGD: if took time to fully realize that indeed: evolution could be seen as a sequence of phase transitions breaking in which certain infinite-dimensional symmetry was spontaneously broken to become just the same symmetry but in longer scale!

   Standard thermodynamics predicts the heat death of the Universe as all gradients gradually disappear. This prediction is problematic for England's argument suggesting that differentiation occurs instead of homogenization. Here the standard view about space-time might be quite too simplistic to overcome the objection. In TGD many-sheeted space-time comes in rescue.

   Here is an example about England's argumentation. It seems intuitively clear that replication increases entropy (it is not however clear whether just the splitting into pieces is even more effective manner to increase entropy!). This would suggest that DDA forces the emergence of replication. Very effective dissipators able to replicate, would increase the total effectiveness in dissipation and be the winners. The proposal to be tested is that bacterial mutations , which are best replicators are also best dissipators.

6.4.2 What Is Missing From England's Theory?

What is missing from England's theory? The answer is same as the answer to the question what is missing from standard physics.

1. What is conscious observer - self?

   Observer, which remains outsider to the physical world in the recent day physics - both classical and quantum. Hence one does not have a theory of consciousness and cannot speak about conscious information. Thermodynamics gives only the notion of entropy as a measure for the ignorance.

   Therefore there is a long list of questions that England's theory does not address. What are the physical correlates of attention, sensory perception, cognition, emotions relating closely to information, etc.? Is there some variational principle behing concious existence, and does it imply evolution? Could second law and DDA be seen as consequences of this variational principle?

   England does not say much about quantum theory since he talks only about thermodynamics but his hypothesis is consistent with quantum theory. The restriction to thermodynamics allows only statistical description and notions like macroscopic quantum coherence are left outside.

2. What is life?

   Again one has a long list of questions.

   What it is to be alive? What distinguishes between living and inanimate systems. What it is to die? How general phenomenon evolution is: does it apply to all matter? Also notions like self-preservation and death are present only implicitly in an example about a population of wine glasses whose members might gradually evolve to survive in an environment populated by opera sopranos.

   One can make also other kinds of questions. What really happens in replication? What is behind genetic code? Etc...

   England is a spiritual person and has made clear that the gulf between science and spirituality is something which bothers him . England even has the courage to use the word "God". Therefore it sounds somewhat paradoxical that England avoids using the concepts related to consciousness and life. This is however the only option if one does not want to lose academic respectability.

6.4.3 How Does England's Theory Relate To TGD?

It is interesting to see whether England's vision is consistent with TGD inspired theory of consciousness, which can be also seen as a generalization of quantum measurement theory achieved by bringing the observer part of the quantum physical world. In TGD framework several new principles are introduced and they relate to the new physics implied by the new view about space-time.

1. The new physics involves a generalization of quantum theory by introducing a hierarchy of Planck constants $h_{eff} = n \times h$ with various quantal length and time scales are proportional to h_{eff}. h_{eff} hierarchy predicts a hierarchy of quantum coherent systems with increasing size scale and time span of memory and planned action. h_{eff} defining a kind of intelligence quotient labels the levels of a hierarchy of conscious entities.

   h_{eff} hierachy labels actually a fractal hierarchy of quantum criticalities: a convenient analogy is a ball at a top of ball at the top..... The quantum phase transitions inreasing h_{eff} occur spontaneously: this is the TGD counterpart for the spontaneous evolution in England's theory. Dark matter is what makes system alive and intelligent and thermodynamical approach can describe only what we see at the level of visible matter.

2. Second key notion is zero energy ontology (ZEO). Physical states are replaced by events, one might say. Event is a pair of states: initial state and final state. In ZEO these states correspond to states with opposite total conserved quantum numbers: positive and negative energy states. This guarantees that ZEO based quantum theory is consistent with the fundamental conservation laws and laws of physics as we understand them although it allows non-determinism and free will. Positive and negative energy states are localized at opposite boundaries of a causal diamond (CD). Penrose diagram - diamond symbol - is a good visualization and enough for getting the idea.

   State function CDreduction (SFR) is what happens in quantum measurement. The first SFR leads to a state which is one in a set of states determined once measurement is characterized. One can only predict the probabilities of various outcomes. Repeated quantum measurements leave the state as such. This is Zeno effect - watched kettle does not boil.

   In ZEO something new emerges. The SFR can be performed at *either* boundary of CD. SFR can occur several times at the same boundary so that the state at it does not change. The state at the opposite boundary however changes - one can speak of the analog of unitary time evolution - and the second boundary also moves farther away. CD therefore increases and the temporal distance between its tips does so also.

   The interpretation is as follows. The sequence of reductions at fixed bounary corresponds to a conscious entity, self. Self experiences the sequence of state function reductions as a flow of time. Sensory experience and thoughts, emotions, etc.. induced by it come from the moving boundary of CD. The constant unchanging part of self which meditators try to experience corresponds to the static boundary - the kettle that does not boil.

Self dies in the *first* reduction to the opposite boundary of CD. Self however re-incarnates. The boundaries of self change their roles and the geometric time identified as distance between the tips of CD increases now in opposite direction. Time-reversed self is generated.

3. Negentropy Maximization Principle (NMP) stating roughly that the information content of consciousness is maximal. Weak form of NMP states that self has free will and can choose also non-maximal negentropy gain. The basic principle of ethics would be "Increase negentropy". p-Adic mathematics is needed to construct a measure for conscious information and the notion of negentropic entanglement (NE) emerges naturally as algebraic entanglement.

   The negentropy to which NMP refers is *not* the negative of thermodynamical entropy describing lack of information of outsider about state of system. This negentropy characterizes the conscious information assignable to negentropic entanglement (NE) characterized by algebraic entanglement coefficients with measure identified as a number theoretic variant of Shannon entropy. Hence NMP is consistent with the second law implied by the mere non-determinism of SFR.

   NMP demands that self during sequence of reductions at the same boundary generates maximum negentropy gain at the changing CD boundary. If self fails, it dies and re-incarnates (in a reduction to the opposite CD boundary more negentropy is generated). Selves do not want to die and usually they do not believe on re-incarnation, and therefore do their best to avoid what they see as a mere death. This is the origin of self-preservation. Self must collect negentropy somehow: gathering negentropic sub-selves (mental images) is a manner to achieve this. Plants achieve this by photosynthesis, which means generation of negentropy and storage of it to various biomolecules. Animals are not so saintly and simply eat plants and even other animals. We are negentropy thieves all.

   Re-incarnation also means increase of h_{eff} and getting to higher level in hierarchy and occurs unavoidably. As in England's theory, evolution occurs spontaneously: it is not climbing to Mount Everest but just dropping down.

4. England says "Some things we consider inanimate actually may already be 'alive'." This conforms with TGD view. Even elementary particles could have self: it is however not clear whether their SFR sequences contain more that one reduction to a fixed boundary - necessary for having a sense about the flow of time. Elementary particles would even cognize: in adelic physics every system has both real and p-adic space-time surfaces as its correlates. It can even happen that system has only p-adic space-time correlates but not the real one: this kind of systems would be only imaginations of real system! This is one of the most fascinating implications of strong form of holography which follows from strong form of General Coordinate Invariance forced by the new view about space-time.

   Clearly the notion of evolution generalizes from biological context to entire physics in TGD. One can speak about p-adic evolution and evolution as increase of h_{eff}. The most abstract formulation is number theoretical: evolution corresponds to the increase of the complexity of extension of rationals to which the parameters characterizing space-time surfaces belong to.

5. Does DDA emerge in TGD framework? NMP demands a lot of SFRs - also at the level of visible matter. The non-determimism of SFR alone means a loss of knowledge about the state of system and an increase of thermodynamical entropy so that living systems would generate entropy very effectively also in TGD Universe at the level of visible matter. If one believes that second law and NET imply DDA as England argues, then also TGD implies it at the level of visible matter. For dark matter the situation is different, since the outcome of SFR is not not random anymore. Seen from TGD perspective England's vision misses what is essential for life - the generation of phases of matter identifiable as the mysterious dark matter.

6. England talks about God. In a theory of consciousness predicting infinite self hierarchy, it is easy to assign the attribute "divine" to the levels of consciousness above given level of hierarchy. Personally I have nothing against calling the Entire Universe "God".

   One could give NMP the role of God. For strong form of NMP SFR would be almost deterministic except for ordinary matter for which entanglement is not algebraic and is

therefore entropic: the universe would the best possible one in dark sectors and the worst one in the visible matter sector - Heaven and Hell! Weak form of NMP makes possible even more effective generation of negentropy than its strong form but allows self to make also stupid things and even SFRs with a vanishing negentropy gain: the outcome is state with no entanglement (system is in very literal sense alone in this state). The world in dark matter sectors is not anymore the best possible one but can become better and does so in statistical sense.

7. Replication is a crucial aspect of being alive. England argues that DDA allows to understand its emergence but does not tell about its mechanism. In TGD framework replication can be understood as an analog of particle decay - say photon emission by electron. This requires however a new notion: magnetic body. In Maxwell's theory one cannot assign any field identity to a physical system but TGD view about space-time forces to assign to a given system its field/magnetic body. The replication occurs primarily at the level of magnetic body carrying dark matter as large h_{eff} phases. Magnetic body replicates and ordinary visible matter self-organizates around the resulting copies of it. The dynamics of dark matter would induce also DNA replication, transcription and mRNA translation, and there are some indications that it is indeed "dark DNA" (dark proton sequences having DNA, RNA, amino-acids, and tRNA as biochemical counterparts), which determines what happens in transcription.

6.4.4 Could One Apply The Thermodynamical Approach Of England In TGD Framework?

It turns out possible to gain amazing additional insights about TGD inspired view of life and consciousness by generalizing England's approach [I125]. Several puzzling co-incidences find an explanation in the thermodynamical framework and the vision about solar system as a living quantum coherent entity gains additional support.

1. The situation considered in England's approach is a system - say biomolecule - in heat bath so that energy is not conserved due the transfer of energy between reactants and heat bath.

2. The basic equation is equilibrium condition for the reaction $i \to f$ and its time reversal $f^* \to i^*$. The initial and final state can be almost anything allowing thermodynamical treatment: states of biomolecule or even gene and its mutation. The ratio of the rates for the reaction and its time reversal is given by the ratio of the Boltzmann weights in thermal equilibrium:

$$\begin{aligned} \frac{R(i \to f)}{R(f^* \to i^*)} &= R \ , \\ R &= e^{-\frac{E_i - E_f}{T}} \ . \end{aligned} \tag{6.4.1}$$

E_i and E_f denote the energies of initial and final state. This formula is claimed to hold true even in non-equilibrium thermodynamics. It is important that the ratio of the rates does not depend at all on various coupling constant parameters. The equilibrium condition must be modified if initial and final states are fermions but it is assumed that states can be described as bosons. Note that in heat bath even fermion number need not be conserved.

3. If the energy eigenstates are degenerate, the ratio R of Boltzman factors must be modified to include the ratio of state degeneracies

$$R \to \frac{D(E_i)}{D(E_f)} \times e^{-\frac{E_i - E_f}{T}} \ . \tag{6.4.2}$$

This generalization is essential in the sequel.

One can imagine two possible reasons for the presence of exponentially large factors compensating Boltzmann weights $D(E_i)$. The first reason is that for $h_{eff} = n \times h$ the presence of n-fold degeneracy due to the n-fold covering of space-time surface reducing to 1-fold covering at its ends at the ends of CD is essential. Second possible reason is that the basic object are magnetic flux tubes modellable as strings with exponentially increasing density of states. These mechanisms could quite well be one and same.

Consider now the basic idea inspired by this formula in TGD framework.

1. Since magnetic flux tubes are key entities in TGD inspired quantum biology, stringy dynamics suggests itself strongly. The situation thus differs dramatically from the standard biochemical situation because of the presence of dark matter at magnetic flux tubes to which one can assign fermion carrying strings connecting partonic 2-surfaces defining correlates for particles in very general sense.

2. The key aspect of stringy dynamics is Hagedorn temperature [B9, B20] (`http://tinyurl.com/yamnafy6`). Slightly below Hagedorn temperature the density of states factor, which increases exponentially, compensates for the Boltzmann factor. Hagedorn temperature is given by

$$T_{Hag} = \frac{\sqrt{6}}{2\pi}\frac{1}{\alpha'} \ , \tag{6.4.3}$$

where α' is string tension. In superstring models the value of string tension is huge but in TGD framework the situation is different. As a matter fact, the temperature can be rather small and even in the range of physiological temperatures.

3. What makes T_{Hag} so special is that in the equilibrium condition reaction and its reversal can have nearly the same rates. This could have profound consequences for life and even more - make it possible.

   In ZEO based quantum measurement theory and theory of consciousness time reversal indeed plays key role: self dies in state function reduction to the opposite boundary of CD and experiences re-incarnation as a time-reversed self. This process is essential element of memory, intentional action, and also remote metabolism, which all rely on negative energy signals travelling to geometric past assignable to time reversed sub-selves (mental images). The above formula suggests that intelligent life emerges near T_{Hag}, where the time reversed selves are generated with high rate so that system remembers and pre-cognizes geometric future as it sleeps so that memory planned action are possible.

4. String tension cannot be determined by Planck length as in string models if it is to be important in biology. This is indeed the case in TGD based quantum gravity. The gravitational interaction between partonic 2-surfaces is mediated by fermionic strings connecting them. If string tension were determined by Planck length, only gravitational bound states of size of order Planck length would be possible. The solution of the problem is that the string tension for gravitational flux tubes behaves like $1/h_{eff}^2$.

   In TGD framework string tension can be identified as an effective parameter in the expression of Kähler action as stringy action for preferred extremal strongly suggested by strong form of holography (SH) allowing the description of the situation in terms of fermionic strings and partonic 2-surfaces or in terms of interiors of space-time surfaces and Kähler action. $1/h_{eff}^2$ dependence can be derived from strong form of holography [K75] assuming electric-magnetic duality for Kähler form, and using the fact that the monopoles associated with the ends have same magnetic and electric charges.

5. The discussion of the analog of Hawking radiation in TGD framework [K75], [L20] led to an amazing prediction: the TGD counterpart of Hawking temperature turns out to be in the case of proton very near to the physiological temperature if the big mass is solar mass. This

suggests that the entire solar system should be regarded as quantum coherent living system. This is also suggested by the general vision about EEG [K15]. Could Hawking temperature be near to the Hagedorn temperature but below it?

One can make this vision more detailed.

1. In ZEO the notion of heat bath requires that one considers reactants as subsystems. The basic mathematical entity is the density matrix obtained by tracing over entanglement with environment. The assumption that dark matter is in thermal equilibrium with ordinary matter can be made but is not absolutely crucial. The reactions transforming visible photons to dark photons should take care of the equilibrium. One could even assume that the description applies even in case of the negentropic entanglement since thermodynamical entropy is different from entanglement entropy negative for negentropic entanglement.

2. In TGD inspired quantum biology one identifies the gravitational Planck constant introduced by Nottale with $h_{eff} = n \times h$ [K75, K45, K37]. The idea is simple: as the strength of gravitational interaction becomes so strong that perturbation series fails to converge, a phase transition increasing the Planck constant takes place. $\hbar_{gr} = GMm/v_0 = \hbar_{eff} = n \times \hbar$ implies that $v_0/c < 1$ becomes the parameter defining the perturbative expansion. h_{gr} is assigned with the flux tubes mediating gravitational interaction and one can say that gravitons propagate along them.

   Note that this assumption makes sense for any interaction - say in the case of Coulomb interaction in heavy atoms: this assumption is indeed made in the model of leptohadrons [K52] predicting particles colored excitations of leptons lighter the weak bosons: this leads to a contradiction with the decay widths of weak bosons unless the colored leptons are dark. They would be generated in the heavy ion collisions when the situation is critical for overcoming the Coulomb wall.

   The cyclotron energy spectrum of dark particles at magnetic flux tubes is proportional to h_{gr}/m does not depend on particle mass being thus universal. In living matter cyclotron energies are assumed to be in the energy range of bio-photons and thus includes visible and UV energies and this gives a constraint on h_{gr} if one makes reasonable assumption about strengths of the magnetic fields at the flux tubes [K65]. Bio-photons are assumed to be produced in the transformation of dark photons to ordinary photons. Also (gravitational) Compton length is independent on particle mass being equal to $L_{gr} = GM/v_0$: this is crucial for macrosopic quantum coherence at gravitational flux tubes.

3. The basic idea is that Hawking radiation in TGD sense is associated with all magnetic flux tubes mediating gravitational interaction between large mass M, say Sun, and small mass m of say elementary particle. How large m can be, must be left open. This leads to a generalization of Hawking temperature [L20] assumed to make sense for all astrophysical objects at the flux tubes connecting them to external masses:

$$T_{GR} = \hbar \frac{GM}{r_S^2 2\pi} = \frac{\hbar}{8\pi GM} \quad . \tag{6.4.4}$$

   For Sun with Schwartschild radius $r_S = 2GM = 3$ km one has $T_{GR} = 3.2 \times 10^{-11}$ eV.

   Planck constant is replaced with $\hbar_{gr} = GMm/v_0 = \hbar_{eff} = n \times \hbar$ in the defining formula for Hawking temperature. Since Hawking temperature is proportional to the surface gravity of blackhole, one must replace surface gravity with that at the surface of the astrophysical object with mass M so that radius $r_S = 2GM$ of the blackhole is replaced with the actual radius R of the astrophysical object in question. This gives

$$T_{Haw} = \frac{m}{8\pi v_0} (\frac{R_S}{R})^2 \quad . \tag{6.4.5}$$

The amazing outcome is that for proton the estimate for the resulting temperature for M the solar mass, is 300 K (27 C), somewhat below the room temperature crucial for life!

Could Hagedorn temperature correspond to the highest temperature in which life is possible - something like 313 K (40 C)? Could it be that the critical range of temperatures for life is defined by the interval $[T_{Haw}, T_{Hag}]$? This would require that T_{Haw} is somewhat smaller T_{Hag}. Note that Hawking temperature contains the velocity parameter v_0 as a control parameter so that Hawking temperature could be controllable. Of course, also $T_{Haw} = T_{Hag}$ can be considered. In this case the temperature of environment would be different from that of dark matter at flux tubes.

4. The condition $T_{Haw} \leq T_{Hag}$ allows to pose an upper bound on the value of the effective string tension

$$\frac{1}{\sqrt{\alpha'}} \geq \frac{m}{4\sqrt{6}v_0}\frac{R_S}{R} \quad . \tag{6.4.6}$$

6.5 About Statistics, Negentropic Entanglement, Hawking Radiation, And Firewall Paradox In TGD Framework

In quantum field theories (QFTs) defined in 4-D Minkowski space spin statistics theorem forces spin statistics connection: fermions/bosons with half-odd integer/integer spin correspond to totally antisymmetric/symmetric states. TGD is not a QFT and one is forced to challenge the basic assumptions of 4-D Minkowskian QFT. In the following it is show that the notion of many-shheeted space-time combined with strong form of holography (SH), Zero Energy Ontology (ZEO), Negentropy Maximization Principle (NMP), hierarchy of Planck constants $h_{eff} = n \times h$ with the identification of h_{eff} as gravitational Planck constant $h_{gr} = GMm/v_0$, $v_0/c \leq 1$ challenges the standard form of spin and statistics connection, suggests that quantum gravitation in astrophysical scales could be highly relevant for life, and also leads to new views about firewall paradox.

1. In TGD framework the fundamental reason for the fermionic statistics are anticommutation relations for the gamma matrices of the "World of Classical Worlds" (WCW). This naturally gives rise to geometrization of the anticommutation relations of induced spinor fields at space-time surfaces. The only fundamental fields are second quantized space-time spinors, which implies that the statistics of bosonic states is induced from the fermionic one since they can be regarded as many-fermion states. At WCW level spinor fields are formally classical.

   Strong form of holography (SH) forced by strong form of General Coordinate Invariance (SGCI) implies that induced spinor fields are localized at string world sheets. 2-dimensionality of the basic objects (string world sheets and partonic 2-surfaces inside space-time surfaces) makes possible braid statistics, which is more complex than the ordinary one. The phase corresponding to 2π rotation is not ± 1 but a root of unitary and the phase can be even replaced with non-commuting analog of phase factor.

   What about the ordinary statistics of QFTs expected to hold true at the level of imbedding space $H = M^4 \times CP_2$? Can one deduce it from the q-variants of anticommutation relations for fermionic oscillator operators - perhaps by a suitable transformation of oscillator operators? Is the Fermi/Bose statistics at imbedding space level an exact notion or does it emerge only at the QFT limit when many-sheeted space-time sheets are lumped together and approximated as a slightly curved region of empty Minkowski space?

2. Zero energy ontology (ZEO) means that physical systems are replaced by pairs of positive and negative energy states defined at the opposite boundaries of causal diamond (CD). CDs form a fractal hierarchy. Does this mean that the usual statistics must be restricted to coherence regions defined by CDs rather than assume it in entire H? This assumption looks reasonable since it would allow to milden the rather paradoxical looking implications of statistics and quantum identify for particles.

6.5.1 Negentropic Entanglement, Quantum Monogamy, And Biology

Interesting questions relate to the notion of negentropic entanglement (NE) and quantum monogamy.

1. Two states are negentropically entangled if their density matrix is proportional to projection operator and thus proportional to unit matrix. This require also algebraic entanglement coefficients. For bipartite entanglement this is guaranteed if the entanglement coefficients form a unitary matrix apart from normalization factor. The so called quantum monogamy theorem has a highly non-trivial implication for NE. In its mildest form it states that if two entangled systems are in a 2-particle state which is pure, the entire system must be de-entangled from the rest of the Universe. As a special case this applies to NE. A stronger form of monogamy states that two maximally entangled qubits cannot have entanglement with a third system. It is essential that one has qubits. For 3-valued color one can have maximal entanglement for 3-particle states (baryons). For instance, the negentropic entanglement associated with N identical fermions is maximal for subsystems in the sense that density matrix is proportional to a projection operator.

   Quantum monogamy could be highly relevant for the understanding of living matter. Biology is full of binary structures (DNA double strand, lipid bi-layer of cell membrane, epithelial cell layers, left and right parts of various brain nuclei and hemispheres, right and left body parts, married couples,...). Could given binary structure correspond at some level to a negentropically entangled pure state and could the system at this level be conscious? Could the loss of consciousness accompany the formation of a system consisting of a larger number of negentropically entangled systems so that 2-particle system ceases to be pure state and is replaced by a larger pure state. Could something like this take place during sleep?

2. NE seems to relate also to the statistics. Totally antisymmetric many-particle states with permutations of states in tensor product regarded as different states can be regarded as negentropically entangled for any subsystem since the density matrix is projection operator. Here one could of course argue that the configuration space must be divided by the permutation group of n objects so that permutations do not represent different states. It is difficult to decide which interpretation is correct so that let us consider the first interpretation.

   The traced out states for subsystems of many-fermion state are not pure. Could fermionic statistics emerge at imbedding space-level from the braid statistics for fundamental fermions and Negentropy Maximization Principle (NMP) favoring the generation of NE? Could CD be identified as a region inside which the statistics has emerged? Are also more general forms of NE possible and assignable to more general representations of permutation group? Could ordinary fermions and bosons be also in states for which entanglement is not negentropic and does not have special symmetry properties? Quantum monogamy plus purity of the state of conscious system demands decomposition into de-entangled sub-systems - could one identify them as CDs? Does this demand that the entanglement due to statistics is present only inside CDs/selves?

3. At space-time level space-time sheets (or space-like 3-surfaces or partonic 2-surfaces and string world sheets by SH) serve as natural candidates for conscious entities at space-time level. At imbedding space level elementary particles associated with various space-time sheets inside given CD would contain elementary particles having NE forced by statistics. But doesn't this imply that space-time sheets cannot define separate conscious entities?

   The notion of finite resolution for quantum measurement, cognition, and consciousness suggests a manner to circumvent this conclusion. One has entanglement hierarchies assignable to the length scale hierarchies defined by p-adic length scales, hierarchy of Planck constants and hierarchy of CDs. Entanglement is defined in given resolution and the key prediction is that two systems unentangled in given resolution can be entangled in an improved resolution. The space-time correlate for this kind of situation are space-time sheets, which are disjoint in given resolution but contain topologically condensed smaller space-time sheets connected by thin flux tubes serving as correlates for entanglement.

   The paradoxical looking prediction is that at a given level of hierarchy characterized by size scale for CD or space-time surface two systems can be un-entangled although their subsystems

are entangled. This is impossible in standard quantum theory. If the sharing of mental images by NE between subselves of separate selves makes sense, contents of consciousness are not completely private as often assumed in theories about consciousness. For instance, stereo vision could rely on fusion and sharing of visual mental images assignable to left and right brain hemispheres and generalizes to the notion of stereo consciousness making to consider the possibility of shared collective consciousness. An interpretation suggesting itself is that selves correspond to space-time sheets and collective levels of consciousness to CDs.

Encouragingly, dark elementary particles would provide a basic example about sharing of mental images. Dark variants of elementary particles could be negentropically entangled by statistics condition in macroscopic scales and form part of a kind of stereo consciousness, kind of pool of fundamental mental images shared by conscious entities. This could explain why for instance the secondary p-adic time scale for electron equal to $T = .1$ seconds corresponds to a fundamental biorhythm.

6.5.2 Quantum Monogamy And Firewall Paradox

Quantum monogamy relates also to the firewall paradox of blackhole physics discussed from TGD viewpoint in [K75].

1. There are two entanglements involved. There is entanglement between Alice entering the blackhole and Bob remaining outside it. There is also the entanglement between blackhole and Hawking radiation implied if Hawking radiation is only apparently thermal radiation and blackhole plus radiation defines a pure quantum state. If so, Hawking evaporation does not lead to a loss of information. In this picture blackhole and Hawking radiation are assumed to form a single pure system.

   Since Alice enters blackhole (or its boundary), one can identify Alice as part of the modified blackhole being entangled with the original blackhole and forming a pure state. Thus Alice would form an entangled pure quantum state with both Bob and Hawking blackhole. This in conflict with quantum monogamy. The assumption that Alice and blackhole are un-entangled does not look reasonable. But why Alice, Bob and blackhole could not form pure entangled 3-particle state or belong to a larger entangled state?

2. In TGD framework the firewall problem seems to be mostly due to the use of poorly defined terms. The first poorly defined notion is blackhole as a singularity of GRT. In TGD framework the analog for the interiors of the blackhole are space-time regions with Euclidian signature of induced metric and accompany all physical systems. Second poorly defined notion is that of information. In TGD framework one can define a measure for conscious information using p-adic mathematics and it is non-vanishing for NE. This information characterizes always two-particle system - either as a pure system or part of a larger system. Thermodynamical negentropy formally defined as negative of entropy characterizes single particle (or ignorance about its state) in ensemble so that the two notions are not equivalent albeit closely related. Further, in the case of blackhole one cannot speak of information going down to blackhole with Alice since information is associated with a pair formed by Alice and some other system outside blackhole like objects or perhaps at its surface. Finally, the notion is hierarchy of Planck constants allows NE in even astrophysical scales. Therefore entangling Bob, Alice, and TGD counterpart of blackhole is not a problem. Hence the firewall paradox seems to dissolve.

3. The hierarchy of Planck constants $h_{eff} = n \times h$ connects also with dark quantum gravity via the identification $h_{eff} = h_{gr}$, where $h_{gr} = 2\pi GMm/v_0$, $v_0/c \leq 1$, is gravitational Planck Planck constant. $v_0/c < 1$ is velocity parameter characterizing system formed by the central mass M and small mass m, say elementary particle.

   This allows to generalize the notion of Hawking radiation [K76] (see `http://tinyurl.com/y9mjddpz` and `http://tinyurl.com/ycm2rs3p`), and one can speak about dark variant of Hawking radiation and assign it with any material object rather than only blackhole. The generalized Hawking temperature is proportional to the mass m of the particle at the gravitational flux tubes of the central object and to the ratio R_S/R of the Schwartschild radius R_S

and radius R for the central object. Amazingly, the Hawking temperature for solar Hawking radiation in the case of proton corresponds to physiological temperature. This finding conforms with the vision that bio-photons result from dark photons with $h_{eff} = h_{gr}$. Dark Hawking radiation could be very relevant for living matter in TGD Universe!

Even more, by extending [K76] (see `http://tinyurl.com/y9pvwb56` and `http://tinyurl.com/ycrml2w3`) Jeremy England's vision about life [I125] (see `http://tinyurl.com/o64rd7o`), one ends up via SH to suggest that the Hawking temperature equals to the Hagedorn temperature assignable to flux tubes regarded as string like objects! This assumption fixes the value of string tension and is highly relevant for living matter in TGD Universe since it guarantees that subsystems can become time-reversed with high probability in state function reduction. The frequent occurrence of time reversed mental images makes possible long term memory and planned action and one ends up with thermodynamics of consciousness. This is actually not new: living systems are able to defy second law and the notion of syntropy was introduced long time ago by Fantappie [J22].

4. Does one get rid of firewall paradox in TGD Universe? It is difficult answer the question since it is not at all clear that there exists any paradox anymore. For instance, the assumption that blackhole represents pure state looks in TGD framework rather ad hoc and the NE between blackhole and other systems outside it looks rather natural if one accepts the hierarchy of Planck constants.

   It would however seems to me that the TGD analog of dark Hawking radiation along flux tubes is quite essential for communications and even more, for what it is to be Alice and Bob and even for their existence! The flux tube connections of living systems to central star and planets could be an essential part of what it is to be alive as I have already earlier suggested with the inspiration coming from $h_{eff} = h_{gr}$. In this framework biology and astrophysics would meet in highly non-trivial manner.

6.6 More Precise View About Remote DNA Replication

Both Luc Montagnier [I94, I95] and Peter Gariaev [I102] have found strong evidence for what might be called remote replication of DNA. I have developed a TGD inspired model for remote replication using the data from Peter Gariaev [K82], who has developed the notion of wave DNA [I81] supported by Montagnier's findings.

Polymer chain reaction (PCR) [I39] provides a manner to build copies of piece of DNA serving as template. Once single copy is produced, it serves as a template for a further copy so that exponential amplification is achieved. Montagnier's and Gariaev's works suggest however that the synthesis of DNA could also occur without a real matrix DNA as remote replication. According to the proposal of Gariaev [I81, I124] DNA template would be remotely represented as what he calls wave DNA. Montagnier [I95] uses 7 Hz ELF radiation to obtain the effect whereas Gariaev [I102] uses scattering of laser light into large interval of frequencies to achieve the effect.

In TGD approach magnetic body containing dark matter with large Planck constant, the associated cyclotron radiation for which energy scale is proportional to effective Planck constant $h_{eff} = n \times h$ having large values implying conjectured macroscopic quantum coherence of living matter, dark analog of DNA represented as dark proton sequences at magnetic flux tubes and accompanying ordinary DNA, plus reconnection of U-shaped magnetic flux tubes assignable to the magnetic bodies of biomolecules and allowing them to recognize each other, are the basic elements. The model has evolved from the attempts to understand water memory and homeopathy in TGD framework [K24].

Both 7 Hz ELF radiation and scattering of laser light would both generate dark photon (large Planck constant) spectrum with a wide spectrum of frequencies but with the same energy which in Gariaev's experiments would naturally be the energy of scatter laser light. The dark photons would provide representation for DNA codons. If 7 Hz frequency radiation involves dark photons with energies of visible photons transforming to ordinary photons before scattering from DNA the outcome would be same as in Gariaev's experiments.

This picture conforms with Gariaev's hologram idea and also with TGD based vision about living matter as a conscious hologram [**?**]. The laser beam that Gariaev has used and the 7 Hz

irradiation (involving dark ELF photons at bio-photon energies) would act as a reference beam allowing to read a biohologram coded by DNA and its magnetic body. The outcome is dark photons with same energy but with varying values of Planck constant and thus with varying frequencies propagating along magnetic flux tubes to the target, which could be exclusion zone (EZ). Flux tubes are characterised by h_{eff} and magnetic field strength B_{end} determining cyclotron frequency (coded by the transversal area by flux quantization if monopole flux is in question). Metabolic energy is needed to create EZ and could be provided either by the radiation itself or by the repeated heating. Negentropic entanglement is generated and creates the correlation between dark (phantom) DNA codons and ordinary DNA codons.

The following involves same elements as the model discussed in [K82] but there are also new elements due to the developments in the model of dark DNA allowing to imagine a detailed mechanism for how water can represent DNA and how DNA could be transcribed to dark DNA. The transcription/association represents a rule and rules are represented in terms of negentropic entanglement in TGD framework with pairs of states in superposition representing the instances of the rule. Transition energy serves as a characterizer of a molecule - say DNA codon - and the entangled state is a superposition of pairs in which either molecule is excited or dark DNA codon is excited to higher cyclotron state with same energy: this requires tuning of the magnetic field and sufficiently large value of h_{eff} at the flux tube. Negentropic entanglement is due to the exchange of dark photons: this corresponds to wave DNA aspect. Dark cyclotron photons also generate negatively charged exclusion zones (EZs) discovered by Pollack and in this process transform part of protons to dark ones residing at the magnetic flux tubes associated with EZs and forming dark proton sequencies.

6.6.1 Some Background

The model for remote replication involves the following basic building bricks.

1. Dark variant of DNA realized as dark proton strings representing dark nuclei.
2. The identification of bio-photons as decay products of dark cyclotron photons with large value of h_{eff} having universal energy spectrum due to the condition $h_{eff} = h_{gr}$.
3. TGD explanation for the fourth phase of water discovered by Pollack [L15] and characterized by negatively charged exclusion zones EZs generated by radiation.
4. A model for the radiative coding of DNA creating 1-1 correlation between ordinary and dark DNA codons and between two dark DNA codons.

Dark DNA as dark proton strings

TGD leads to a model of nuclei as nucleons strings [L2]. The model generalizes to the dark matter sector [L2, K24].

1. I have proposed the notion of dark DNA realized as dark proton sequences (3 quark states), which I have argued ton basis of a simple model to form representations for DNA, RNA, amino-acids and even tRNA is central for TGD inspired biology. Biochemistry would define only a secondary representation for more fundamental realization of genetic code and analogs of basic biomolecules in terms of dark nuclear physics.

   I have conjectured that translations, transcription, etc generalize and apply to pairs of ordinary and dark and dark and dark DNA and amino-acids. One could even consider that dark DNA would make possible induction of genetic changes: transfer dark DNA inside germ cells and transform them to ordinary DNA and attach to existing DNA. If dark DNA can be generated by radiation as wave DNA notion suggests then radiation from other cells to germ cells could induced genetic changes. Living systems would have kind of Research and Discovery apartment developing new candidates for genes. Evolution would be the opposite for blind random trials.

2. I have also proposed that immune system could have developed from what is basic mechanism of homeopathy and water memory. The magnetic bodies of water clusters mimic invader

molecules - or rather their magnetic bodies. What is needed is a representation for cyclotron frequencies so that radiation would emerge in this phase. Cyclotron frequency spectrum would represent the invader and the simplest mimicry of invader molecule would be water structure with magnetic body characterized by same cyclotron frequency spectrum: water memory in short. Also the braiding of the magnetic body of the invader might be mimicked.

Protein folding might be a chemical representation for this braiding and the proteins of immune system might mimic the braidings of the magnetic bodies of the invader molecules. DNA in turn would give a symbolic representation of proteins allowing to construct them when needed. Ordinary DNA and proteins would have been preceded by dark DNA and dark proteins. I have even proposed an interpretation of genetic code based on the idea that it represents the dynamical evolution of braiding of the magnetic body - or 2-braiding [K62].

The basic mechanism of directed attention or sensing the presence of the invader molecule would be reconnection of U shape flux tubes of the magnetic bodies of the two system. Also resonant interaction by cyclotron radiation inducing cyclotron transitions is expected to be an essential piece of the mechanism. Magnetic body of water cluster could tune the thickness of flux tube so that the magnetic field is same as that in the flux tube of invader molecule so that primitive consciousness and act of free will would be involved.

3. Suppose that DNA codes for proteins, their cyclotron frequency spectrum and their braiding and knotting in protein folding in turn representing invader molecule. Is the frequency spectrum all that is needed to represent DNA and construct its dark variant? The experiments of Benveniste and followers [I71, I72] suggest that invader molecules are indeed represented by the cyclotron frequency spectrum alone. This would suggest connection with wave DNA concept.

Universality of cyclotron energy spectrum and bio-photons as decay products of dark photons

There are good empirical motivations [K76] to expect that the cyclotron energy spectrum is universal and in the range of bio-photon energy spectrum. This is achieved if h_{eff} is proportional to the mass m of the charged particle so that cyclotron energy $\hbar_{eff}eB/m$ is independent of mass and same for all charged particles.

Universality follows also from the condition that gravitational and biological Planck constants are identical: $h_{gr} = h_{eff}$, where $\hbar_{gr} = GMm/v_0$ is the gravitational Planck constant introduced by Nottale and assigned with the flux tubes mediating gravitational interaction in TGD Universe. The condition states that electromagnetic and gravitational flux tubes have same the value of effective Planck constant meaning that also gravitation would become a key player in biology.

Fourth phase of water, EZs, and metabolic role of cyclotron radiation

The experiments of Pollack [L15] suggest a partial answer to the question. in terms of what he calls fourth phase of water containing negatively charged regions, exclusion zones (EZ) of size up to 200 micrometers.

1. Irradiation of water by visible light generates negatively charged regions which he calls exclusion zones (EZs). The energy goes to the formation of electric voltage between exterior and interior and is analogous to cell membrane potential. Predecessor of cell could be in question. Some fraction of protons must go outside the system and my proposal is that it goes to magnetic flux tubes and forms dark proton sequences defining the analogs of basic bio-molecules. The $H_{1.5}O$ stoichiometry of EZs [L15] characterizing also earlier findings suggesting that one fourth of protons of water are dark in attosecond time scale (not visible in electron scattering and neutron diffraction) suggests that every fourth proton disappears from EZ. This anomaly was one of the strong motivations for taking the idea about dark matter as large h_{eff} phases seriously [K18].

   These structures would be involved also with water memory and homeopathy and immune system would have emerged from these. Free energy researchers know these regions quite

well [H1] (no-one of course takes them seriously!) and they can be generated by just feeding energy to system used as metabolic energy. In homeopathy the mechanical agitation would do this and induce replication and perhaps even evolution of the resulting primitive lifeforms. Cavitation, use of strong electric field, maybe even heating used in PRC, etc... are possible mechanisms of energy feed.

2. The cyclotron radiation at cyclotron frequencies associated with flux tubes emanating from DNA codons could provide the energy needed to induce the formation of EZs. This would be the first function for the radiation.

3. If the DNA end of flux tube contains dark proton in state which corresponds to the DNA in one-one manner then the mass of the dark proton state would assign to it a unique cyclotron frequency distinguishing between DNA codons. The challenge is to understand the mechanism of DNA dark DNA pairing and dark DNA-dark DNA pairing and one expects resonant binding by exchange of dark cyclotron photons.

Pairing ordinary and dark DNA codons and two identical dark DNA codons by negentropic entanglement

One should understand the pairing of ordinary and dark DNA. As a matter fact, this pairing defines a realization of the genetic code as a physical 1-1 correlation of DNA codons with some physical states. I have consider this kind of realizations also in the model of DNA as topological quantum computer. The following realization relies on resonant interaction by exchange of dark cyclotron photons and can be seen as radiation based.

1. The most natural association between ordinary and dark DNA would via energy resonance. The energy for some molecular transition of DNA (in bio-photon energy range by argument below) would be same as cyclotron energy for the codon with large value of $h_{eff} = n \times h$ making cyclotron energy large.

2. By suitably tuning the value of the magnetic field B associated with the flux tube accompanying ordinary DNA codon the dark cyclotron energy can be tuned to be equal to the value of some biochemical transition energy of DNA, which is in visible and UV range typically - that is in the energy range of bio-photons.

3. Classically DNA codon and its dark variant can be thought of as exchanging forth and back dark photon at resonance frequency and become strongly correlated in this manner like tennis players during game. Quantum mechanically one has quantum entangled Schrödinger cat like state in which state pairs have same total energy but individual states do not have well-defined energy.

4. The correlation between dark proton states at two ends of flux tube would be realized as formation of bound state via resonant exchange of dark cyclotron photons. Negentropically entangled [K32] superposition for which simplest the possible form is $|n\rangle|n+1\rangle + |n+1\rangle|n\rangle$ of paired cyclotron states would be generated. DNA and dark DNA codons would pair to a negentropically entangled state in similar manner. Recall that in TGD framework negentropic entanglement (NE) carries potentially conscious information: the state represents a rule whose instances correspond to the state pairs in the superposition [K32].

5. One can consider also 3-particle NE of DNA codon and 2 dark DNA codons which is superposition of three 3-particle states with one particle excited to higher energy state with the same energy. DNA codon would be excited chemically and dark codons excited to cyclotron state $(n \to n+1)$. 3-dimensional permutation symbol defines this kind of state. Also NE for larger number of particles is possible.

The tuning of the flux tube magnetic field to make cyclotron energy equal to chemical transition energy is possible for arbitrary biochemical transition energies and the association of dark proton states to arbitrary biomolecules is in principle possible via same mechanism. This would be essentially a symbolic representation of biomolecule, a name for molecule. If one has some number of different molecules able to form sequences, these sequences can be remotely reconstructed by

using the cyclotron frequencies and transversal flux tubes associated with the template to generate the EZs and the name of the polymer to which the building bricks bind resonantly.

If the condition $h_{eff} = h_{gr}$ holds true, one can use instead of dark proton sequences sequences of *any* dark charged particles - say electrons and ions. Hence almost an unlimited repertoire of representations arises. These correspondences need not to be one-one. For instance, DNA-amino-acid 64-to-20 correspondence is possible to realize with the help of dark variants of DNA codons and amino-acids and also the partially or totally dark variants of this correspondence are possible.

This pairing mechanism would allow resonant interactions of the ordinary DNA codons in water and dark DNA codons induced by the dark cyclotron radiation and could play key role also in ordinary DNA replication and also in the remote replication reported by Montagnier [I95] and Gariaev [K82]. A phase transition reducing h_{eff} would bring ordinary and dark codon together and ordinary biochemistry would take care of the rest. Clearly, this mechanism would also allow biomolecules connected by magnetic flux tubes to find each other in molecular soup with pairing following by a phase transition reducing h_{eff}.

6.6.2 Does Remote Replication Apply Same Mechanism As MimicryOf Invader Molecules In The Case Of Water Memory?

Somehow the irradiation of water sample with the cyclotron radiation generated by real DNA should induce or be involved with the generation of dark DNA representing the ordinary DNA and the PCR process would use this dark DNA as template an involves pairing of ordinary and dark DNA nucleotides. How this could happen in TGD Universe?

The mechanism of remote DNA replication without chemical template would be essentially the same as in the TGD based model of water memory [K24] underlying also the model of homeopathy circumventing the ultra-naive skeptic argument that homeopathy is not possible because the density of molecules dissolved in water is practically zero.

The cyclotron frequency spectrum allows to create EZ whose magnetic body mimics the invader molecule. Resonant formation of negentropically entangled pairs would define a realization of genetic code based on radiation and dark cyclotron radiation would give rise to the formation of EZs and accompanying dark proton sequences.

In the recent case invader molecule would be replaced with DNA expressing its presence using dark cyclotron radiation propagating along the flux tubes transversal to codons and forming part of the magnetic body of DNA. The magnetic flux tube of ordinary DNA codon realizing dark proton sequence as dark variant of DNA codon would generate its own representation by generating EZs in water.

The rules would be following.

1. Magnetic fields at U-shaped flux tubes associated with codons and dark codons must be equal so that also cyclotron frequencies coding for dark proton masses and therefore for dark proton states would be equal so that frequency and energy resonance is possible and negentropically entangled state is formed. This assigns by resonance mechanism to the second end of flux tube same dark proton state as to the end near ordinary DNA. Recall that U-shape is essential for bio-super-conductivity based on large value of h_{eff} making possible large and negative spin-spin interaction energy for electrons of pair located at parallel flux tubes [K6, K41].

   As described, binding is generated by resonant exchange of dark cyclotron photons between the ends which are in superposition of different cyclotron states. Magnetic field value in turn corresponds directly to ordinary DNA codon - or rather its transition in bio-photon energy range. It is essential that the value of magnetic field codes for ordinary DNA codon via a biochemical transition energy associated with it. One can imagine that magnetic body can tune the value of field by changing the transversal area of the flux tube carrying monopole flux (possible in TGD due to the CP_2 topology). Similar tuning would be involved when the magnetic bodies assignable to EZs detect possible invader molecules. Interestingly, the impurity molecules inside EZs are removed by unknown mechanism citebbioPollackYoutube.

2. Dark DNA codons associated with DNA would have U-shaped flux tubes which for large h_{eff} would extend to the water sample containing building bricks of DNA and catalyst. The

flux tubes associated with dark DNA and building bricks of ordinary DNA would reconnect resonantly and lead to remote replication of DNA strand.

This option is definitely not the only possibility one can imagine but represents the general principle. For instance, one can consider using only DNA-dark DNA complex and inducing h_{eff} increasing phase transition transferring the dark DNA strand to the volume of the water sample. The mechanism allows also to consider remote translation of genes to proteins. The possible medical applications of this in a situation in which the DNA of the patient has suffered a mutation causing a disease are obvious.

6.7 TGD Inspired Model For The Formation Of Exclusion Zones From Coherence Regions

There is a talk of Mae-Wan Ho (`http://tinyurl.com/ybbyn4pc`) in Conference on the Physics, Chemistry and Biology of Water 2014. It is a very nice representation and I learned new facts highly relevant for my own work.

Some background articles might be helpful. Mae-Wan Ho [I112] has proposed that there exists superconducting liquid crystal water aligned with collage fibres. Giudice et al [I68] have proposed that water dynamics is at the root of metamorphosis in living matter: this involves the notion of water coherent region (CD) with size scale of 1 micrometer. I have not considered this notion in TGD framework earlier but TGD strongly suggests that the four Gaussian Mersennes $M_{G,k}$, $k = 151, 157, 164, 167$ with corresponding p-adic length scales coming as $L(k) = 2^{(k-151)/2} times L(151)$, $L(151)$=10 nm are important in biology: $k = 167$ corresponds to 2.5 micrometers. Pollack and et al [I145, I126] have introduced the concept of exclusion zone (EZ) with size scale of 200 nm and related notion fourth phase of water. TGD inspired model of EZ involves in essential manner dark protons at magnetic flux tubes assignable to EZ [K76, K62].

The main points of Mae-Wan Ho's talk are following.

1. Protons make water a conductor, maybe even superconductor. In TGD framework the statement would be that dark protons flowing along magnetic flux tubes make this possible. Personally I believe that electronic and even ionic Cooper pairs are are involved and TGD based model of cell membrane [K47] assumes these super-conductivities relying on the notion of dark matter realizes as $h_{eff} = n \times h$ phases.

2. The water associated with collagen networks appears as superconductor and superfluid in nano-scales. Also this is very attractive idea and if the $h_{eff} = h_{gr}$ condition holds as some arguments suggest, then superfluidity allowing macroscopic quantum coherence with gravitational Compton length having no dependence on the mass of particle becomes possible [K76]. This is due to two facts. First, one has $\hbar_{gr} = GMm/v_0$, where M can be identified as dark part of the Earth's mass, m is the mass of the particle and v_0 is velocity parameter. Secondly, Compton length is inversely proportional to the mass. One of the strange effects involved with superfluidity is fountain effect explained elegantly by macroscopic quantum gravitational coherence: water would effectively defy gravitation: this effect might allow testing of the hypothesis.

6.7.1 CDs And Ezs

Mae Wan-Ho talked about and compared two notions: CDs (coherent domains of water with size of about micrometer postulated by quantum field theoreticians, in particular Emilio del Giudice) and EZs (exclusion domains with size about 200 micrometers discovered by Gerald Pollack and collaborators experimentally). Note that in Zero Energy Ontology (ZEO) I talk about causal diamonds (CDs), which are typically much larger than CDs of Giudice et al.

1. Inside EZ the water forms layered structure consisting of hexagonal layers and the stoichiometry is $H_{1.5}O$ so that every fourth proton must be outside EZ (proton is not accompanied by electron if charge separation takes place: EZ is indeed negatively charged so that one obtains different pHs inside EZ and in its exterior). This state is experimentally heavier than ordinary water.

2. So called tetrahedral or 4-coordinated water is assigned with CDs. CDs and EZs could correspond to two different p-adic length scales in TGD framework. This state would be less dense than ordinary water. Both CD and EZ contain plasma of almost free electrons. CDs are excited to 12.06 eV just.5 eV below the ionizing potential 12.56 eV..5 eV which is the nominal value of metabolic energy quantum - probably not an accident.

6.7.2 TGD Inspired Model For CDs And Ezs

I try my best to summarise some very interesting points of the talk and develop in more detail TGD inspired model for EZs and their formation, and the TGD view of metabolism leading to a prediction of new form of metabolism involving dark UV photons from Sun.

1. The splitting of ordinary water H_2O to $2H^+ + 2e^- + O$ is a key step in photosynthesis. In particular, it produces oxygen without which which we cannot survive. The splitting process involves two ionizations. The ionisation energy of the first electron 12.56 eV and in ultraviolet much above the metabolic energy quantum around.5 eV. How the splitting of water can be achieved at all? This looks like a very real problem!

2. CDs/EZs could be the solution to the problem. Inside CD the energy for the splitting of water is much smaller due to the fact that electrons are almost free as already mentioned: if the splitting energy equals to the so called formation energy, it is about.41 eV for CD: nothing but the metabolic energy quantum! Also at the interace of EZ just above the boundary of EZ the electronic states are excited and only an energy of.51 eV - known as formation energy - is needed for the splitting. This suggests that metabolic energy quanta are used to generate EZs and/or CDs in the fundamental step metabolism. Also irradiation at these energies generates CDs/EZs.

3. My layman logic says that formation energy for EZ must correspond to the energy needed to increase the size of /EZ by a minimum amount. In TGD model this would mean creating one proton-electron pair such that electron remains inside the EZ, whose size thus increases and proton becomes dark proton at dark magnetic flux tube. This step would be also a key step in the splitting of water. Splitting of water and growth of EZ would be essentially the same process. In the case of CD it would seem that charge separation takes place inside CD in the splitting and proton can go outside.

   What comes in mind that the formation of CDs requiring large excitation UV energy of 12.06 eV precedes that of EZs. After the formation of CD and almost free electrons only metabolic energy quantum per proton is required to kick single proton to dark magnetic flux tube. This would conform with the fact that CD radius is about 200 times larger than that of CD meaning that volumes are related by a factor $8 \times 10^6 \simeq 2^{23}$. The formation of EZ would transform tetrahedral water to the hexagonal $H_{1.5}O$ and suck protons to dark protons at magnetic flux tubes. If this picture is correct, the proper identification of formation energy for CD would be as absorption energy for CD equal to 12.06 eV and in UV. Recall that bio-photon spectrum extends to UV and dark photons with this energy could be responsible for the formation of CDs. This would adde dark photons transforming to bio-photons to the picture.

   The formation of EZ can be seen as pulling out one ordinary proton from ordinary water just above the surface of the EZ and making it dark proton at a magnetic flux tube assignable to the EZ and perhaps connecting it to neighboring EZ for form a quantum coherent network. Dark proton would serve as a current carrier and make water a conductor and perhaps even super-conductor. Even superfluidity can be considered.

4. The metabolic energy quantum.5 eV can be also assigned with hydrogen bond. Could the process of generating dark proton and increasing the size of EZ by one electron involve cutting of the hydrogen bond binding the proton to the water outside. If so then the only thing keeping the excited water inside CD as a coherent phase would be the bond energy of hydrogen bonds! Maybe this is too simplistic.

I have proposed earlier that hydrogen bonds are short magnetic flux flux tubes, which can suffer h_{eff} increasing phase transition. These flux tubes could in turn experience reconnections with U shaped large h_{eff} flux tubes and get connected to the dark web. Mae-Wan Ho also tells that the transfer of proton from covalent OH bond to the middle of hydrogen bond happens with a considerable probability. Could this step precede the increase of h_{eff} and reconnection? This would give a connection with hydrogen bonding about which Mae Wan-Ho also talked about. These naive models of course cannot be correct in detail but give hopes about fusion of existing chemical thinking and new quantal notions.

5. A process bringing in mind the formation of EZs occurs as one perturbs molecular biosystems - that is feeds energy into it. The system "wakes up" from "winter sleep", the globular proteins, which are in resting state with hydrogen bonds at their surface forming kind of ice layer unfold and protein aggregates are formed. Molecular summer begins and ceases when the energy feed is over. Cellular winter begins again. Maybe cellular summer is just temporary formation of EZ layers around the protein involving melting of hydrogen bonds and generation of dark protons making system conscious!

6.7.3 Is A New Source Of Metabolic Energy Needed?

What remains to be understood is the process generating CDs: where could the UV photons with energy 12.06 eV come? Clearly a new form of metabolism is involved and the only source of energy seems to be the Sun!

1. Solar radiation cannot however provide UV photons as ordinary photons since UV radiation at these wavelengths is absorbed by the atmosphere. In TGD framework a reasonable candidate for dark radiation with energies in UV range is dark cyclotron radiation with energy $E = h_{eff} \times f$: biophotons would be produced in the transformation of dark cyclotron photons to ordinary photons.

2. Could part of solar UV radiation transform to dark UV photons at magnetic flux tubes of even size scales larger than that of Earth predicted by the model of EEG and arrive along them through the atmosphere? The presence of a new source of metabolic energy is in principle a testable prediction: is the energy feed from the visible part of solar radiation really enough to cover the metabolic energy needs? Here one must however take into account the fact that the UV energy would be received by water. The water from which CDs are eliminated would not allow photosynthesis.

To sum up, if the proposed picture is correct photosynthesis involves formation of EZs and cellular respiration the inverse of this process. As discussed earlier, the purpose of metabolic processes would be basically generation and transfer of negentropic entanglement assignable to large h_{eff} states.

6.8 Was Ribosome The First Self-Replicator?

I encountered a link to apopular article (see `http://tinyurl.com/nl2wybc`) describing a highly interesting work [I131] by M. Root-Bernstein and R. Root-Bernstein (daughter and father). The title of the popular article "Forget the selfish gene: Evolution of life is driven by the selfish ribosome, research suggests". As a matter of fact, the article itself is not selling anything of type "selfish X", a dogma which to my opinion is more or less dead: synergy and quantum coherence are much more promising notions relevant to biomatter. "Selfish X" is a paradigm, which suits much better to the description of cancer. The title of the article "The ribosome as a missing link in the evolution of life" would have been much more appropriate also for the popular article.

First a summary of motivations by authors. The basic problem relates to the emergence of life and there are many theories. The models can be divided to "genetics first" and "metabolism first" type models.

1. RNA world is basic example of "genetics first" models. The problem of the "genetics first models" is that it is difficult to understand how prebiotic life could have coped before the

complex molecular machinery of metabolism. The second problem of RNA world is that polynucleotides and proteins almost certainly co-evolved. So called compositional replication models start from this assumption but have difficulties in explain replication schemes. Both approaches fail to explain how complex cells emerged from molecular evolution. It is however known that lipid layers of cell membrane are emergent structures not coded by genes (soap films).

2. Second class of models try to proceed from complexity to simplicity by assuming the first replicator (pro-cell typically) but are not able to answer the question "What before this?". The natural assumption is that simple bio-molecules gradually evolved to polymers and polymer aggregates and eventually cell membrane emerged.

According to authors, the challenge is to bridge the gap between self-replicating polymers and fully functional cell by identifying intermediate structures able to replicate, restore and replicate information, capture metabolic components and energy, and transform all these into biochemical networks.

6.8.1 Trying To Catch The Idea

The basic idea of the authors is simple and brilliant. Ribosome is the transcription machinery transforming DNA to proteins. Also the first replicator must have contained the transcription machinery. Perhaps the first replicator was minimal and contained just this machinery! Perhaps ribosome or its predecessor ("pre-ribosome") indeed was the first self-replicator. One would have beautiful self-reference: ribosome would be the recipe for making a copy about the recipe! Brings in mind Gödel-Escher-Bach!

This assumption is highly non-trivial. In the following I try to sketch for myself what this could mean. In the following I drop "pre"or notational convenience with understanding that ribosome, RNA, amino-acid etc. means "pre-ribosome", "pre-RNA", "pre-amino-acid", "pre-tRNA" etc.. In TGD framework pre-ribosome could be of non-biochemical nature and realized at the level of dark matter.

1. It seems natural to assume that the basic raw material consisted of RNA and amino-acid molecules in the environment. Ribosome could use them to build copies of itself. The question how these were generated will not be considered now.

2. Ribosome consists of rRNA and proteins and uses tRNA to associated to mRNA sequence amino-acid sequence. If ribosome was the first replicator realizing genetic code as mRNA-amino-acid correspondence it had to use its own rRNA as a template for the translation to a corresponding protein.

   If nothing has changed after the emergence of the recent replication mechanisms, the testable prediction is that ribosome amino-acids are images of rRNA sequences under genetic code. One of course expects that the stricture of ribosome has not conserved in precise sense so that this prediction could be too strong.

3. tRNA is a molecule of form RNA-X-amino-acid and rRNA should have contained the genetic information allowing to transcribe and translate the RNA and amino-acid polymers appearing in tRNA.

According to [I131] these predictions are indeed tested in the work considered for Escheria Coli bacterium and it is found that the findings are consistent with the hypothesis.

On basis of these observations one can try to imagine how the ribosome or its predecessor "pre-ribosome" might have replicated.

1. Both the basic units of RNA sequences and corresponding amino-acid polymers of rRNA had to replicate. The most economic assumption is that this occurred simultaneously.

2. One can imagine that rRNA "gene" and the protein coded by it arranged themselves so that they were parallel. The amino-acid coded by rRNA codon acted as a catalyzer for the attachment of a conjugate of rRNA codon to the growing rRNA sequence just as in DNA

replication promoter catalyzes the replication. rRNA codon in turm acted as a catalyzer for the addition of new amino-acid to the growing protein. tRNA molecules of form RNA-X-amino-acid from the environment provided the needed RNA codon and amino-acid.

Remark: I have already earlier considered an RNA world scenario in which amino-acids of tRNA catalyzed the replication of RNA sequences [K19]. When DNA emerged, the roles would have changed and amino-acid sequence was formed instead of the replication of RNA.

This replication differs from ordinary transcription. In transcription incoming mRNA sequences produce amino-acid sequences as tRNAs attach to the mRNA codons of mRNA attached to the ribosome. tRNA looses its amino-acid but keeps RNA. Now tRNA loses both amino-acid and RNA codon and only the unit X in tRNA? RNA-X-amino-acid remains.

At some step of evolution the replication of rRNA would have ceased to occur and tRNA would have kept its RNA in the double translation process. Is this possibly biologically?

3. Concerning tRNA there are many possibilities. One can imagine that ribosome and Xs could have served as co-replicators. The reaction $X \to RNA - X - amino - acid$ and its inverse could have occurred spontaneously. The resulting complex would have attached to the end of RNA-amino-acid sequence associated with some portion of mRNA just as it does in ordinary translation. In the replication or ribosome RNA-X-amino-acid would have attached to ribosome and X: s would have been produced in the replication of X forming a part of ribosome. In the environment the attachment of RNA and corresponding amino-acid to X would have taken place.

A possible objection is based on ontogenesis-recapitulates-phylogeny vision (ORP). The replicating pre-ribosomes should be still there but they are not. There should be some very simple mechanism preventing the replication but still one can ask whether the ribosomal replication could not occur in special circumstances.

6.8.2 How The Pre-Ribosome As First Replicator Relates To TGD Approach?

TGD framework predicts that replication as a splitting of 3-surfaces to two copies is a fundamental mechanism of quantum TGD analogous to the $1 \to 2$ decay of elementary particle and the replication of DNA, cells, etc... should reduce to a hierarchy of replications starting from long length scales and proceeding as replications at shorter length scales with master slave relationship between the subsequent levels of the scale hierarchy.

This identification of replication as a mere splitting of 3-surfaces saying nothing about what happens for the quantum states associated with them is too general to allow to talk about unique primary replicator. If one however restricts the consideration to systems consisting of RNA and amino-acid sequences the idea about ribosome as primary replicator becomes highly non-trivial.

In TGD framework it is possible that pre-biopolymers were not bio-polymers but their dark counterparts formed from dark protons sequences at magnetic flux tubes with states of dark proton in 1-1 corresponds with DNA, RNA, amino-acids and tRNA. If so pre-ribosome was realized at the level of dark matter as dark ribosome - a complex formed by dark analogs of bio-polymers.

If so, then pre-ribosome consisting of dark matter at flux quanta could be the primary replicator and the formation of its bio-molecular counterpart would be induced from that of dark pre-ribosome like the dynamics of slave in master slave hierarchy.

This raises questions. How does this replication proceed? Does ribosome still replicate as all other biological structures do and induce replication of low ever level structures in the dark matter hierarchy? Does the ordinary biomatter induced at the lowest level of hierarchy would only make visible this replication?

In the following I briefly summarize the basic TGD based notions involved in attempt to answer these questions.

4-D self-organization and magnetic body

One class of questions concerns the roles of self-organization and genetices. Even the definition of the notion of self-organization is poorly defined. In TGD zero energy ontology (ZEO) forms the

basic framework of both quantum TGD proper and its applications to consciousness and biology. In zero energy ontology (ZEO) self-organization is replaced with self-organization by quantum jump sequence leading to the emergence of not only 3-D spatial patters but also of 4-D behavioral patterns: one can say that living system is 4-dimensional and also its geometric past changes in quantum jumps (Libet's findings).

1. Various motor actions of magnetic body appear as basic processes of the quantum self-organization. This includes braiding and knotting, h_{eff} changing phase transitions changing the lengths fo flux tubes, reconnections allowing to build connections between different system consisting of flux tube pairs, and also replication. Also signalling by dark photons is an essential part of the picture and the general hypothesis is that dark photons have same universal energy spectrum as bio-photons and thus in the energy range of molecular transition energies.

2. Replication in TGD framework occurs at the fundamental level as a replications of 3-surface and is completely analogous to $1 \to 2$ decay for point elementary particle. This replication could take place for the magnetic flux quanta representing various biopolymers and higher level structures and induced the replication at the level of visible matter. As noticed, this replication is not enough in biology and must be accompanied by the replication of the quantum states associated with 3-surfaces.

3. One key question is how the bio-molecular processes arranged into a functional network. Here the hypothesis that magnetic flux tubes form a 3-D grid analogous to coordinate grid with points of grid at intersections of 3 flux tubes and flux tubes as coordinate lines is very attractive. This Indra's web would be behind the gel like structure of cellular water and make it single coherent unit. Behavioral modes would be time evolutions of this grid: motor actions of the magnetic body - or hierarchy of them.

Does dark matter induced the dynamics of visible biomatter?

The idea that dark matter induces the dynamics of biomatter is extremely attractive since the enormous complexity of biochemistry would be only adaptation to the dynamics of the much simple almost topological dynamics of the master represented as flux tubes carrying dark matter.

1. In TGD framework there are good reasons to believe that water contained the prebiotic life forms as dark analogs of various biomolecules consisting of dark proton sequences at magnetic flux tubes with the states of dark proton in 1-1 correspondence with various bio-polymers (DNA, RNA, amino-acids, tRNA). These string like objects would be dark nuclei but with a large value of Planck $h_{eff} = n \times h$ constant and with same size scale as biopolymers. The proposal is that they are present also in living matter and that is interaction between various levels based on dark photons which give bio-photons as decay products.

2. All the basic processes such as transcription, translation, and replication would be realized already at this level. The analogs of these processes assigning to dark analogs of biopolymers the biopolymers themselves would have evolved later. (ORP) suggests that ordinary biopolymers are accompanied by parallel flux tubes carrying dark protons sequences representing them. Ordinary manner would condense around dark matter.

   The strongest assumption is that dark processes induce their bio-chemical counterparts as biomolecules attach to the magnetic flux tubes for which they form images at the level of visible matter. This might explain why strong dehydration leads to denaturation of biomolecules and why denatured biomolecules are not biologically active. Dark DNA would represent the "soul" of DNA not present in denatured DNA! Same of course would apply to other biopolymers: the loss of dark matter would induce the in vivo $\to$ in vitro transformation.

   I have proposed the identification of dark counterparts of RNAs and amino-acids as complex braided and knotted structures with braiding carrying information making possible topological quantum computation like processes and topological realization of memory. DNA would provide a symbolic representation coding also the braiding characteristics of the dark amino-acid sequence. Dark amino-acid sequence would represent the braiding physically ad dark DNA as a sequence of symbols.

Cyclotron frequencies are crucial for communication and the strength of magnetic field on flux tubes emanating transversally from dark amino-acid sequence would be determined by the state of dark proton. The correspondence between dark RNA and amino-acid would be determined by the condition that cyclotron frequencies are identical for the corresponding dark proton states (DNA and mRNA, RNA and amino-acid) so that resonant interaction is possible.

3. This picture conforms with the chemical properties of DNA, RNA and proteins.

   (a) RNA does not appear as double strands and in unfolded form is much less stable than DNA. This conforms with the fact that DNA serves as an information storage providing symbolic representation of RNA and amino-acids including their folding or at least braiding. RNA in turn would provide the concrete representation for braiding and folding.

   (b) DNA double strand is stable against hydrolysis but only inside cell - this could be due to the fact that the phase of water is ordered and ice-like so that it cannot induce hydrolysis by providing water molecules - perhaps the fourth phase of water discovered by Pollack and leading to the formation of dark proton sequences in TGD framework is in question.

   (c) The braiding structure of DNA is repetitive and carries no information. This conforms with the idea that DNA and its dark variant provide a purely symbolic representations in terms of genetic code for the corresponding amino-acid- and RNA polymers including also their braiding.

4. One can invent objections against the hypothesis that the dynamics of biopolymers is induced from that for their dark variants.

   (a) RNA is not stable against hydrolysis but it can gain stability by folding. Thus the shape of RNA molecule would not be determined by its dark variant in conflict with induction hypothesis. One can however consider the much weaker possibility that dark sector determines only topological dynamics. Only the braiding of the fold RNA molecules would determined by the braiding of dark variant.

   (b) DNA double strand is stable and braided in repetitive and very simple manner. If chemistry determines the stability of the DNA double strand then DNA double strand would induce the braiding of dark DNA strand rather than vice versa. Now one can argue that if dark DNA appears as double strand this forces the repetitive braiding.

To how high level can one continue this parallelism. For instance, does it make sense to talk about dark variants of cell and cell membrane? Can one tell whether it was pro-cell or bio-molecules that emerged first? It seems that all these structures could have emerged simultaneously. What emerged was dark matter and its emergence involved the emergence of all the others. Hens and eggs emerged simultaneously.

1. Here the findings of Pollack about the generation of exclusion zones, which are negatively charged regions of water obeying exotic stoichiometry $H_{1.5}O$, are suggestive. The TGD based model assumes that a phase transition generating dark protons sequences at flux tubes of magnetic body outside the EZ takes place. The self-organization at the level of ordinary matter would generate dark matter at quantum criticality - a basic aspect of self-organization process leading to higher hierarchy levels taking the role of master. Dark matter would be the master or rather - there would be entire hierarchy of masters labelled by the values of h_{eff}. I have also considered the possibility that the generation of large h_{eff} phases happens at criticality quite universally so that life would be universal phenomenon rather than random thermodynamical fluctuation.

2. EZs with sizes about 200 microns (size of cell) could have been the prebiotic cells. There is also evidence that EZs consist of structures with size of order micron called coherent regions (CDs to be not confused with Causal Diamonds!). Could they have been the predecessors of

the cell nuclei inside which dark DNA would be stable? The TGD model for the formation of EZs assumes that they are formed from CDs under irradiation.

This picture leads also to a view about metabolism predict that UV radiation with energies about 12.6 eV must play a key role in metabolism. The proposal is that this radiation arrives as dark photons along magnetic flux tubes of the magnetic body and excites water molecules inside CDs so that they are energetically at distance of about.5 eV from the splitting of OH bond. The excitation of water molecules inside CDs by metabolic energy quantum of nominal value.5 eV transforms this phase to EZs of Pollack.

Emergence of life as emergence of dark matter?

Many basic questions of biology seem to be hen-egg questions such as "genetics or metabolism?", "cell membrane or biomolecules?", "DNA or RNA?", "RNA or amino-acids?", etc.. This suggests that there exists a deeper level and emergence at this level induced the emergence at the level of biochemistry and cell biology.

In TGD the emergence of living systems would reduce to the emergence of dark matter as large h_{eff} phases of ordinary matter taking place at quantum critical and perhaps even critical systems [K75].

1. The question whether genetics or metabolism emerged first ceases to be relevant in this framework, where basic physics provides candidates for the fundamental mechanisms of metabolism (for instance liberation of zero point kinetic energy when the p-adic length scale of space-time sheet (magnetic flux tube) increases).

   Also genetic code would have been realized already before biochemistry if dark proton sequences provided the counterparts for the fundamental biomolecules. The dark biology as dark nuclear physics would make itself visible via biochemistry induced by it. We would see directly the dynamics of dark matter just by looking living systems!

2. If one takes this picture seriously, then also pre-RNA and various other pre-biopolymers could have been realized in terms dark proton sequences associated with dark magnetic flux tubes. The dark replication process could have been the arrangement of RNA and amino-acid flux tube portions in parallel and replication of the dark proton sequences with the help of the analog of tRNA attaching to the corresponding amino-acid. In this framework the notion of dark ribosome makes sense. It would however replicate only in cell replication.

3. In the biochemical scenarios also the emergence of DNA looks like mystery. In TGD framework dark DNA could have emerged at the same time as dark RNA and dark amino-acids as CDs and EZs emerged and make the stable presence of also ordinary DNA inside CDs and EZs. All basic biomolecules and prebiotic cell and metabolism would have accompanied the emergence of CDs and EZs under the irradiation of water feeding metabolic energy and giving rise to prebiotic photosynthesis (note that the negative net charge of DNAs could be due to the fact that part of protons is at dark flux tubes). Dark DNA could be interpreted as an information storage representing the braiding patterns of dark RNA and dark amino-acids symbolically.

4. In this framework the basic step of the replication is the generation of flux tube parallel to the flux tube from which one forms copy or map (say in DNA replicationandtranscription). How this happens?

   A possible answer to the question relies on the earlier proposal that living system involves kind of coordinate grid formed from magnetic flux tubes serving as coordinate lines and meeting each other at the points of the grid . [K62]. The replication process would involved translation of nearby flux parallel flux tube of the grid near to a given flux tube assignable to say DNA strand as a first step - maybe by h_eff reducing phase transition for flux tubes orthogonal the flux tube. After this the building bricks of the new biomolecule would be brought along either of the remaining locally orthogonal flux tubes - perhaps by h_{eff} reducing phase transition. The basic structure would be this Indras web containing visible matter at its nodes with dynamics consisting of magnetic motor actions.

This vision involves of course considerable challenges. One should model the dark ribosome counterparts of the replication process for dark DNA, transcription of dark DNA to dark mRNA, translation of dark mRNA to dark amino-acids, and also possible self-replication of dark ribosome.

6.9 Potential "missing link" in chemistry that led to life on Earth discovered

In the attempts to understand pre-biology the basic challenge is to understand how the needed short RNA, DNA, and amino-acid sequences managed to form. Phosphorylation (see `http://tinyurl.com/y732fsd3`) is known to be crucial for this process and means energization in standard bio-chemistry. Organic phosphate (see `http://tinyurl.com/cx9ukv9`) possesses somewhat mysterious high energy phosphate bond, which stores energy and makes possible metabolism: in metabolic ATP with three phosphates transforms to ADP with two phosphates by giving one phosphate with high energy phosphate bond to the acceptor molecule, which is therefore phosphorylated.

In the recent biology phosphorylation of various biomolecules such as DNA, RNA, amino-acid sequences is catalyzed by proteins known as enzymes known as phosphorylases. Kinase is one particular enzyme transferring phosphate from ATP to the acceptor molecule. Proteins consist of amino-acids and would not be present in RNA world, which serves almost as a standard model for the prebiotic period. Ribozymes are catalysts formed from RNA but they catalyze typically only the reversal of phosphorylation.

6.9.1 The problem and its possible solution

The phosphorylation of short nucleotide sequences and amino-acid sequences, and also lipids making possible formation of small cell membrane like structures is necessary for the formation of larger structures from their building bricks. As noticed, ribozymes catalyze only dephosphorylation. How RNA was phosphorylated during RNA era or were the amino-acid present all the time?

The popular article with the title "*Potential 'missing link' in chemistry that led to life on Earth discovered*" (see `http://tinyurl.com/y9s56xnx`) tells about a mechanism allowing phosphorylation during RNA era in absence of enzymes. The discovery [I84] (see `http://tinyurl.com/y9kvgl24`) is that an organic molecule known as diamidophosphate (DAP) (see `http://tinyurl.com/y88vecs2`) having chemical formula $PO_2(NH_2)_2^{-1}$ could do the job in presence of water and imidazol. Imidazol (see `http://tinyurl.com/y8vgfr42`) has chemical formula$C_3N_2H_4$ and is a molecule possessing aromatic hetero-cycle consisting of 3 C atoms and 2 N atoms.

Remark: Pyrimidine (see `http://tinyurl.com/k3vxl9b`) in turn is aromatic hetero-6-cycle consisting of 4 C atoms and 2 N atoms and having formula $C_4N_2H_4$. DNA (see `http://tinyurl.com/cpndtse`) has as basic building bricks phosphates PO_4^- having valence bonds with deoxy-ribose (see `http://tinyurl.com/qxv9kg8`) molecules (containing 5-rings with 4 C atoms and one O). Each sugar has valence bond with N of nucleoside C, T, A or G. C and T are pyrimidines with single aromatic 6-ring and A and G are purines obtained by fusing imidazol 5-ring and pyrimidine 6-ring to obtain purine double ring. By replacing one OH of de-oxyribose of DNA with H one obtains RNA.

DAP could solve several problems simultaneously: how the short sequences of RNA (later DNA) and amino-acids were formed, and how the predecessors of cell membranes emerged. It is not however clear to me whether this process could have been fast enough or whether the slowness only made the first step painful.

6.9.2 How could the discovery relate to TGD inspired quantum biology?

It is interesting to interpret the discovery in TGD framework. The basic question is whether the presence of dark atoms and electrons in bio-molecule distinguish between atomic physics, in-organic chemistry, and organic chemistry. Usually organic chemistry is defined to be chemistry of carbon compounds, typically hydrocarbons. Could it be that the formation of hydrocarbons involves dark variants of proton and electron identified as $h_{eff} = n \times h$ variants of ordinary proton and electron?

From atomic physics to chemistry

How could one proceed from atomic physics to atomic physics to chemistry in TGD framework. The basic question is how to understand valence bond: it is not at all clear whether mere Schrödinger equation allows to understand it. Could the emergence of dark electrons allow their delocalization and formation of valence bonds? It has been known for decades that the heating of rare-earth metals leads to a mysterious loss of some valence electrons and the explanation would be the energy provided by heating kicks them to higher energy states by making some valence electrons dark [L33]. The explanation would be in terms of dark electron orbitals for valence electrons which have radii scaled up by factor n^2 and are analogous to Rydberg states identified as orbitals with large value of principal quantum number and having very large radius.

The dark variants of atoms have binding energy scale reduced by factor $1/n^2$ so that their formation requires energy feed (perhaps radiation at required frequencies). One or more valence electrons of ordinary atom could be dark so that the size of the orbital is scaled up by factor n^2. The valence bond central for chemistry in general and in particular for basic biopolymers could contain dark electrons delocalized because of larger value of n than for the non-valence electrons. Note that one could be $n = n_0 > 1$ for ordinary atoms making in principle possible atoms with $n < n_0$ with anomalous large binding energy also for the filled shells as the findings of Randel Mills indeed suggest [L23].

Surprisingly, dark electrons would be essential in ordinary chemistry thought to reduce to standard model physics! The increase of n reduces binding energy scale and requires energy feed. This would allow to understand why anabolism (see `http://tinyurl.com/c8x8avz`) - that is generation of biopolymers from their building blocks by generating valence bonds - requires energy feed and why catabolism (see `http://tinyurl.com/cbx99fv`) - the splitting of biopolymers to their building blocks by splitting the valence bonds liberates energy.

The valence bonds would be classified by the value of n and it is quite possible that in organic chemistry the values of n are larger than in in-organic chemistry. Could this mean that valence bonds H and C and N and O have higher values in bio-chemistry? Also the valence bonds between O and H in water could have larger value of n.

To sum up, the transition from atomic physics to ordinary chemistry involved generation of dark electrons associated with valence bonds. The value of n for dark electrons can vary and allow hierarchy of evolutionary steps with increasingly delocalized valence electrons.

From chemistry to bio-chemistry

What about the step leading to a genuine bio-chemistry involving genetic code? Magnetic body (MB) is the basic aspect of biochemistry according to TGD. Pollack effect [L15] (see `http://tinyurl.com/y8uxocch`) leading to the formation of negatively charged regions - exclusion zones (EZs) - would involve generation of dark protons at magnetic flux tubes of MB with electrons left to the EZ - possible as ordinary particles [L15]. Also Pollack effect requires feeding of energy, say as irradiation by photons.

DNA is stable against spontaneous hydration only inside cell membrane. This suggests that the EZs of Pollack containing partially dark water molecules satisfying effectively the stoichiometry $H_{3/2}O$ allowed to stabilize DNA. Therefore EZs are excellent candidates for the predecessors of cell.

The TGD inspired proposal is that DNA strand for which each phosphate has negative unit charge is companied by dark analog of DNA consisting of dark protons such that the states of 3-proton units are in one-one correspondence with DNA, RNA, tRNA and amino-acids and the degeneracies of the vertebrate genetic code (number of codons coding for given amino-acid) come out correctly [L21] (see `http://tinyurl.com/jgfjlbe`). A more general picture is that ordinary chemistry is kind of shadow for the dynamics of dark matter at magnetic flux tubes doing its best to emulate it. This would explain also why genetic code has also other variants.

It would be the emergence of dark protons with large enough value of n, which would distinguish between ordinary chemistry and bio-chemistry. Water is basic element of life and hydrogen bonding is responsible for the formation of water clusters - certainly one of the key aspects of bio-chemistry. Hydrogen bonds (see `http://tinyurl.com/bntn28n`) appear between highly electronegative (see `http://tinyurl.com/pbh6r6c`) atoms such as O, N, and F (electronegativity

is roughly the tendency to attract electrons). What distinguishes hydrogen bond from valence bond is that it is proton rather than electron, which is delocalized. This suggests that the delocalized proton is dark proton at magnetic flux tube connecting the hydrogen bonded molecules.

The emergence of metabolism

In the proposed framework the first basic aspect of life would be the generation of dark electrons and protons using energy feed and their transfer between molecules and their generation by providing the needed energy.

1. Metabolism (anabolism) would provide the energy needed to transform ordinary atom (that is electron bound to it) to a dark atom with large value of $h_{eff}/h = n$. This requires energy since the binding energy is proportional to $1/n^2$ and reduced in the process. This is quite generally true for all dark variants of quantum states. One can say that the increase of the complexity of the system by increasing n characterizing its "IQ" requires metabolic energy (in adelic physics [L35, L34] "IQ" has a concrete interpretation as cognitive resources). Therefore the first steps of prebiotic life was the emergence of energy feed mechanism making possible the increase of n.

2. I have considered the possibility that the period of prebiotic life preceding the the emergence of chemical storage of energy used dark nucleosynthesis [L29] (see `http://tinyurl.com/y7u5v7j4`) as the source of metabolic energy. The recently discovered life-like properties [I103] in a very simple system consisting of negatively charged plastic balls in the plasma of Ar^+ ions allows to develop rather detailed ideas about this phase of life [L32] (see `http://tinyurl.com/yassnhzb`).

3. A fundamental question is about the step leading to the chemical storage of metabolic energy to valence bonds with non-standard value of n. Solar radiation could have generated both negatively charged EZs identifiable as possible predecessors of cell membrane and valence bonded molecules storing metabolic energy.

About bio-catalysis

Without bio-catalysis biochemical reactions leading to the formation of biopolymers and cell membrane would be quite too slow. Here phosphorylation enters the game.

1. The TGD based model for bio-catalysis relies on the temporary reduction of $h_{eff} = n \times h$ liberating energy kicking the reactants over potential wall. After this step the catalyst - at least in the ideal situation - receives the energy and the atom becomes dark again.

2. Acid catalyst gives a proton and base catalyst gives an electron. Most bio-catalysts are acid catalysts. The TGD based interpretation should rely on the possibility of dark valence electrons and dark protons at flux tubes. Since base catalysts are associated with non-organic chemistry, the identification of the electron given by base catalyst as dark electron looks natural. Acid catalysts would give dark proton.

Bio-catalysts are usually activated by phosphorylation and de-activated by de-phosphorylation but there are exceptions to this rule. This can be understood if the catalyst activates a molecule acting as a switch for a reaction. Catalysts related to phosphorylation are known as phosphotransferasess (see `http://tinyurl.com/y87crqad`) and contain kinases transferring phosphate from ATP to the acceptor molecules.

Phosphatases (see `http://tinyurl.com/ybf9onba`) remove phosphate from the target molecule: they are hydrolases (see `http://tinyurl.com/y88zayj7`) and use water to remove the phosphate and to hydrate the molecule.

The difference between organic and inorganic phosphates

Phosphate appears as too variants: organic and inorganic.

1. Organic phosphates bound to biomolecules have charge -1. Some electrons of organic phosphate ion have transformed to valence electrons and are therefore dark. Also some protons - one dark proton per dark electron to not affect the observed charge in short scales - would be dark and at the magnetic body of the organic phosphate. Both dark protons and dark electrons would be present and give rise to somewhat mysterious high energy phosphate bond.

2. Free phosphate in water environment appears in ionized variants $H_nPO_4^{n-4}$ and is regarded as in-organic and have negative charge 4-n. In inorganic phosphate some dark protons and ordinary electrons giving rise to the negative charge have combined to hydrogen atoms. The larger the number of hydrogens is, the higher the level of inorganicity is.

   The fractions of variants of free phosphate in water depend on pH characterizing the density of protons present. Could pH in fact characterize the fraction of dark protons at magnetic flux tubes? Or could it also characterize the fraction of dark hydrogen atoms present. Similar question applies to the counterparts of pH for other biologically important ions.

About phosphorylation and the interpretation of DAP

At chemical level phosphorylation attaches phosphate ion to the hydroxyl group (R-OH) of the acceptor molecule. At deeper level phosphorylation would give dark electron to the acceptor molecule and dark proton to its MB. Phosphorylation would increase the quantum coherence length: the formation of short RNA, amino-acid sequences and of cell membrane like structures would be a basic example of this.

What about the interpretation of the role of DAP in this framework? DAP has charge -1 as also the phosphate bound to DNA and RNA have (in ATP the outermost phosphate has charge -2). DAP is very similar to the phosphate in DNA and RNA and expected to carry high energy phosphate bond. In TGD framework it would possess both dark valence electrons and dark protons at magnetic flux tubes with only one ordinary electron responsible for the charge of DAP. Due to the properties of phosphatase the phosphorylation would be very simple process at the level of dark electron and proton. Hence DAP and imidazole could make possible the phosphorylation.

About dephosphorylation and phosphoryl transfer

The scanning of web shows that some sources talk of dephosphorylation and some sources about phosphoryl transfer reactions and it remained unclear to me whether the two terms really have the same meaning. In any case, in TGD framework one can distinguish between these notion. Dephosphorylation could mean either phosphoryl transfer (transfer of phosphate between donor and acceptor molecules) or "dropping" of organic phosphate to water environment and giving it negative additional negative charge (the transfer would be now to water environment) and making it inorganic.

1. Phosphoryl would transfer removes PO_4^- group and presumably also the associated dark proton from the target and transfers them to the acceptor molecule and its MB. I have proposed that reconnection of flux tubes transforms the flux tubes entering to the donor molecule to that associated with the acceptor molecule so that dark proton is automatically transferred. In ATP-ADP process the phosphate group and presumably also the dark proton and electron would be transferred to the acceptor molecule from ATP. ADP is dephosphorylated and acceptor phosphorylated.

2. In "dropping" the outcome would be in-organic phosphate denoted by P_i, which is a mixture of HPO_4^{-2} and $H_2PO_4^{-1}$. One interpretation is that 1 or 2 dark protons from magnetic flux tubes have transformed to ordinary protons and combined with electrons to form hydrogen atoms. This operation would reduce the number of dark particle and thus the "evolutionary level" of the system.

Dephosphorylation is known to lead to a decomposition of the donor molecule to smaller structures, indicating the reduction of h_{eff}/h and thus of quantum coherence length. In RNA world dephosphorylation would be catalyzed by ribozymes and in some important cases also in

the recent biology. Dephosphorylation would reduce quantum coherence length and lead to the decomposition of structures to smaller ones: mRNA splicing is one example of this. Catabolism of nutrients and the decay process of dead organic matter provide further basic examples.

Catabolism (see `http://tinyurl.com/cbx99fv`) of nutrients and the decay process of dead organic matter suggest what happens. In the first preliminary step of catabolism catalysts are involved. At the second step of catabolism inorganic phosphate is formed, which suggests that the number of dark protons is reduced in the process. This conforms with the reduction of the value of $h_{eff}/h = n$.

6.10 Some aspects of TGD inspired quantum biology

TGD based explanation for the findings relies on the basic notions of TGD inspired quantum biology. The basic notions are magnetic body (MB) and hierarchy of Planck constants $h_{eff} = n \times h_0$ [K75, K76] emerging from the adelic physics as a prediction [L35, L34] but originally proposed on basis of anomalous effects of ELF em fields in living matter. The anatomy of MB has remained unclear hitherto but in this article a detailed model allowing to understand the formula $h_{gr} = h_{eff}$ for gravitational Planck constant and leading to a further formula for h_{gr} relating magnetism and gravitation.

A further central notion is TGD based model for water memory as the ability of the MB of water to control the thickness of its flux tubes to entrain with external frequencies and reproduce them. This is a central element in TGD based view about immune system and homeopathic effects [K24]. Cancer would reduce to a disease of the MB of the living system to high degree determined by the MB of water. Details of the bio-chemistry and even cell membrane dynamics would have surprisingly minor role in the model.

6.10.1 Is the cosmological constant really understood?

The interpretation of the coefficient of the volume term as cosmological constant has been a long-standing interpretational issue and caused many moments of despair during years. The intuitive picture has been that cosmological constant obeys p-adic length scale scale evolution meaning that Λ would behave like $1/L_p^2 = 1/p \simeq 1/2^k$ [**?**].

This would solve the problems due to the huge value of Λ predicted in GRT approach: the smoothed out behavior of Λ would be $\Lambda \propto 1/a^2$, a light-cone proper time defining cosmic time, and the recent value of Λ - or rather, its value in length scale corresponding to the size scale of the observed Universe - would be extremely small. In the very early Universe - in very short length scales - Λ would be large.

It has however turned out that I have not really understood how this evolution could emerge! Twistor lift seems to allow only a very slow (logarithmic) p-adic length scale evolution of Λ [L52]. Is there any cure to this problem?

1. Could one consider the *total* action for preferred extremals - at least flux tubes - as proportional to effective cosmological constant Λ_{eff}? Since magnetic energy decreases with the are of string like $1/p \simeq 1/2^k$, where p defines the transversal length scale of the flux tube, one would have effective p-adic coupling constant evolution of Λ_{eff} approaching to Λ, which must be extremely small.

   The corresponding size scale would correspond to the density of the magnetic energy equal to that of dark energy. Flux tubes with quantized flux would have thickness determined by the length scale defined by the density of dark energy: $L \sim \rho_{vac}^{-1/4}$, $\rho_{dark} = \Lambda/8\pi G$. $\rho_{vac} \sim 10^{-47}$ GeV^4 (see `http://tinyurl.com/k4bwlzu`) would give $L \sim 1$ mm, which would could be interpreted as a biological length scale (maybe even neuronal length scale).

2. But can Λ be very small? In the simplest picture based on dimensionally reduced 6-D Kähler action this term is not small in comparison with the Kähler action! If the twistor spheres of M^4 and CP_2 give the same contribution to the induced Kähler form at twistor sphere of X^4, this term has maximal possible value!

The original discussions in [?, ?] treated the volume term and Kähler term in the dimensionally reduced action as independent terms and Λ was chosen freely. This is however not the case since the coefficients of both terms are proportional to $1/\alpha_K^2 S$, where S is the area of the twistor sphere which is same for the twistor spaces of M^4 and CP_2 if CP_2 size defines the only fundamental length scale. I did not even recognize this mistake.

The proposed fast p-adic evolution of the cosmological constant would have extremely beautiful consequences. Could the original intuitive picture be wrong, or could the desired p-adic length scale evolution for Λ be possible after all? Could dynamics somehow give it? To see what can happen one must look in more detail the induction of twistor structure.

1. The induction of the twistor structure by dimensional reduction involves the identification of the twistor spheres S^2 of the geometric twistor spaces $T(M^4) = M^4 \times S^2(M^4)$ and of T_{CP_2} having $S^2(CP_2)$ as fiber space. What this means that one can take the coordinates of say $S^2(M^4)$ as coordinates and imbedding map maps $S^2(M^4)$ to $S^2(CP_2)$. The twistor spheres $S^2(M^4)$ and $S^2(CP_2)$ have in the minimal scenario same radius $R(CP_2)$ (radius of the geodesic sphere of CP_2. The identification map is unique apart from $SO(3)$ rotation R of either twistor sphere. Could one consider the possibility that R is not trivial and that the induced Kähler forms could almos cancel each other?

2. The induced Kähler form is sum of the Kähler forms induced from $S^2(M^4)$ and $S^2(CP_2)$ and since Kähler forms are same apart from a rotation in the common S^2 coordinates, one has $J_{ind} = J + R(J)$, where R denotes the rotation. The sum is $J_{ind} = 2J$ if the relative rotation is trivial and $J_{ind} = 0$ if R corresponds to a rotation $\Theta \to \Theta + \pi$ changing the sign of $J = sin(\Theta) d\Theta \wedge d\Phi$.

3. Could p-adic length scale evolution for Λ correspond to a sequence of rotations - in the simplest case $\Theta \to \Theta + \Delta_k \Theta$ taking gradually J from $2J$ at very short length scales to $J = 0$ corresponding to $\Delta_\infty \Theta = \pi$ at very long length scales? A suitable spectrum for $\Delta_k(\Theta)$ could reproduce the proposal $\Lambda \propto 2^- k$ for Λ.

4. One can of course ask whether the resulting induced twistor structure is acceptable. Certainly it is not equivalent with the standard twistor structure. In particular, the condition $J^2 = -g$ is lost. In the case of induced Kähler form at X^4 this condition is also lost. For spinor structure the induction guarantees the existence and uniqueness of the spinor structure, and the same applies also to the induced twistor structure being together with the unique properties of twistor spaces of M^4 and CP_2 the key motivation for the notion.

5. Could field equations associated with the dimensional reduction allow p-adic length scale evolution in this sense?

   (a) The sum $J + R(J)$ defining the induced Kähler form in $S^2(X^4)$ is covariantly constant since both terms are covariantly constant by the rotational covariance of J.

   (b) The imbeddings of $S^2(X^4)$ as twistor sphere of space-time surface to both spheres are holomorphic since rotations are represented as holomorphic transformations. This in turn implies that the second fundamental form in complex coordinates is a tensor having only components of type $(1,1)$ and $(-1,-1)$ whereas metric and energy momentum tensor have only components of type $(1,-1)$ and $(-1,1)$. Therefore all contractions appearing in field equations vanish identically and $S^2(X^4)$ is minimal surface and Kähler current in $S^2(X^4)$ vanishes since it involves components of the trace of second fundamental form. Field equations are indeed satisfied.

   (c) The solution of field equations becomes a family of space-time surfaces parametrized by the values of the cosmological constant Λ as function of S^2 coordinates satisfying $\Lambda/8\pi G = \rho_{vac} = J \wedge (*J)(S^2)$. In long length scales the variation range of Λ would become arbitrary small.

6. If the minimal surface equations solve separately field equations for the volume term and Kähler action everywhere apart from a discrete set of singular points, the cosmological constant affects the space-time dynamics only at these points. The physical interpretation of

these points is as seats of fundamental fermions at partonic 2-surface at the ends of light-like 3-surfaces defining their orbits (induced metric changes signature at these 3-surfaces). Fermion orbits would be boundaries of fermionic string world sheets.

One would have family of solutions of field equations but particular value of Λ would make itself visible only at the level of elementary fermions by affecting the values of coupling constants. p-Adic coupling constant evolution would be induced by the p-adic coupling constant evolution for the relative rotations R for the two twistor spheres. Therefore twistor lift would not be mere manner to reproduce cosmological term but determine the dynamics at the level of coupling constant evolution.

7. What is nice that also $\Lambda = 0$ option is possible. This would correspond to the variant of TGD involving only Kähler action regarded as TGD before the emergence of twistor lift. Therefore the nice results about cosmology obtained at this limit would not be lost.

6.10.2 The notion of magnetic body

Magnetic flux tubes and field body/magnetic body (MB) are basic notions of TGD implied by the modification of Maxwellian electrodynamics [K62, K27, K47]. Actually a profound generalization of space-time concept is in question. Magnetic flux tubes are in well-defined sense building bricks of space-time - topological field quanta - and lead to the notion of field body/MB as a field identity assignable to any physical system: in Maxwell's theory and ordinary field theory the fields of different systems superpose and one cannot say about magnetic field in given region of space-time that it would belong to some particular system. In TGD only the effects on test particle for induced fields associated with different space-time sheets with overlapping M^4 projections sum.

The hierarchy of Planck constants $h_{eff} = n \times h_0$, where h_0 is the minimum value of Planck constant, is second key notion. h_0 need not correspond to ordinary Planck constant h and both the observations of Randell Mills [L23] and the model for color vision [L42] suggest that one has $h = 6h_0$. The hierarchy of Planck constants labels a hierarchy of phases of ordinary matter behaving as dark matter.

Magnetic flux tubes would connect molecules, cells and even larger units, which would serve as nodes in (tensor-) networks [B12] [L22]. Flux tubes would serve as correlates for quantum entanglement and replace wormholes in ER-EPR correspondence proposed by Leonard Susskind and Juan Maldacena in 2014 (see `http://tinyurl.com/y7za98cn` and `http://tinyurl.com/ydckw5u7`). In biology and neuroscience these networks would be in a central role. For instance, in brain neuron nets would be associated with them and would serve as correlates for mental images [L28, L43]. The dynamics of mental images would correspond to that for the flux tube networks.

6.10.3 Hierarchy of Planck constants, space-time surfaces as covering spaces, and adelic physics

From the beginning it was clear that $h_{eff}/h = n$ corresponds to the number of sheets for a covering space of some kind. First the covering was assigned with the causal diamonds. Later I assigned it with space-time surfaces but the details of the covering remained unclear. The final identification emerged only in the beginning of 2017.

Number theoretical universality and hierarchy of extensions of rationals

Number theoretical universality (NTU) leads to the notion of adelic space-time surface (monadic manifold) involving a discretization in an extension of rationals defining particular level in the hierarchy of adeles defining evolutionary hierarchy. The formulation of this vision is proposed in [L25, L34, L35].

The key constraint is NTU for adelic space-time containing sheets in the real sector and various padic sectors, which are extensions of p-adic number fields induced by an extension of rationals which can contain also powers of a root of e inducing finite-D extension of p-adic numbers (e^p is ordinary p-adic number in Q_p).

One identifies the numbers in the extension of rationals as common for all number fields and demands that imbedding space has a discretization in an extension of rationals in the sense that the preferred coordinates of imbedding space implied by isometries belong to extension of rationals for the points of number theoretic discretization. This implies that the versions of isometries with group parameters in the extension of rationals act as discrete versions of symmetries. The correspondence between real and p-adic variants of the imbedding space is extremely discontinuous for given adelic imbedding space (there is hierarchy of them with levels characterized by extensions of rationals). Space-time surfaces typically contain rather small set of points in the extension ($x^n + yn^2 = z^n$ contains no rationals for $n > 2$!). Hence one expects a discretization with a finite cutoff length at space-time level for sufficiently low space-time dimension $D = 4$ could be enough.

After that one assigns in the real sector an open set to each point of discretization and these open sets define a manifold covering. In p-adic sector one can assign 8:th Cartesian power of ordinary p-adic numbers to each point of number theoretic discretization. This gives both discretization and smooth local manifold structure. What is important is that Galois group of the extension acts on these discretizations and one obtains from a given discretization a covering space with the number of sheets equal to a factor of the order of Galois group.

Effective Planck constant as dimension of extension of rationals and number of sheets of space-time surface as covering space

$h_{eff}/h_0 = n$ was identified from the beginning as the number of sheets of poly-sheeted covering assignable to space-time surface. The number n of sheets would naturally a factor of the order of Galois group implying $h_{eff}/h = n$ bound to increase during number theoretic evolution so that the algebraic complexity increases. Note that WCW decomposes into sectors corresponding to the extensions of rationals and the dimension of the extension is bound to increase in the long run by localizations to various sectors in self measurements [K32]. Dark matter hierarchy represents number theoretical/adelic physics and therefore has now rather rigorous mathematical justification. It is however good to recall that $h_{eff}/h = n$ hypothesis emerged from an experimental anomaly: radiation at ELF frequencies had quantal effects of vertebrate brain impossible in standard quantum theory since the energies $E = hf$ of photons are ridiculously small as compared to thermal energy.

Indeed, since n is positive integer evolution is analogous to a diffusion in half-line and n unavoidably increases in the long run just as the particle diffuses farther away from origin (by looking what gradually happens near paper basket one understands what this means). The increase of n implies the increase of maximal negentropy and thus of negentropy. Negentropy Maximization Principle (NMP) follows from adelic physics alone and there is no need to postulate it separately. Things get better in the long run although we do not live in the best possible world as Leibniz who first proposed the notion of monad proposed!

Formula for the gravitational Planck constant and some background

The formula

$$\hbar_{gr} = \frac{GM_D m}{v_0} \tag{6.10.1}$$

for the gravitational Planck constant was originally introduced by Nottale [E5]. Here v_0 is a parameter with dimensions of velocity: I have considered argument allowing to deduce information about the value of $\beta_0 = v_0/c$ as the ratio of the M^4 size of the system and the size of its magnetic body [L39]. Values of order $\beta_0 \sim 10^{-3}$ are encountered.

Since m disappears from the predictions by Equivalence Principle it is not at all clear what kind limitations one has for m and one can even assume that m corresponds to particle mass without change in predictions. In Nottale's original formula m is mass of planet and M_D the mass of Sun but m could be even mass of elementary particle without change in predictions. The assumption has been $m/M_D << 1$. The replacement of M_D with total mass $M_D + m$ and m by reduced mass $M_D m/(M_D + m)$ does not affect the formula and the asymmetry between m and M_D would become more natural asymmetry between total mass and reduced mass.

For $Mm < v_0 m_{Pl}^2$ one must have $h_{gr} = h$, which suggests that quite generally one must have $m \geq \sqrt{v_0} M_{Pl}$ and $M \geq \sqrt{v_0} M_{Pl}$. The formula is non-relativistic but one can consider a relativistic generalization in which m and M are replaced by energies [K37] .

The formula is expected to hold true at the magnetic flux tubes mediating gravitational interaction. M_D has been interpreted as dark gravitational flux at the gravitational flux tubes with a fixed value of h_{eff} and should be a fraction of the total gravitational flux M. These flux tubes define $n_{gr} = h_{eff}/h_0$-sheeted covering of M^4.

Also a more general formula

$$h_{gr} = h_{eff} \quad , \quad h_{eff} = n_{gr} \times h_0 \quad , \quad h = 6h_0 \quad . \tag{6.10.2}$$

has been assumed. The support for the formula $h = 6h_0$ is discussed in [L23, L42]. The value of h_{gr} can be very large unlike the value of h_{eff} associated with say valence bonds.

One important implication of the formula is that the cyclotron energy spectrum does not depend on the mass of charged particle at all and is therefore universal. The assumption has been that the spectrum is in visible and UV range assignable to bio-photons [K65, K66]. One can however consider also the possibility that also the energies between the thermal energy at physiological temperature and visible photon energies are allowed.

What does one really mean with gravitational Planck constant?

There are important questions related to the QFT-GRT limit of TGD.

1. What does one mean with space-time as covering space?

The central idea is that space-time corresponds to n-fold covering for $h_{eff} = n \times h_0$. It is not however quite clear what this statement does mean.

1. How the many-sheeted space-time corresponds to the space-time of QFT and GRT? QFT-GRT limit of TGD is defined by identifying the gauge potentials as sums of induced gauge potentials over the space-time sheets. Magnetic field is sum over its values for different space-time sheets. For single sheet the field would be extremely small in the present case as will be found.

2. A central notion associated with the hierarchy of effective Planck constants $h_{eff}/h_0 = n$ giving as a special case $\hbar_{gr} = GMm/v_0$ assigned to the flux tubes mediating gravitational interactions. The most general view is that the space-time itself can be regarded as n-sheeted covering space. A more restricted view is that space-time surface can be regarded as n-sheeted covering of M^4. But why not n-sheeted covering of CP_2? And why not having $n = n_1 \times n_2$ such that one has n_1-sheeted covering of CP_2 and n_2-sheeted covering of M^4 as I indeed proposed for more than decade ago [K39] but gave up this notion later and consider only coverings of M^4? There is indeed nothing preventing the more general coverings.

3. $n = n_1 \times n_2$ covering can be illustrated for an electric engineer by considering a coil in very thin 3 dimensional slab having thickness L. The small vertical direction would serve and as analog of CP_2. The remaining 2 large dimensions would serve as analog for M^4. One could try to construct a coil with n loops in the vertical direction direction but for very large n one would encounter problems since loops would overlap because the thickness of the wire would be larger than available room L/n. There would be some maximum value of n, call it n_{max}.

   One could overcome this limit by using the decomposition $n = n_1 \times n_2$ existing if n is prime. In this case one could decompose the coil into n_1 parallel coils in plane having $n_2 \geq n_{max}$ loops in the vertical direction. This provided n_2 is small enough to avoid problems due to finite thickness of the coil. For n prime this does not work but one can of also select n_2 to be maximal and allow the last coil to have less than n_2 loops.

   An interesting possibility is that that preferred extremal property implies the decomposition $n_{gr} = n_1 \times n_2$ with nearly maximal value of n_2, which can vary in some limits. Of course, one of the n_2-coverings of M^4 could be in-complete in the case that n_{gr} is prime or not divisible by nearly maximal value of n_2. We do not live in ideal Universe, and one can even imagine that the copies of M^4 covering are not exact copies but that n_2 can vary.

4. In the case of $M^4 \times CP_2$ space-time sheet would replace single loop of the coil, and the procedure would be very similar. A highly interesting question is whether preferred extremal property favours the option in which one has as analog of n_1 coils n_1 full copies of n_2-fold coverings of M^4 at different positions in M^4 and thus defining an n_1 covering of CP_2 in M^4 direction. These positions of copies need not be close to each other but one could still have quantum coherence and this would be essential in TGD inspired quantum biology [L41].

   Number theoretic vision [L34, L35] suggests that the sheets could be related by discrete isometries of CP_2 possibly representing the action of Galois group of the extension of rationals defining the adele and since the group is finite sub-group of CP_2, the number of sheets would be finite.

   The finite sub-groups of $SU(3)$ are analogous to the finite sub-groups of $SU(2)$ and if they action is genuinely 3-D they correspond to the symmetries of Platonic solids (tetrahedron,cube,octahedron, icosahedron, dodecahedron). Otherwise one obtains symmetries of polygons and the order of group can be arbitrary large. Similar phenomenon is expected now. In fact the values of n_2 could be quantized in terms of dimensions of discrete coset spaces associated with discrete sub-groups of $SU(3)$. This would give rise to a large variation of n_2 and could perhaps explain the large variation of G identified as $G = R^2(CP_2)/n_2$ suggested by the fountain effect of superfluidity [L48].

5. There are indeed two kinds of values of n: the small values $n = h_{em}/h_0 = n_{em}$ assigned with flux tubes mediating em interaction and appearing already in condensed matter physics [L31, L42, L23] and large values $n = h_{gr}/h_0 = n_{gr}$ associated with gravitational flux tubes. The small values of n would be naturally associated with coverings of CP_2. The large values $n_{gr} = n_1 \times n_2$ would correspond n_1-fold coverings of CP_2 consisting of complete n_2-fold coverings of M^4. Note that in this picture one can formally define constants $\hbar(M^4) = n_1\hbar_0$ and $\hbar(CP_2) = n_2\hbar_0$ as proposed in [K39] for more than decade ago.

2. Planck length as CP_2 radius and identification of gravitational constant G

There is also a puzzle related to the identification of gravitational Planck constant. In TGD framework the only theoretically reasonable identification of Planck length is as CP_2 length $R(CP_2)$, which is roughly $10^{3.5}$ times longer than Planck length [L48]. Otherwise one must introduce the usual Planck length as separate fundamental length. The proposal was that gravitational constant would be defined as $G = R^2(CP_2)/\hbar_{gr}$, $\hbar_{gr} \simeq 10^7\hbar$. The G indeed varies in un-expectedly wide limits and the fountain effect of superfluidity suggests that the variation can be surprisingly large.

There are however problems.

1. Arbitrary small values of $G = R^2(CP_2)/\hbar_{gr}$ are possible for the values of $\hbar_{gr}$ appearing in the applications: the values of order $n_{gr} \sim 10^{13}$ are encountered in the biological applications. The value range of G is however experimentally rather limited. Something clearly goes wrong with the proposed formula.

2. Schwartschild radius $r_S = 2GM = 2R^2(CP_2)M/\hbar_{gr}$ would decrease with $\hbar_{gr}$. One would expect just the opposite since fundamental quantal length scales should scale like $\hbar_{gr}$.

3. What about Nottale formula [E5] $\hbar_{gr} = GMm/v_0$? Should one require self-consistency and substitute $G = R^2(CP_2)/\hbar_{gr}$ to it to obtain $\hbar_{gr} = \sqrt{R^2(CP_2)Mm/v_0}$. This formula leads to physically un-acceptable predictions, and I have used in all applications $G = G_N$ corresponding to $n_{gr} \sim 10^7$ as the ratio of squares of CP_2 length and ordinary Planck length.

Could one interpret the almost constancy of G by assuming that it corresponds to $\hbar(CP_2) = n_2\hbar_0$, $n_2 \simeq 10^7$ and nearly maximal except possibly in some special situations? For $n_{gr} = n_1 \times n_2$ the covering corresponding to $\hbar_{gr}$ would be n_1-fold covering of CP_2 formed from n_1 n_2-fold coverings of M^4. For l $n_{gr} = n_1 \times n_2$ the covering would decompose to n_1 disjoint M^4 coverings and this would also guarantee that the definition of r_S remains the standard one since only the number of M^4 coverings increases.

If n_2 corresponds to the order of finite subgroup G of $SU(3)$ or number of elements in a coset space G/H of G (itself sub-group for normal sub-group H), one would have very limited number of values of n_2, and it might be possible to understand the fountain effect of superfluidity [L48] from the symmetries of CP_2, which would take a role similar to the symmetries associated with Platonic solids. In fact, the smaller value of G in fountain effect would suggest that n_2 in this case is larger than for G_N so that n_2 for G_N would not be maximal.

New constraint between h_{gr} and h_{eff}

Cyclotron frequencies and energies in magnetic field B and charged particle with charge Ze and mass m are proportional to the ZeB/m. The energy spectrum of bio-photons would be covered by a spectrum of magnetic field strengths B. A special field strength $B_{end} = 0.2$ Gauss has emerged in biological applications from the beginning and the first guess is that it defines a lower bound for the spectrum of visible photon energies [L40, L37, L51]. One can fix the value of h_{gr} and therefore of GM_D/v_0 if one requires that dark photon frequency of say $f_l = 10$ Hz corresponds to the lower bound $f_h = 400$ THz for visible frequencies as $h_{gr} = f_h/f_l$: in this case would would have $n_{gr} = 4 \times 10^{13}$.

The variation of B means variation of cyclotron frequency and I have proposed that the audible frequencies correspond to a spectrum of B for the flux tubes involved with hearing [K43], and that even 12-note scale represent in terms of rational frequency ratios might have a preferred role [L12, L50].

The formula $h_{gr} = h_{eff}$ is not enough to fix the model completely. A formula fixing the relationship between B and GM_D/v_0 would be needed. This formula should be consistent with $h_{gr} = h_{eff}$. Dimensional analyst would start from the geometry of the situation.

Magnetic flux tubes are characterized by two parameters: length L_c and radius R_B.

1. Length scale naturally corresponds to the cyclotron wave length

$$L_c = \lambda_c = \frac{1}{f_c} = \frac{2\pi m}{ZeB} \quad . \tag{6.10.3}$$

   L_c is proportional to the mass m of the charged particle so that charge particles with different mass are with different mass flux tubes with different length and therefore different onion-like layers of MB. Charged dark particles are like books about different topics at different shelves so that living matter is extremely well-organized: something totally different from a chaotic soup of charged ions.

2. The radius of the flux tube is obtained from the flux quantization. For ordinary cylindrical flux tube with constant B the condition is $BS = k\hbar$ and for $S = \pi R^2$ the radius would be

$$R_B(h,k) = \sqrt{\frac{k\hbar}{\pi eB}} = \sqrt{\frac{k}{\pi}} L_B \quad , \quad L_B = \sqrt{\frac{\hbar}{eB}} \quad . \tag{6.10.4}$$

   .

   For $k = 1$ and for $B = B_{end} = .2$ Gauss one has $R_B(h,1) = 3.3$ μm to be compared with p-adic length scale $L(167) = 2.5$ μm assignable to Gaussian Mersenne $M_{G,167} = (1+i)^{167} - 1$. Magnetic length L_B is in this case $L_B = 5.8$ μm slightly larger than $L(169)$.

3. For $h_{eff} = n \times h_0$, $h = 6h_0$ the formula would generalize to

$$R_B(h_{eff},k) = \sqrt{\frac{k\hbar_{eff}}{\pi eB}} = \sqrt{\frac{n}{6}} R_c(h,k) = \sqrt{\frac{nk}{6}} R_B(h,1) \quad . \tag{6.10.5}$$

   Note that here n is rather small such as the value of n assignable to valence bonds.

4. The natural guess is that this formula applies at the small part of the MB restricted to the "biological body" of the living system defining that part of system, which corresponds to relatively small values of h_{eff}. The value of h_{eff} would indeed vary, being larger than h for instance for valence bonds [L31]. For dark flux tubes with small value of n the radius would be scaled up by $\sqrt{n}$ such as biological system for fixed value of B. Same happens if the value of flux is scaled by m.

   For the simplest flux tubes carrying monopole flux having string world sheet as M^4 projection geodesic sphere as CP_2 projection, the cross section is not circular disk but CP_2 geodesic sphere with radius R. I this case R is fixed. The M^4 projection of these objects is however unstable against thickening and for spherical cross section- think of two disks glued along boundaries but having different CP_2 projections, the area is $4\pi R^2$, where R corresponds to the radius of M^4 projection. Area is reduced by factor 4 from that for non-monopole flux tube and radius is reduced by factor 1/2.

One can guess the additional constraint on h_{gr} without more detailed analysis of what MB really is using dimensional analysis and I will postpone this analysis later.

1. The first natural guess is that one has

$$\frac{h_{gr}}{h_0} = n_{gr} = x\frac{L_c}{R_B(h_{eff},k)} = x(6\pi)^{3/2}\frac{1}{(nk)^{1/2}}\frac{L_B}{l_C(m)} \quad ,$$
$$L_B = \sqrt{\frac{\hbar}{eB}} \quad , \quad l_C(m) = \frac{\hbar}{m} \quad . \tag{6.10.6}$$

   x is some numerical constant. h_{gr}/h_0 is proportional to the ratio l_B/l_C of the magnetic length and Compton length $l_C = m/\hbar$ of the charged particle.

2. Alternative guess replaces the radius of the magnetic flux tube with the magnetic length L_B.

$$\frac{h_{gr}}{h_0} = n_{gr} = x\frac{L_c}{L_B} == x6^{3/2}\pi\frac{1}{n^{1/2}}\frac{L_B}{L_C(m)} \quad , \tag{6.10.7}$$

   This formulas is related by factor $\sqrt{k}pi$ the first formula and has no dependence on h. It is difficult to say anything about exact value of the numerical constant x.

3. h_{gr} is proportional to m so that the formulas are consistent with $h_{gr} = h_{eff}$ formula. Combining these formulas one obtains

$$\frac{GM_D}{h_0 v_0} = \frac{r_S(M_D)}{2} = x2\pi\sqrt{\frac{n}{6Z}}\sqrt{\frac{\hbar}{eB}} \quad . \tag{6.10.8}$$

   This formula does not depend on m and gives the value of GM_D/v_0 assignable to the flux tubes carrying magnetic field with strength B and particles with charge Z. One can say that the Schwartschild radius $r_S = 2GM_D$ characterixing M_D is proportional to magnetic length. The first option gives

$$r_S(M_D) = x \times 2 \times 6^{1/2}\pi^{3/2}\frac{1}{(nk)^{1/2}}v_0 l_B \quad . \tag{6.10.9}$$

   For Earth Schwartschild radius is $r_{S,E} = 8.87$ mm and if $M_D < M_E$ holds true, one obtains for a given value of v_0 upper bound for the magnetic length and therefore lower bound for

B. I have considered in [L39] a model for v_0 and combining this model for this formula, one obtains rather strong constraints on the parameters and also on the minimal value of B. The order of magnitude for v_0 is $v_0 \sim 10^{-3}$.

M_D/v_0 would not depend on the mass of the charged particles at the flux tube (universality) but would depend on their charge Z unless the parameter x has a compensating $Z-$dependence. Therefore electrons and their Cooper pairs would have different value of GMD/v_0. One could perhaps interpret r_S/v_0 as analog of star radius applying to particular dark matter part of Earth. It would be considerably larger than Schwartchild radius.

4. Note that the condition $GM_Dm/v_0 = n_{gr}\hbar$ can be written as

$$r_S(M_D) = 2n_{gr}l_C \quad . \tag{6.10.10}$$

Estimate of G/G_N from the delocalization at magnetic flux tubes

The following argument is for a situation in which the mass m corresponds to the mass of ion. By Equivalence Principle m however disappears from the formulas involving gravitational interaction of Earth, and cyclotron frequencies remain invariant for cyclotron BE condensate. Therefore the formulas apply for the BE condensate ions with total mass equal to a multiple of Planck mass $m_P = \hbar_0/R$.

The de-localization length of dark matter wave functions in the gravitational field is much longer than for ordinary value of Planck constant: essentially the height to which particle can rise with given initial velocity V_0 in the gravitational field with gravitational constant G. This would conform with the idea that dark particles are delocalized at the flux tubes in the scale of cyclotron wave-length.

The condition that the height h for the orbit equals to cyclotron wavelength gives an estimate for G_N/G. One can estimate the height $h = R - R_E$ from energy conservation assuming that particle has initial vertical velocity V_0 at the surface of Earth and cyclotron wavelength λ_c:

$$\frac{V_0^2}{2} = \frac{G}{G_N}\left[\frac{GM}{R_E} - \frac{GM}{R}\right] \quad ,$$

$$h = \lambda_c = \frac{1}{f_c} = \frac{2\pi m}{neB} \quad .$$

One obtains an estimate for G/G_N as

$$\frac{G}{G_N} = V_0^2\frac{(R_E+h)R_E}{r_S h} \quad , \qquad R = R_E + h \quad ,$$

$$h = \frac{\lambda_c}{n} = \frac{1}{nf_c} = \frac{2\pi m}{neB} \quad . \tag{6.10.11}$$

This gives

$$\frac{G}{G_N} = nV_0^2 \times \frac{R_E(R_E+\frac{\lambda_c}{n})}{r_S\lambda_c} = nV_0^2 \times \frac{R_E(R_E+\frac{2\pi eB}{neBm})}{r_S} \times \frac{eB}{2\pi m} \quad . \tag{6.10.12}$$

The condition that value of G/G_N is constant quantizes the value of V_0. For small value of h one has $V_0^2 n \simeq constant$. For $R_E \sim \lambda_c$ and nV_0^2 is of order unity, the order of magnitude would be $G/G_N \sim R_E/r_S \sim 7 \times 10^8$.

6.10.4 What can one say about the detailed anatomy of the MB?

The details of the anatomy of the MB have remained rather fuzzy hitherto. The following is an attempt to formulate more explicitly and coherently the earlier ideas scattered in books and articles about TGD. There are several empirical facts and theoretical constraints that one can use.

1. There is the notion of dark DNA as dark nuclei consisting of sequences of dark protons. The notion of dark nucleus is central concept in TGD based model of "cold fusion" [L29]. Dark proton sequences are parallel with and in the vicinity of ordinary DNA strands and ordinary codons and dark proton triplets representing them [L21] are paired.

2. Pollack effect [L15] [L15] for water is assumed to generate dark DNA. Part of protons go to the flux tube and negative charge is generated in ordinary matter and ends to negative charge of phosphates associated with the ordinary DNA nucleotides. Ordinary DNA would pair with dark DNA serving as predecessor and controller of ordinary DNA. Also RNA, amino-acids, and tRNA would have dark predecessors and similar pairing would occur.

3. Experiments of Peter Gariaev et al - in particular the discovery of phantom DNA [I82] - and of Montagnier [I95] [L8] provide further valuable information.

Consider now what MB could look like.

1. MB has two parts. The small part has size of the physical system consisting of ordinary matter plus parts with relatively small h_{eff} assignable to structures such as valence bonds. The flux tubes of this part of MB connect parts of the system to a network and tensor network is an excellent mathematical model for what is involved. Flux tubes serve as topological correlates for entanglement and even prerequisites for it.

   In living matter one can imagine that the basic units of ordinary matter - say cells - are organized at parallel flux tubes. For $B_{end} = .2$ Gauss, which seems to define an especially important endogenous magnetic field, the radius r_B is of cell size. The value of proton cyclotron frequency is 300 Hz in this case and happens to correspond to the rotation frequency of the "shaft" of the ATPase as power generator.

   60 Hz frequency was found to lead to a transformation of cancer cells to ordinary ones and this suggests that cyclotron frequency for $B = B_{end}/5$ is involved. The flux tubes would contain 5 cells in their cross section and one can argue that dark proton quantum coherence at gravitational flux tubes with this thickness could give rise coherence in 5-cell length scale and lead to the cure of cancer.

2. The large part of MB - with size of the order Earth radius for $f_c = 60$ Hz corresponds to long flux tubes with large effective Planck constant $h_{gr}/h_0 = n$. Effective value of Planck constant is indeed in question since n_{gr} is the number sheets of the space-time surface as covering space and Planck constant has value h_0 (rather than $h = 6h_0$) at each sheet of the covering. At QFT limit sheets are effectively replaced with single one, and one must allow the "real" Planck constant to have non-standard values.

   What space-time surface as covering does mean has been already discussed, and it seems that the identification as $n = n_1 \times n_2$ covering, where n_1 is the number of sheets as covering of CP_2 realized in the recent case as disjoint flux tubes in M^4 and n_2 is the number of sheets as covering of M^4. Gravitational constant identified as $G = R^2/\hbar_2$ would allow to avoid unphysical predictions since n_2 could be limited to a rather narrow range by symmetry considerations.

   The cyclotron energies are scaled up by $h_{eff}/h_0 = n_{gr}$ and whatever the detailed anatomy of MB is this must be understood. Effectively one has n_{gr} photons with ordinary cyclotron energy and their energies sum up. This can be understood if the flux tubes define n_{gr}-fold coverings of M^4.

3. $h_{gr} = n_{gr}h_0$ correspond to quantum coherence in very long length scales whereas in the scale of organism the value of n is relatively small. The simplest idea is that n_{gr} disjoint flux tubes with small value of n and with given thickness determined by flux quantization coming

from the living system combine to form single n_{gr}-sheeted flux tube with length given by $L_c = \lambda_c = 2\pi m/ZeB$ having no dependence on h_{eff}.

This would be like a large number of cables combining a single cable. The threads of the cable would be now on top of each other in CP_2 direction! A rather exotic space savings! This would combine the sensory information coming from the separate flux tubes to a single super-cable and make the control of the system easy. Central nervous system would have spinal chord as an analogous unit both geometrically and functionally albeit in totally different scale. One of the first proposals was that MB provides an almost topographic representation of the biological body [K28].

One can estimate the volume of the region with coherence forced by quantum gravitational coherence as $V_{gr} = n_{gr}V(unit)$, where $V(unit)$ is the volume of the basic unit presumably determined by flux tube radius. If $V(unit)$ equals to volume a^3 of cube with side a, V_{gr} corresponds to a cube with side $a_{gr} = n_{gr}^{1/3}a$.

The assumption that the energies of EEG photons in alpha band with $f = 10$ Hz correspond to ordinary photons at the lower end of the bio-photon spectrum having frequency 400 THz gives n_{gr} as $n_{gr} = 4 \times 10^{13}$. For $n_{gr} = 4 \times 1013$ and $a = 5$ μ m giving lower bound for the volume of neuron one would have $a_{gr} = 0.2$ m, roughly the size scale of brain.

4. The natural interpretation of the super-cables is as gravitational flux tubes. The gravitational flux associated with the ordinary flux tubes would combine to the dark gravitational flux tubes involving n_1 parallel flux tubes in M^4, each of them consisting of n_2 flux tubes on top of each other in CP_2 direction. This combination could take place repeatedly. Could the parameter M_D in $h_{gr} = n_{gr}h_0$ correspond to the portion of the Earth's gravitational flux flowing along these flux tubes? The sum of the masses M_D should over values of field strengths and charged particle masses should give the total mass M_E of Earth if the guess is correct.

   One must of course be extremely cautious in interpretations. For instance, flux tubes carrying Kähler charge the flux tubes should be closed and give rise to a kind of Dirac monopole like structure with return flux. This would mean that gravitational flux returns back, possibly along different space-time sheets. But the flux lines are closed also for the ordinary magnetic fields. Can this really be consistent with the Newtonian view about gravitation in which gravitational flux flows to infinity? The answer is far from obvious: the many-sheeted space-time in which space-time sheets are glued along the boundaries would that part of the flux can return and part goes to larger space-time sheets and in principle there is no largest space-time sheet so that one would obtain effectively monopoles.

5. An entire fractal hierarchy of magnetic field strengths is predicted. A good guess is that field strengths are given by p-adic length scale hypothesis, that is have scales given by $B(k) \propto 1/L(k)^2$, where $L(k) \propto 2^{k/2}$ is the p-adic length scale assignable to $p \simeq 2^k$. This would mean hierarchy of flux tubes with radii $L(k)$ and at each level the combination to super-cables representing gravitational flux tubes would take place.

   One has $M_D \propto v_0/\sqrt{B} \propto v_0 2^{k/2}$. For a fixed value of v_0, the sum can converge only if the number of p-adic length scales involved is finite. The radius R_E of Earth certainly gives this kind of upper bound and corresponds to a rather modest value of k ($L(151)$ correspond to 10 nm) . Also v_0 can depend on p-adic length scale. The sizes of living organisms give a more stringent upper bound on k.

6.10.5 Water memory and homeopathy

There is a lot of support about the representation of water memory as extremely low frequencies (ELF) of radiation associated with water [I71, I72]. These ELF frequencies can be stored electronically and they produce the same effects as the bio-active chemical, whose presence induced these frequencies in water. At the age of IT the idea about the existence of representations of bio-active molecules as frequency patterns able to induce the biological effects of molecules without the presence of molecules should not raise grave objections. For instance, brain generates this kind of representations by entrainment to external frequencies and water might play a crucial

role also here. Few years ago HIV Nobelist Montagnier did experiments giving support for water memory and the procedure involved a part very similar to that used in preparing homeopathic remedies [I95] [L8].

The description of water memory in TGD Universe would look like follows.

1. In TGD framework these frequencies would correspond to cyclotron frequencies assignable to MBs of molecules, and immune system is proposed to have emerged from the ability of water to mimic the MBs of invader molecules and learning to recognize them [K24] by resonant coupling at these frequencies.

   This would take place via entrainment made possible by the variation of the thickness of the flux tube inducing variation of the cyclotron frequency. In entrainment the cyclotron frequency of the flux tube would co-incide with the external frequency. MB having flux tubes with modified thickness would be able to produce cyclotron radiation at the these frequencies and couple to the invader molecule resonantly. The coupling would involve also topological part as reconnection of flux tubes with same thickness and carrying same charged particles to make resonance possible.

   One can visualize living systems as systems having magnetic tentacles consisting of U-shaped flux tubes forming thus locally pairs of flux tube tubes and searching for flux similar flux tubes of other systems, in particular bio-active molecules. The recognition of invader molecules is a crucial part of immune systems and this mechanism would be an essential part of immune action besides cyclotron resonance.

2. In TGD universe water is very special substance in that it contains both ordinary water and its dark variant. What makes it dark is that dark magnetic flux tubes representing long hydrogen bonds are present for some portion of water [L49] (see `http://tinyurl.com/y8fvwbp9`): the length of bonds scales as n or perhaps even n^2. The presence of these flux tubes makes any liquid phase a network like structure, and one ends up with a model explaining an anomaly of thermodynamics of liquids at criticality known already in Maxwell's time. This leads to a model explaining the numerous anomalies of water in terms of the dark matter.

   For instance, the dark part of water with non-standard Planck constant transforms to ordinary water in freezing. As a consequence, a large amount of energy is liberated. This explains why water has anomalously large latent heat of fusion. One can also understand why the volume of water increases in freezing and decreases in heating in the interval 0-4 °C. The anomalies of water are largest at physiological temperature $T_{phys} \sim 37$ °C suggesting that the dark portion of water is largest at T_{phys}. Dark fraction of water would be essential for life.

3. Pollack effect [L15] (see `http://tinyurl.com/oyhstc2`) requiring feed of energy - as IR radiation for instance - generates so called exclusion zones (EZs), which are negatively charged regions. A fraction of protons from water must go somewhere and the TGD inspired proposal [L15] (see `http://tinyurl.com/gwasd8o`) is that the protons transform to dark protons at magnetic flux tubes. The dark variants of particles quite generally have higher energies than ordinary ones and energy feed provides the needed metabolic energy go make the protons dark. In the case of homeopathy and water memory mechanical agitation creates provides the metabolic energy and would generate EZs accompanied by dark proton sequencies at flux tubes [K24].

4. The MB of water would be also a key central part of MB of the living system acting as intentional agent receiving sensory input from biological body and controlling it. Biochemistry would be kind of shadow dynamics. The ions provided by the living system would reside at the flux tubes of MB provided by water and as found the lengths of flux tubes and also the value of $h_{eff} = h_{gr}$ at the would distinguish between different ions. The gravitational flux tubes formed by combination of n_{gr} ordinary flux tubes to n_{gr} flux tubes with the same M^4 projection defining a covering of M^4 would define the large part of MB serving as intentional agent and communications would occur at cyclotron frequencies.

   Cell membranes would produce what I call generalized Josephson radiation, which would couple resonantly to cyclotron Bose-Einstein condensates at the flux tubes. Nerve pulse

patterns would induce frequency modulation allowing to code sensory input represented by them and send it to MB which in turn could send control signals through genome [K44, K15, K17, K53].

MB would be the seat of primary form of genetic code. Dark protons sequences at flux tubes representing genetic code [L21] and the analogs of the other basic biomolecules are realized in water.

6.10.6 What the view about magnetic body could mean at the level of DNA and other basic bio-molecules?

A more precise vision about the anatomy of MB leads to a flux of ideas and questions. Flux tubes from identical basic units (cells, DNA, identical proteins, etc) combine to form single many-sheeted flux tube so that the incoming flux tubes have same M^4 projection being on top of each other in CP_2 direction. This super cable is like umbilical chord! The structures form a Bose-Einstein condensate in abstract topological sense.

This opens fascinating possibilities for understanding of dark DNA..

1. Cells have identical DNAs. Earlier I have assumed that magnetic flux sheets go through DNA in transversal direction and that dark DNA in some sense is sequence of dark proton triplets associated with flux tubes. Furthermore, DNA transcription requires that there are transversal flux tubes emerging from codons or perhaps even from nucleotides as flux tubes inside codon flux tube.

   How to combine these views together with new view about combination of the DNAs flux tube to larger superstructure, one DNA from each cell in structure?

2. For single DNA each codon would correspond to 3-proton units organized linearly into a sequence. Each 3-proton unit must have a flux tube transversal flux to DNA strand and located at 2-D sheet. This brings in mind the structure of spine as anatomical and neurobiological analogy. This suggests that dark DNA codons formed by 3-proton units should be associated with these horizontal flux tubes in 2-D locally planar surface going through DNA.

3. These structures from $n_{gr} = h_{gr}/h_0 = h_{eff}/h_0$ separate cells should combine to single n_{gr}-sheeted gravitational flux tube with sheets on top of each other with same M^4 projection. This would be dark DNA at the level of MB. It would seem that given codon of each DNA must contribute a dark proton triplet so that there would be n_{gr} dark proton triplets at given flux tube which is however very long. The size scale - that is the length of the flux tube - is that of Earth typically and fixed by the cyclotron wave length λ_c.

   This would give a concrete topological meaning to quantum quantum coherence at the level of MB of bio-system. Also a view about how lower level conscious entities integrate to larger ones: one can imagine entire fractal hierarchy of structures integrating to larger structures integrating... In particular, altered states of consciousness could correspond to this kind of temporary integrations to higher level structures. Same should apply to other basic biological structures: cells, proteins, RNA, tRA. Dark realization of the genetic code predicts the dark variants of these biomolecules.

   This picture conforms with adelic physics [L35, L34] in which n_{gr} corresponds to the dimension of extension of rationals: the larger the value of n_{gr}, the higher the algebraic complexity and level of conscious intelligence.

4. Where are the dark protons and various dark ions at dark flux tubes? Along entire long flux tubes with length of order cyclotron wavelength for given charged particle? Or inside the organism?

   The model of dark DNA allows only the latter option. They must reside at the short portions of the magnetic flux tubes inside organism. For instance, the dark protons of dark DNA are associated with flux tubes parallel and in immediate vicinity of ordinary DNA strand and codon and dark codon a paired like codon and its conjugate in ordinary DNA.

   What makes these particles dark is that they are controlled by the gravitational flux tube and form a non-local quantum coherent unit containing n_{gr} particles.

This raises a long series of questions and fantastic challenges for visual imagination.

1. How do DNA and its conjugate relate at this level: do DNA and conjugate correspond to single closed long flux tube forming part of the "umbical chord" far from biological body?

2. What replication of DNA could mean topologically at the level of this super-DNA? What about description of transcription and translation at these super-levels. Are the ordinary replication, etc.. induced from this super level as mere shadow processes: this would explain their mysterious coherence?

3. What sexual reproduction and associated recombination of chromosomes could mean at super level? What does the growth of organisms mean at super level? Addition of new sheets to super DNA and its variants so that n_{gr} defined as the number of basic units grows and organism becomes more and more quantum intelligent?

Chapter 7

More Precise TGD View about Quantum Biology and Prebiotic Evolution

7.1 Introduction

This work is an attempt to clarify the relation of the basic notions of TGD and TGD inspired biology - in particular the vision about prebiotic evolution - to chemistry and to the standard views about prebiotic evolution. There are frustratingly many different approaches and I have been working hardly to see whether TGD could allow to identify the common denominator of these approaches.

1. The works of Fröhlich [I109] and Del Giudice [I68] [D6] have served as a theoretical background in many attempts to develop quantum view about biology and consciousness. The first key idea is that weak em fields with frequencies, which correspond to energies much below the thermal energy in ordinary quantum theory, induce coherence/synchrony - maybe even quantum coherence - and that metabolic energy can be stored into Bose-Einstein condensate type states (`https://www.youtube.com/watch?v=RjF1_eDEsqc`). For instance, the work of Blackman [J8] and others in turn suggests that cyclotron frequencies in magnetic field of .2 Gauss have effects on vertebrate brain.

   Living systems are full of electrets and dipoles and charge separation in water environment is key aspect of living matter. Fröhlich sees electric dipoles and dipole oscillations as something fundamental. Also microtubule based view about consciousness relies on the ideas of Fröhlich. Del Giudice introduces the notion of coherence regions with size of about 1 micron as regions of water. Pollack [L15] has discovered exclusion zones (EZs) as a characteristic of what he calls fourth phase of water. Charge separation occurs in EZs created in presence of gel: EZ is negatively charged and obeys $H_{3/2}$ stoichiometry instead of the usual. Part of protons goes outside EZ. Water clathrates (`https://en.wikipedia.org/wiki/Clathrate_hydrate`) have size scales in the same range as EZs and could be precursors of EZs.

   Questions: What does the coherence/synchrony forced by oscillating external emf really mean? Does it really create Bose-Einstein condensates for oscillatory modes coupled with it? How coherence regions and EZs emerge? Frequency clearly matters as in quantum theory but the photon energies are typically far below thermal energy: how can external emfs with extremely low frequencies have quantal effects?

2. The experimental work carried out to understand prebiotic evolution has led to various insights but no unified view exists. Urey and Miller [I26] found that amino-acids emerge from simpler building blocks in an environment believed to mimic the boundary region between water, dry land, and atmosphere. The recipe for the prebiotic soup was simple: take simplest biomolecules such as NH_3, CH_4, water, lightnings to feed energy (they might have also some other functions), and assume reducing atmosphere. By adding some further simple

ingredients also adenine essential for metabolism, was generated in this kind of environment. It has however become clear that the atmosphere very probably was not reducing.

Question: Is it possible to imagine any counterpart for the reducing atmosphere?

3. There is also a vision that clays represented prebiotic life. Clays form complex chemical and geometric structures consisting of layers microscopically, and also replicate by simply splitting to two. One can even speculate about a simple predecessor of genetic code. Perhaps chemical life evolved in symbiosis with clays.

   Phyllosilicates (`https://en.wikipedia.org/wiki/Category:Phyllosilicates`) - in particular kaolinite and montmorillonite - are most studied clays. There is large variant of them containing basic biologically important ions in their lattice structure. Montmorillonites adsorb amino-acids and RNA nucleotides and promote polymerization of oligomers of RNA although the lengths of the resulting oligomers are considerably shorter than required by RNA world. DNA is not obtained since it is highly unstable in ordinary water. Even vesicles formed by double lipid layers are formed and could serve as predecessors of cells. But something is clearly missing.

   Questions: What is needed to get longer RNA strands and perhaps even DNA? How could one obtain prebiotic genetic code? What kind of environment could contain the biologically important atoms/ions in particular phosphate ion?

4. One can try to combine the experimental vision with the theoretical visions of Fröhlich and Del Giudice and with the experimental discoveries of Blackman and Pollack. This leads to ask whether the layers phyllosilicate structures could generated frequencies which promote coherence (maybe even quantum coherence) in living matter. It is now known (as I learned from Hans Geesink) that phyllosilicates have positive effects on health. Maps are constructed for their frequency spectrum and it is even found that they can serve as kind of frequency storage - this is analogous to water memory [K24]. Even cyclotron frequencies assignable to .2 Gauss magnetic field have been identified, and there is evidence that the powers of 3 and 2 about these frequencies are also biologically important. Quite generally, the THz/microwave region for which energies are below thermal energy (kT paradox) seems to be of special importance.

   Questions: Could basic biomolecules and surfaces of phyllosilicate layers in interaction with water have been predecessors of the recent chemical life? Water clathrates can contain various elements and probably also phyllosilicate crystals: could their transformation to EZs be an essential step in prebiotic evolution?

TGD suggests an answer to the questions posed above.

1. In TGD Universe dark matter corresponds to ordinary matter with large value $h_{eff} = n \times h$ of effective Planck constant. The oscillating classical em fields are classical correlates for dark photons. This solves the kT paradox. The forced oscillations are induced by absorption of these quanta: macroscopic quantum coherence forces the coherence of ordinary biomatter.

   The additional assumption $h_{eff} = h_{gr} = GMm/v_0$ [K76, K45] (to be explained in more detail later) implies universal energy spectrum for dark cyclotron photons and their transforms to ordinary photons can be identified as bio-photons [K65] in energy range containing visible and UV frequencies. Generalized Josephson radiation from membrane proteins acting as generalized Josephson junctions has also a branch for which energy spectrum is universal but frequencies depend on h_{eff}. These two dark photon species are used by magnetic body to control, coordinate, and communicate with ordinary matter in living systems.

2. In TGD framework one can do without coherence regions (one could perhaps identify them as special cases of Pollacks EZs), which can be much larger. The basic observation is that for a pair of hydrogen bonded water molecules the reaction $2H_2O \rightarrow H_3O_2^- +$ dark proton require UV photon with energy of O-H bond of about 5.15 eV. Water clathrates (`https://en.wikipedia.org/wiki/Clathrate_hydrate`), whose importance Hans Geesink emphasizes [L19], are good candidates for the precursors of EZs since they have size scale in the same range as EZs and contain hydrogen bonded water. Quantum criticality suggests

that this process should occur spontaneously as a chain reaction. This is achieved in the same manner as in nuclear fusion if the dark protons at the flux tube fuse to nuclear strings giving rise to dark nuclei.

If dark nuclear binding energy transforms as Coulomb energy under scalings of h_{eff} inducing similar scaling of the size of the system, the nuclear energy scale of MeV scales down to 1-10 eV - depending on the value of h_{eff}. An attractive guess is that the energy range of bio-photons corresponds to that for dark nuclear binding and excitation energies. Their spontaneous transformation to ordinary nuclei would liberate energy could at least partially explain the evidence for bio-transmutations. Also the relation to cold fusion is interesting.

Dark nuclear binding energy is liberated as dark photons decaying into bunches of ordinary photons inducing further reactions $2H_2O \rightarrow H_3O_2^- +$ dark proton also other kind of dark ionizations. The size of EZs varies from about 1 micron to 100 microns. Suppose that the size scale of EZ corresponds to the wavelength of dark photon with energy of order dark nuclear binding, and that h_{eff} is such that the nuclear binding energy corresponds to the lower end about 1 eV in the range of bio-photon energies. If so then h_{eff}/h varies in the range $1 - 100$. This would be the total number of dark photons resulting in the decay to ordinary photons.

In this process ordinary protons transform dark protons at magnetic flux tubes outside EZ. Dark ionization differs from ordinary ionization only in that the proton is dark. The difference between dark and ordinary ionization would define the borderline between ordinary and bio-chemistry (or dark chemistry). Chemical quantum criticality is possible also for other cations and also anions and all biologically important ions can appear as dark ions.

3. Dark proton states correspond to states of DNA, RNA, amino-acids and tRNA and therefore provide a fundamental representation of genetic code. The dark ionization of -O-H:s of any linear molecular structure generates dark proton sequence. In particular, the -O-H in phosphate of DNA nucleotide can become O^- plus dark proton, so that one has pairing or DNA with dark proton sequence carrying the genetic information. This splitting can occur also for amino-acids containing -O-H as standard part and also for ATP. Dark ionization can also occur for -O-H:s at of phyllosilicates layers and at their 1-D boundaries. Depending on the correlation between dark proton states and phyllosilicate units one could have an analog of genetic code. One can also imagine formation of DNA, RNA, etc... as their inorganic forms "steal" dark proton sequence from phyllosilicate: dark proton sequence would serve as a template. This would make possible very effective generation of complex biopolymers.

4. As Geesink emphasizes [L19], clays are good candidates for the key structures in prebiotic evolution since they can replicate. One can even speculate with an analog of genetic code. Phyllosilicates containing -O-H groups are especially interesting: they can adsorb basic biomolecules and induce their polymerization to oligomers. They also induce a formation of vesicles formed from lipid bilayer and serving as a candidate for a predecessor of cell. DNA is the problem and has led to a scenario known as RNA world. Phyllosilicates are also known to generate radiation with positive health effects.

   The natural and testable hypothesis is that the presence of EZs allows to circumvent the difficulties of the standard RNA world scenario and also generate DNA and biologically active phosphates containing the mysterious phosphate bond as ionized dark proton. The dark magnetic flux tubes and UV photon energy needed to generate EZs could be provided by gel in Pollacks's experiments and by electric discharges in Urey-Miller experiment. Also dark photons from the formation of dark nuclei decaying to bunches of bio-photons provide this energy.

   Water clathrates serving as precursors of EZs can contain atoms and perhaps even micrometer sized phyllosilicate crystals, which could catalyze the formation of biomolecules at their surfaces as a dark nuclear fusion chain reaction. Clathrate could also develop phospholipid bilayer around it - kind of primitive cell membrane. A possible objection is that Pollack observed that EZs repel impurities from their interior. What "inpurity" exactly means is of course a crucial question.

5. Prebiotic life could have evolved in underground oceans - even below the Earth's crust. The metabolic energy feed could have come as dark photons from the core, whose temperature is rather near to that of solar radiation. Also dark photons from solar radiation could have contributed. EZs could have been generated by dark UV quanta accompanying lightnings. Dark photons would propagate along dark magnetic flux tubes through the crust and transform to bio-photons in underground oceans (this is not the only possibility).

   Geesink [L19]mentions that FIR and THz/microwave radiation is accompanies the clathrate aerosols in atmosphere, which suggests the importance of atmosphere. If EZs generated by solar radiation from clathrates are present, this radiation could be dark and have energies above thermal energy and propagate along dark magnetic flux tubes. EZs could also transform ordinary solar radiation to dark radiation so that the radiation from atmosphere could enter underground oceans as dark radiation.

   In Cambrian explosion the radius of Earth was doubled (in TGD Universe cosmic expansion occurs in rapid jerks at the level of astrophysical objects in given scale) the underground life was burst to the surface of Earth [L45].

Possible technological implications of this picture - if true - are quite impressive. Cold biofusion could make possible artificial generation of technologically important elements and the mechanism generating EZs could make possible creation of artificial intelligent life forms involving silicates and water.

7.2 Background

Recently I have had very interesting discussions with Hans Geesink (`http://tinyurl.com/ya73ydrq`) and have also received a lot of highly interesting material from Hans, in particular his book "Proposal for a quantum field theory about coherence concerning non ionizing radiation" [L19], which can be found from his blog (`http://tinyurl.com/yd4cqpgn`). His views have much in common with my own vision and differences are especially useful since they force to direct attention to ideas that I have not directed enough attention.

7.2.1 About Experimental Work Of Hans Geesink

I was contacted by Hans Geesink, who works in BioTech Silicates, which tries to develop technology intended to reduce negative health effects caused by man-made non-thermal non-ionizing radiation involving typically frequencies from ELF (EEG region) to far infrared region. These effects are caused by EMFs from antennae, mobile phones, and power cables. Perception tests are carried out to see the possible effects on well-being.

Using the words of Geesink:

We have measured more precisely the resonances of the phyllosilicate minerals (used to compensate negative biological effects caused by non thermal non ionizing radiation; having multiple stacked sheets; each platelet 1 nanometer thick, and in stacks of micrometers, and total lengths of more than earth diameter, able to be organized as a metamaterial, nearly all types of ions incorporated in and between the platelets and we measured: quantized light, IR and FIR spectra properly ordered in powers of 2, and ratios of 1:2, 2:3, and adding multiple frequencies of 2 and 3.

The general vision is that weak external em fields oscillating at frequencies utilized by biosystems to coordinate their behavior by inducing coherent oscillations make possible coherence and perhaps even quantum coherence. The man-made emfs tend to destroy this coherence and weak emfs would restore the coherence if the frequencies are correct. Phyllosilicates seem to provide the materials producing the correct frequencies.

7.2.2 Some Theoretical Ideas

In his articles Geesink has done hard work in building a unified view about the enormous literature related to the biosystems and quantum coherence. Geesink sees the role of classical oscillating em fields central in biology. These fields somehow give rise to the coherent behavior of biomatter and perhaps even quantum coherence. Fröhlich is one of the pioneers, who thought that electric dipoles

and dipole oscillations could be central in living matter and give rise to analogs of Bose-Einstein condensates. A further important notion would be that of coherence region developed by Del Giudice as a quantum field theoretical (QFT) concept important for understanding of quantum biology. Unfortunately, this notion is not established experimentally unlike the exclusion zones (EZs) discovered by Pollack. In the following I try to relate these ideas to TGD framework.

Fröhlich's ideas

Fröhlich [I109] (see `http://tinyurl.com/yas9sv49`) proposes the importance of liquid crystals (`http://tinyurl.com/mcqtmd8`) and electric dipoles in biology. Cell membrane is only one example of liquid crystal and electret important in biology. Already Becker [J6] demonstrated that electric potentials serve as correlates of consciousness. Fröhlich suggests the importance of the longitudinal em modes assignable to dipole oscillations and metabolic energy storage as analogs Bose Einstein condensates (`http://tinyurl.com/y7utzsv8`). For instance, the tubulins inside microtubules are electric dipoles and Hameroff was the first researcher to propose that they might be important for consciousness. I have myself developed this idea from TGD perspective in a model of anesthetes based on electric fields associated with microtubules and give rise also to Becker's DC currents as supra-currents inside microtubules [K44].

One can imagine that dipole oscillations are quantized just like sound waves. Mathematically this is not a problem. The simplest situation corresponds to electrons oscillating in unisono with respect to the ionic lattice and accompanied by an electric field varying in a periodic manner. These oscillations can propagate and define longitudinal electric waves analogous to longitudinal sound waves.

Personally I am a little bit skeptic about quantizing the plasma oscillations but I might be wrong - also acoustic oscillations are quantized. The point is that the density of electrons appears in the formulas for frequencies, which suggests that a phenomenological description is in question. But the density of particles appears also in the frequency for sound waves and we talk fluently about phonons!

I would propose that both phonons and plasma waves have a genuine quantum description at deeper level. In TGD this deeper level would correspond to strings connecting points of partonic 2-surfaces serving as carriers of fermion number. The oscillations of strings would be fundamental besides the oscillations of their ends. Even elementary particles would consist of pairs of wormhole contacts in turn consisting of two partonic 2-surfaces at parallel space-time sheets and connected by strings and string oscillations would represent the fundamental phonons. Phonons would be 2-particle phenomenon and photons single particle phenomenon. This two-particle aspect is missing from QFT description. In string model description only the string aspect is present. In TGD both are involved and this is crucial for obtaining macroscopic gravitationally bound states: in TGD framework string model is doomed to be only a model of gravitation in Planck length scale.

Fröhlich uses the phrase "Governed by negentropy". The notion of negentropy has somewhat fuzzy content in standard physics framework.

1. Fantappie [J22] introduced the notion of syntropy, which in zero energy ontology (ZEO) can be regarded as entropy but with different arrow of time. Spontaneous self assembly would be a process, which would be decay in the reversed direction of time and obey time reversed second law.

2. I have talked about Negentropy Maximization Principle and number theoretic negentropy [K32, K77]. NMP defines the basic variational principle behind state function reduction central for both TGD and TGD inspired theory of consciousness.

   Number theoretical entropy is a variant of Shannon entropy for which the probabilities appearing as arguments of logarithms are replaced with their p-adic norms: this requires that probabilities are rational or at least algebraic numbers. If the entanglement probabilities do not belong to the algebraic extension of rationals used, the entanglement is rather stable since it requires a phase transition to large algebraic extension.

   he final states of state function reduction can have non-vanishing rational entanglement probabilities with projector as a density matrix: this corresponds to entanglement matrix proportional to unitary matrix. The number theoretic entanglement entropy is negative for

these states and one can say that entanglement carries information. NMP is not in conflict with second law: the thermodynamical ensemble entropy characterizes the average particle of ensemble and entanglement entropy characterizes pair of systems. Second law would however hold true only when restricted to the visible sector with standard value of Planck constant.

3. The most powerful implications of NMP in Zero Energy Ontology (ZEO) are precise identification of self as the sequence of state function reductions at a fixed boundary of causal diamond (CD). This leads to the understanding of metabolism and homeostasis as the attempt of conscious entities (selves) to survive: the "death" of self occurs in the first state function reduction to the opposite boundary of CD and actually means re-incarnation in geometric past as far as sensory input is considered. Selves do not however know about this(!) and fight for survival trying to gather negentropy associated with sub-selves to satisfy the needs of NMP. Metabolism is at deeper level gathering of negentropy resources as negentropic entanglement and nutrients are carriers of the negentropic entanglement. This picture is a powerful guideline in attempts to understand how the prebiotic life was initiated.

Forced coherence, coherence regions, and exclusion zones (EZs)

The notion of forced coherence is crucial idea behind the development of devices allowing to reduce the negative health effects caused by man-made non-thermal non-ionizing radiation. Coherent em fields at various frequencies are assumed to play a key role in bio-coordination and artificially generated emfs interfere with this coordination causing negative health effects.

The use of phyllosilicate based devices is argued to help to re-establish the coordination if the generate radiation at frequencies important for maintaining biological coherence via external weak synchronizing signal (for illustration of synchrony see `http://tinyurl.com/nu7cchs`). If phyllosilicates indeed achieve they might have played important role in prebiotic evolution.

Del Giudice [D6] [I68] has introduced the notion of coherence region. These regions would have size of order 1 micrometer and would be characterized by both acoustic and plasma oscillations induced by the synchronizing external fields. Velocity of propagation is dramatically reduced.

I have considered a model of coherence regions as a phase of water in which certain fraction of -O-H bonds of water molecules are excited to high energy state with energy abound 4.8 eV and near the bond breaking energy about 5.15-5.3 eV so that only metabolic energy quantum of about in the range .05-.3 eV is needed to break these bonds. Note that $.05 \times Z$ eV corresponds to the minimal energy assignable to protein Josephhson junctions of neural membrane and that .3 eV is slightly below the nominal value of metabolic energy quantum with nominal value of .5 eV. This would give rise to the formation of fourth phase of water discovered by Pollack [L15]. It however turns out that one can do without coherences regions in TGD framework.

The Exclusion Zones (EZs) of Pollack are generated in water bounded by gel in presence of irradiation by visible light. They have sizes up to 100 micrometers - the size of large neuron - are a fundamental concept in TGD inspired attempts to understand living matter. EZs have high electron density and obey the stoichiometry $H_{3/2}O$. Part of protons must go outside the EZ and TGD inspired proposal is that they go to dark protons at magnetic flux tubes.

Electrons inside EZ have large Fermi energy above thermal energy - maybe even of order 1 eV as in condensed matter - and could be key players in TGD based mechanism of bio-superconductivity. The electrons would be transferred to magnetic flux tubes as dark electrons at quantum criticality. EZs would accompany all bio-active molecules in particular DNA, which has charge -e per nucleotide associated with the phosphate. Also microtubules possess GTP molecules with same charge. The basic problem is to understand how the EZs and coherence regions or clathrates as their possible precursors can be created.

Quantum criticality is a key notion of quantum TGD and TGD inspired biology but has been discussed also by other scientists. For instance, Stuart Kauffman has developed this notion [I135] (`http://tinyurl.com/y74r8gwp`). There are of course many views about quantum criticality: the characteristic difference between TGD inspired proposal [K75] and other proposals is that quantum theory is generalized by introducing the hierarchy of Planck constants $h_{eff} = n \times h$ labeling a fractal hierarchy of isomorphic sub-algebras of so called super-symplectic algebra having the structure of conformal algebra.

Water clathrates

Geesink emphasizes [L19] the importance of water clathrates or clathrate hydrates (`http://tinyurl.com/y97q54bp`) - crystalline water based solids resembling ices and consist of hydrogen bonded water. Clathrates contain also guest molecules such as small non-polar molecules (typically gas molecules) and polar molecules with large hydrophobic moieties (parts) trapped inside "cages" of hydrogen bonded frozen water molecules. Methane is one gas trapped in deposits of methane clathrate. Clathrates appear also at outer planets, moons, and trans-Neptunian objects.

The size scale range for clathrates varies from 1-100 micros and is same as for EZs of Pollack and the natural identification would be as precursors of EZs. This makes clathrates ideal prebiotic structures inside which molecular life could have evolved.

Geesink notices also the importance of atmospheric aerosol of water clathrates as emitters of radiation in FIR and THz/microwave region inducing coherence and transition betweens protein conformations and Rydberg states (`http://tinyurl.com/y8s8bolj`). Rydberg states themselves could be excited by UV radiation. The absorption of solar light could transform also atmospheric clathrates to EZs.

7.3 Basic TGD Based Vision About Quantum Biology

From TGD point of view the findings discussed by Geesink in his article [L19] are highly interesting for several reasons. Geesink underlines the importance of external classical fields as inducers of coherence which differs from ordinary coherence in that there is external energy feed as in self-organizing systems, and also the importance of coherence regions of size about 1 micrometer. This raises questions.

1. Is the coherence really quantal or is it the external classical fields classical correlates for quantum coherence? Can one really speak about Bose-Einstein condensates of longitudinal oscillations of electric or is a more fundamental quantum description needed?

2. Do the coherence regions of del Giudice exist except as theoretical entities? What is their origin in TGD Universe if they exist? Could the EZs of Pollack- , which certainly exist - involve the fusion of coherence regions accompanied by a phase transition to $H_{1.5}O$ stoichiometry generating charge separation. Or could one do without coherence regions as separate entities and perhaps identify them with EZs? Or could water clathrates replace them as precursors of EZs? Note that theoretically the size of coherence regions would be about 1 micrometers whereas the sizes of EZs vary up to 200 micrometers. The clathrate option looks to me highly attractive.

3. Another option is based on the hypothesis that dark proton sequences are dark nuclei and their binding energy scales like $1/L$, L the size scale of dark nucleus measured in nanoneters. If so, the binding energy of dark nuclei per dark proton would be in UV range. The process could proceed spontaneously as dark fusion. Dark proton sequences would be formed and emit UV photons with energy near 5 eV, which in turn would excite O-H near to the criticality so that a radiation with energy of energy near metabolic energy quantum can generate the dark proton and hydrogen bonded $H_3O_2^-$. Metabolic energy could induce this process.

4. Geesink reports that the phyllosilicate minerals created in the interaction of water with silicate minerals and possessing characteristic -O-H groups have positive health effects and can be used to reduce the negative effects caused by man-made non-ionizing radiation. When doped with biologically important ions they produce specific biological effects characterizing the ion and also the cyclotron frequencies assigned to .2 Gauss magnetic field by Blackman are detected.

   This leads to a series of questions.

   (a) Could the physics of phyllosilicate-water system involve EZs and possibly also coherence regions in a key role? -O-H groups and their ionized variants $-O^-$ are a common denominator of both water, biologically active phosphate and there of DNA and RNA nucleotides as well as phospholipids containing phosphate, of amino-acids, etc...

Could the transformation of -O-H to -O^- plus dark proton be the fundamental reaction generating dark protons. Note that this transformation would be dark counterpart for what what happens as acid gives up proton. For instance, a fraction of water molecules characterized by pH decomposes to OH^- and H_3O^+ ions. In presence of EZ this process would produce dark H^+ rather than H_3O^+ ions.

This generalizes to other cations and also to anions. The distinction between dark anion/cation (usually proton/electron) is the boundary between non-organic chemistry and bio-chemistry.

(b) Phyllosilicates involve all biologically important ions: did their dark variants emerge already in the prebiotic phase in the interaction of water with phyllosilicate? What is this interaction? Could the process -O-H to -O^- also phyllosilicates in interaction with fourth phase of water and transform also the biologically important ions to their dark counterparts and at the same time ionize the mineral surface?

5. What makes possible coherent generation and liberation of metabolic energy? Is this a quantum coherent process or chain reaction as the model for the generation of EZ suggests or are both options realized?

6. Quantum criticality and dark variants of biologically important ions. What is the mechanism giving rise to the pairing of the biopolymers with their dark analogs at magnetic flux tubes? How dark ions such as K^+,Na^+, Ca^{++}, Cl^- are generated? Could the interaction of water with EZs provide a prebiotic mechanism for the generation of these dark ions?

7. Cell membranes consisting of double lipid layers are in TGD Universe Josephson junctions and Josephson currents between them generate Josephson radiation with energy, which is just above the thermal energy and have frequency proportional to $1/h_{eff}$ and thus give rise to classical counterpart of THz radiation known to be important in the interaction of phyllosilicates with living matter. It is known that vesicles consisting of lipid bilayers are formed in water-montmorillonite system. Could the predecessor of cell emerge in water-phyllosilicate interaction?

   Phyllosilicates appear in bi- and triple-layered structures and are semiconductors. Could they act - perhaps in presence of EZs - as high temperature superconductors in the sense that their resistance would be associated only with the ends of the "wires" (the resistance would be thus independent of length)? Could a charge separation develop in the presence of EZs so that there would be potential difference through the layered structure? Could the layers form Josephson junctions generating radiation with energy above thermal energy and frequency determined by the value of h_{eff}? The lattice spacing for layered structures is of order 1 Angstrom so that one expects Josephson energy ZeV to have order of magnitude of 10^2 eV.

8. Doped phyllosilicates are also catalysts and could have served as prebiotic bio-catalysts. A highly attractive idea is that both prebiotic molecules, atoms of various elements, and phyllosilicate crystals were trapped inside water clathrates so that all important building bricks of bio-molecules would have been automatically inside EZs after their birth.

7.3.1 How Could External Fields Induce Coherence?

By general arguments (Planck constant istoo small) the coherence induced by classical fields in visible matter is like forcing soldiers to march in the same pace and should not be regarded as a genuine quantum coherence. Quantum coherence would be at deeper level and allows to understand why the external classical field is coherent in long scales. In TGD Universe resonance frequencies of EEG etc... perform this task in brain functioning and dark EEG photons are behind EEG mediating sensory information to magnetic body and control commands back to biological body [K15]. (Quantum) criticality is the key notion: at (quantum) criticality large h_{eff} dark matter phases can appear. In applications one should try to identify quantum critical aspects of systems considered.

In TGD framework dark cyclotron photons having oscillating fields as classical correlates and with energy $E = h_{eff} \times f$ above thermal threshold would be inducers of coherence. This

picture solves the kT paradox, which originally led to $h_{eff} = n \times h$ hypothesis, which can be now deduced from the number theoretic vision about TGD [K77]. Dark cyclotron photons could transform to ordinary photons in energy conserving manner and have biophotons as their decay products with energies in visible and UV range. $h_{eff} = h_{gr}$ hypothesis [K76] implies that dark cyclotron photons and therefore also bio-photons have universal spectrum reflecting the spectrum of magnetic field strengths.

The model for cell membrane as generalized Josephson junction can act also as an ordinary Josephson junction and thus allows also a piece of spectrum with Josephson photon energy coming as multiples of $E = ZeV$, V resting potential, where Z is the charge of the superconducting charge carrier. Just in the vicinity of thermal threshold for $Z = 2$ (Cooper pairs or Ca^{+2}, Mg^{+2}). Dark Josephson radiation with energies near thermal energy and with frequency inversely proportional to $1/h_{eff}$ so that arbitrary low frequencies would be obtained. These dark photons have always same energy irrespective of the value of h_{eff}.

THz/microwave frequency range is considerably below the thermal threshold for the ordinary value of Planck constant and dark Josephson photons with appropriate value of Planck constant could be transformed to these photons. The simplest transformation is the decay of the $n = h_{eff}/h$ sheeted space-time surface to n sheets each carrying ordinary THz photon. Also energy conserving decay to single photon can occur. The values of Planck constant would not be very large for THz range if Josephson photons are in question. The dark THz/microwave photons emitted by say EZs generated from atmospheric water clathrates by solar radiation could propagate through the crust along magnetic flux tubes to the underground oceans.

The basic mechanism in the interaction of dark matter with visible matter would be phase transition transforming dark photon to ordinary photon(s) in energy conserving manner. All particles can be in dark phase and this makes possible super-conductivity and superfluidity.

7.3.2 Coherence Regions And EZs

The proposal of del Giudice is that what he calls coherence regions/domains play a central role in biology and are induced by oscillating external fields by forcing units of visible matter to march in the same rhythm. In TGD framework one must take a skeptic attitude towards the existence of coherence regions postulated by del Giudice. To my best knowledge there is no direct experimental support for coherence regions and they might be identifiable as special cases of EZs.

1. EZs of Pollack are an experimental fact and are generated in presence of gel phase and incoming radiation. The open question is whether gel phase also serves as an energy source or does it have some kind of control function feeding in information. It might well be that coherence regions of del Giudice are not needed and the water clathrates serve as natural precursors of EZs. The transition *hydrogen bonded* $2H_2O \rightarrow H_3O_2^-$ + *dark proton* could be induced by UV light as breaking of -O-H bond.

   EZs carry negative electronic charge and part of protons would become dark and would be transferred to the dark magnetic flux tubes. Dark protons form sequences, which could be seen as scaled up variants of atomic nuclei in the first approximation. The states of dark proton in the model that I have proposed are in one-one correspondence with DNA, RNA, amino-acids, and 40 tRNA states [K24]. The coherence regions could be created by UV light splitting -O-H bonds and possibly also other kinds of bonds to the verge of phase transition. Later various options for the energetics of coherence regions are discussed.

   The simplest assumption is that nuclear binding energy transforms as Coulomb potential in the scaling of $h \rightarrow h_{eff}$ scaling also the system size. If so, the dark nuclear energy spectrum could be that for bio-photons and basic bio-molecules. The transformations of dark nuclei to ordinary nuclei could take place and would provide new source of nuclear power and ability to artificially generate elements: there is indeed evidence for biofusion [C3, C9].

2. If the coherence regions of del Giudice exists they must relate closely with EZs. The simplest TGD inspired analog would be as micron sized regions as regions near criticality of a phase transition of water to fourth phase of Pollack. The simplest guess is that Josephson energy quantum for cell membrane (above $.05 \times Z$ eV) or energy quantum somewhat below metabolic energy quantum $\sim .5$ eV is needed to transform H_2O stoichiometry to $H_{1.5}O$ so that EZ would

be obtained. Hence the Josephson radiation from membrane protein Josephson junctions could have a role in the control of EZs. On the other hand, the hydrogen bonds EZs with high enough bond energy would be stable against absorption of Josephson radiation and metabolic energy quanta.

The proposal is that fourth phase of water realizes genetic code at the level of dark nuclear physics and ordinary biomatter has condensed around the dark matter. DNA, etc. are paired to the dark proton sequences representing their dark variants and transcription and translation occurs at the dark level primarily and ordinary biomatter makes this visible. The recent finding that so called knocked out genes are transcribed correctly [I98] (`http://tinyurl.com/y9849jkz`) supports this view [K76].

7.3.3 Quantum Criticality Bio-Chemically

Quantum criticality [K75] has become key concept of quantum TGD and TGD inspired biology. Quantum criticality allows to understandard the hierarchy of Planck constants and also its relationship to p-adic length scale hypothesis, whose origin reduces to number theoretic vision about TGD [K77]. Dark matter phases characterized by $h_{eff} = n \times h$ accompany any quantum critical system, maybe even thermodynamimcally critical systems. The challenge is to find concrete realizations of quantum criticality in various scales. In biology biochemical realization is of special interest.

The basic aspect of quantum criticality is that the increase of h_{eff} occurs *spontaneously* since the process corresponds to increase of negentropy and NMP states that negentropic entanglement resources of the Universe are increasing as kind of Akashic records or cosmic library. At the level of selves this means that self "dies" and re-incarnates as its time reversal. Selves fight for survival and try to grow their negentropic resources to satisfy the requirements of NMP. This leads to metabolism and homeostasis characterizing living systems. The emergence of life would not be extremely rare accident but doomed to occur spontaneously sooner or later by basic law telling what happens in state function reduction in TGD Universe obeying Zero Energy Ontology (ZEO). Hence the process should occur spontaneously and increase h_{eff}.

1. The basic question is how quantum criticality is realized biochemically. Are the molecules excited near to a critical energy at which a dark ion at magnetic flux tube is generated and a phase transition analogous to that leading from ordinary to fourth phase of water occurs? Or are large systems near criticality to a generation of dark phase as the general vision about quantum criticality of TGD Universe suggests.

2. A natural assumption is that metabolic energy quantum should be able to induce the phase transition producing dark particles at criticality. Could dark photons in visible and UV range accompany criticality at the level of single molecule? Are cell membrane and neuronal membrane quantum critical systems and how they differ?

3. Dark variants of biologically important ions residing at magnetic flux tubes are in fundamental role in TGD inspired quantum biology. In particular, dark proton states are proposed to give rise to the dark analogs of DNA, RNA, amino-acids, and tRNA. The pairing of ordinary DNA/RNA/amino-acids with their dark analogs is expected to be fundamental in biology and transcription and translation are proposed to take place at dark level as the recent experimental findings indicate. How is this pairing realized? How ordinary DNA becomes paired with dark DNA or is it already paired with it?

4. What could be the fundamental mechanism liberating metabolic energy coherently? This question will be discussed later.

The role of fourth phase of water

Pollack's EZs [L15] and fourth phase of water should be in key role.

1. EZs are generated under conditions equivalent with those prevailing in Pollack's experiments (water bounded by gel plus irradiation). Charge separation occurs: EZ is negatively charged

and dark protons reside at magnetic flux tubes. This process could occur also for systems in contact with water such as phyllosilicates. Cations (in particular protons) or anions at these surfaces could be transferred to magnetic flux tubes. Dark proton sequences could realize the genetic code.

2. -O-H bond near quantum criticality would become -O^- in the formation of EZs - most naturally from water clathrates since also EZs have crystal structure. Actually much more general process can be considered: also the -O-H bonds associated with say phyllosilicates in contact with EZ could suffer the same fate. O^- appears in the phosphates associated with XTPs of DNA n and RNA nucleotides, phospholipids, and with GTPs of microtubules. Are all these O^-:s accompanied by dark proton in some spin state at parallel magnetic flux tube. In the case of DNA there should be a correlation between the code letter A, T, C, G and dark proton state. Could the 3-electron state possibly assignable to the codon be same as 3-quark state of corresponding dark proton? In particular DNA as topological quantum computer could involve pairing of dark protons associated with DNA and with phospholipids by flux tubes which can become braided.

3. -O-H bonds associated with O=C-O-H is the basic building brick of amino-acid and could make it acid that is able to donate H^+ received by water molecule becoming H_3O^+. Could amino-acid become biologically active as -O-H becomes -O^- plus dark proton at flux tube possibly defining dark proton sequences dark variant of amino-acid as dark proton sequences? Another possibility is that he phosphorylation of amino-acids brings associates dark protons with amino-acids and can even generate dark nuclei. There should be a correlation with spin state of dark proton and amino-acid side-chain if genetic code is realized.

4. There is no need to restrict this mechanism to -O-H$\rightarrow O^-$. Any chemical bond could be kicked near to criticality either by the combination of dark and p-adic phase transitions liberating zero point kinetic energy or by dark photons absorbed in the time reversal of Bose-Einstein condensation. This would allow generation of dark variants of biologically important ions by EZs associated with phyllosilicates.

One could test this vision empirically by looking whether EZs induce generation of DNA sequences or at least dehydration of DNA and checking whether EZs could stabilize DNA against hydrolysis. Also the interaction between EZs and phyllosilicates could be studied.

Simplest model for the formation of fourth phase of water

The basic ideas about quantum criticality apply to the formation of EZs and possibly existing coherence regions serving as their predecessors. The simplest model for the formation of EZs discussed in the following does not require coherence regions at all and could occur spontaneously as a chain reaction. This is what Occam's razor suggests.

The simplest option does not require pre-existing coherence regions. The basic idea is simple: radiation at visible light induces the transition $2H_2O \rightarrow H_3O_2^- +$ dark proton where water molecules are hydrogen bonded. If dark protons at magnetic flux tubes fuse to form dark nuclei, they liberate dark gamma rays. If they decay to ordinary photons with correct energy they induces further transitions which ca decay to ordinary photons. If their energies are correct they induce further transitions $2H_2O \rightarrow H_3O_2^- +$ dark proton and EZ is generated as a nuclear chain reaction.

1. $H_{3/2}O$ is stoichiometric shorthand for hydrogen bonded $H_3O_2^-$ molecule forming a loosely bound lattice structure with lattice binding energy small compared to the molecular bond energies. A pair of hydrogen bonded water molecules forming H_2O–H-O-H structure ("–" denotes for hydrogen bond) could suffer dark ionization by giving up dark proton so that $H_3O_2^-$ molecule is formed. The dark proton would be transferred to the dark magnetic flux tube. The bond energy of O-H bond is 5.15 eV (`http://tinyurl.com/yccmm7mm`) is in the first approximation the net energy needed to transform $2H_2O$ to $H_3O_2^- +$ dark proton directly. This corresponds to UV energy. This is of course extremely rough estimate.

2. The objection is that the large negative electronic charge gives the system very large Coulomb energy so that it explodes. A possible manner to circumvent the problem is that dark protons

fuse to dark nuclear strings and liberate nuclear binding energy, which compensates the Coulombic energy and stabilizes the system. Dark nuclear fusion would liberate dark gamma rays decaying into ordinary photons. If the photons have energies in the range of visible and UV photons they could generate more $H_3O_2^-$ molecules and the generation of EZ could proceed as a chain reaction. Hence dark phase of protons would be generated spontaneously in accordance with NMP and the resulting phase would be stable. These photons can also induce dark ionization of other biologically important ions appearing as anions or cations.

Dark proton sequences could also transform more complex nuclei containing dark neutrons and in TGD framework also exotic nuclei with charged bonds between nucleons are possible. The transformation of dark nuclei to ordinary ones would provide a new mechanism of nuclear fusion producing various elements outside solar core. There is indeed evidence for bio-transmutations [C3, C9]. I have discussed this possibility as a possible explanation of Lithium anomaly [L2]. One can even ask whether the prebiotic life could have generated some of the needed atomic nuclei artificially!

3. Gel phase in Pollack's experiments could provide the dark magnetic flux tubes for protons. In experiments of Urey and Miller electric discharges accompanied by magnetic flux tubes would do the same rather than providing metabolic energy as one might also imagine. This could be tested by replacing electric discharges with gel in the analogs of Urey-Miller experiments. Lightnings would have the same role in the evolution of prebiotic life. Dark flux tubes might have been associated with the magnetic fields of Earth. The endogenous magnetic field from the experiments of Blackman [J8] has value $2B_E/5$, $B_E = .5$ Gauss is the magnetic field of Earth.

Second option is that coherence regions of del Giudice are created first. A subset of -O-H bonds is first transformed near criticality by UV light with energies around 4.8 eV as coherence regions are formed. After that metabolic energy quantum kicks the molecules over the threshold for the formation of H_3O_2 and liberates about 2 eV per bond. The burst of these ~ 2 eV photons should have been detected so that this option is not plausible. There is also the problem due to the fact that two many O-Hs could be taken to the criticalityandboth -O-H bonds of given water molecule could be taken to criticality.

Could dark proton sequences at flux tubes form dark nuclei?

In TGD framework nuclei correspond to nuclear strings [**?**]onsisting of strings formed from dark protons and neutrons. Neutrons and protons could even form their own dark strings. Therefore dark proton sequences could but need not to fuse to dark nuclear strings with some nuclear binding energy and liberate the nuclear binding energy in the process.

Suppose that the fusion can occur so that a dark proton created in dark ionization is bound to an already existing dark proton sequence representing dark nuclear string at magnetic flux tube. By a naive extrapolation the binding energy would be same as in ordinary nuclear physics and would be measured in MeV range assignable to gamma rays. This estimate is probably wrong. As already explained, the nuclear binding energy could more naturally behave as $1/h_{eff}$ - like Coulomb energy- and nuclear excitation energy spectrum would be naturally in bio-photon energy range. The situation could become analogous to nuclear fusion liberating large amounts of energy. This would conform with NMP and with the idea that formation of large h_{eff} phases occurs spontaneously.

In the case of linear structures containing -O-H sequences with small enough distance dark nuclear fusion can be imagined. Could the fusion occur at phyllosilicate surfaces and generate dark analogs of DNA codons as highly stable structures? Could the fusion occur as a chain reaction liberating large amounts of energy at biophoton energies and lead to a formation of dark proton sequences with some maximum length dictated by Coulomb repulsion?

Could DNA nucleotides associate with these dark codons? If O^- associated with phosphates inside cell nucleus can can combine with ordinary protons the hydrolysis of DNA can occur inside nucleus. The pairing of DNA and dark proton sequence by connecting magnetic flux tubes could prevent hydrolysis.

One prediction would be that the negative charge of DNA (one units per single nucleotide) is screened by dark proton sequences in vivo in the scale of the system formed by DNA and dark

proton sequence. Usually it is believed to be screened by Na^+ counter ions. If the distance between DNA and dark proton sequences is large enough, a local screening by Na^+ counter ions can indeed occur. What happens inside cell nucleus is far from clear to me.

Could dark nuclei collapse to ordinary nuclei?

One can also wonder whether the phase transition $h_{eff} \to h$ could produce ordinary nuclei and liberate energy in nuclear energy range. Could living matter be at criticality against nuclear explosion? The occurrence of bio-transmutations has been indeed claimed [**?**] This possibility would mean a manner to generate both nuclear energy and generate artificially those elements, which are depleted.

The observation that the isotope ratios reported to appear in the cold fusion experiment of Andrea Rossi are the natural ones (`http://tinyurl.com/yd8wka4w`) has been used to claim that the E Cat reactor developed by Rossi [**?**]s fraud. Lithium anomaly however forces to ask how large fraction of ordinary matter emerged via dark fusion in interstellar space, and how large fraction was generated in the stellar cores. Could even the fusion in stellar cores have occurred as dark fusion at magnetic flux tubes followed by a phase transition to ordinary matter?

One can argue that since the increase of h_{eff} and generation of negentropic entanglement (NE) occurs spontaneously, the fusion to ordinary nuclei must be a rare process. NMP suggests strongly that the existing NE must be transferred from the dark nucleus - magnetic flux tube - shortening to ordinary nuclear string in $h_{eff} \to h$. If this NE is associated with the transversal flux tubes connecting dark protons of the nuclear string with other similar system, the transfer could take place by reconnection of flux tubes with those of second analogous system (the model for DNA as TQC assumes that flux tubes connect dark protons assignable to DNA codons and lipids of nuclear/cell membrane [K17]). The transfer of single transversal flux tube connecting A and B to that connecting C and D would require two reconnections: AB+ CD$\to$ AC+ BD $\to$ AB+CD. CD would have no NE in the initial situation and would have that of AB in the final situation whereas AB would have no NE. The probability that all flux tubes are doubly reconnected within a reasonable time span is expected to be small and only light nuclei might be generated. The occurrence of biofusion however suggest that this objection might be circumvented in some quantum critical situations.

Decay of very energetic dark photons to low energy photons

It is known that X and gamma rays accompany lightnings (`http://tinyurl.com/cr5e6tz`). This is impossible in standard physics since X and gamma rays should be absorbed in atmosphere. I have proposed that that this radiation as also the radiation at lower energies propagates along magnetic flux tubes as dark photons.

Suppose that dark proton sequences indeed fuse to dark nuclei and liberate large amount of energy in the process as dark analogs of gamma rays but possibly much lower energy in the energy range of dark bio-photons and possessing much longer wave-length than usually. These dark photons can decay to ordinary photons and an interesting possibility is that this range includes visible photons (bio-photon energy range is a good in lack-of-anything-better-guess).

Could this decay promote the visible light promoting the generation of EZ? If this were the case the formation of living matter could take place as a chain reaction as NMP encourages to think. Similar chain reaction could have taken place also in prebiotic circumstances, where lightnings could have provided the initiating photons and perhaps also dark photons in dark nuclear binding energy range decaying to visible photons initiating the process. Same could have happened in Urey-Miller experiments.

Anomalies possibly related to EZs

There are several anomalies which might allow explanation in terms of EZs.

1. Tesla studied what happens in di-electric breakdown and was perhaps the first experimentalist to discover dark matter. Critical phenomenon is in question and could in TGD Universe be accompanied by the formation of dark matter - perhaps even dark nuclear matter accompanied by liberation of energy. Also dark radiation with wavelengths proportional to h_{eff}

making possible long range communications and energy transfer could be involved [K64]. The most fascinating phenomenon reported by Tesla was charge separation in length scales much longer than one might have expected and could directly reflect the generation of dark charged particles.

2. The article of Kanarev and Mizuno [D8] reports findings supporting the occurrence of cold fusion in NaOH and KOH hydrolysis. The situation is different from standard cold fusion, where heavy water D_2O is used instead of H_2O. I have considered this finding in [L2]. Obviously the mechanism generating dark proton sequences as dark nuclear fusion could explain the findings of Kanarev and Mizuno.

3. The irradiation of salt water with microwaves induces the "burning" of water with a visible flame [D1]. The phenomenon is believed to involve the breaking of salt water into oxygen, hydrogen and salt. If EZ is formed this could mean formation of H-O-H–$OH_2 \rightarrow H_3O_2^- +$ dark proton. Nuclear fusion need not be initiated since polymer structures are absent. The burning process could be induced by microwaves accompanied by dark photons having energy in the energy range of UV photons and transforming to UV photons.

4. Free energy anomalies are not taken seriously by the main stream since they are not consistent with energy conservation in standard physics framework. I have proposed they they could be understood in terms of generation of dark proton sequences and cold fusion liberating energy [K71].

   The so called Brown's gas [H1] (might be same as fourth phase of water) produced from water by electrolysis is reported to be able to melt metals at much below the melting temperature. The explanation would be that the presence of metal initiates transition to ordinary nuclei liberating nuclear energy. The original explanation was quite not like this [K71] although the energy was assigned with dark proton sequences. Another interpretation is that the process generating dark proton sequences continues.

5. There is also analogy of charged water clusters (EZs) with two poorly understood phenomena: steam electricity [H3] (`http://tinyurl.com/y977k2es`) and waterfall ionization. Also thunder cloud charge separation and sonoluminescence might involve the formation of charged water clusters.

How biosystems could control protein dynamics?

Hans Frauenfelder et al propose a unified model of protein dynamics based on experimental findings [I90]. The key proposal is that protein dynamics is slaved by the hydration shell and by the bulk solvent. The dynamics of master should be slower than that of slave. The conformational motions of proteins have time scale in the range 1 ns-1 s. The frequencies corresponding to the splitting of hydrogen bonds are above 10 THz and hence splitting dynamics is faster than protein dynamics. Therefore the claimed master-slave relation looks strange at the first glance. One can however think that the cleaving of hydrogen bonds defines the control dynamics as dynamics of switching and is much faster process than processes occurring between switchings. Changing the position of switch would correspond to a catastrophe in catastrophe theoretic formulation. The dynamics at a given sheet of catastrophe is indeed slow except at the critical lines defining its boundaries [A20].

This suggests that various phases of water define environments for water controlling the behavior of proteins. If the phase is hydrogen bonded water clathrate, the protein finds itself inside "ice" layer and cannot move. Protein folding would represent a basic example of this situation. When the hydrogen bonds disappear due to the melting of the EZ around protein by the splitting of protein-water and water-water hydrogen bonds, protein becomes able to change its conformation and protein un-folding can occur. The "ice" layer around protein can melt by the feed of external energy at energies below metabolic energy quantum. This radiation could arrive as dark photons from dark magnetic body decaying into bunches of ordinary photons with same frequency and inducing fast melting of the entire layer. The bulk solvent could control large scale protein motions by changing the viscosity achieved by modifying the density of hydrogen bonds. Protein would move in the direction where the resistance is smallest.

In ZEO the reverse process would correspond to melting but in non-standard time direction. One can interpret the situation also in terms of consciousness theory. The period between folding and unfolding would define self and the control action would generate the time reversal of self.

But "who" is the master? In TGD framework it would be naturally the dark magnetic body containing at its flux tubes dark proton sequences associated with proteins. The motor actions of the magnetic body would induce those of proteins. The only condition is that the inherent protein dynamics is fast enough to follow the dynamics of water. The fingerprints of biomolecules are in energy region .05-.25 eV (this is also the energy range for hydrogen bond energies) and the frequencies are above 10 THz. Therefore the time scales of protein dynamics would actually reflect those of dark magnetic body.

The modelling of protein folding as a random process in which system tries all options and ends up to the bottom of potential well representing the final configuration has problems: the basic paradox is that the folding should take extremely long time. If protein folding is macroscopic quantal self-organization process governed by NMP in present of large h_{eff} phases, these problems might be circumvented. Folding could to high extent reduce to the folding of the underlying magnetic flux tube structure: proteins would follow automatically if they are surrounded by the "ice" layer of ordered water.

The following considerations provide additional insights in the attempts to build a model for protein folding. There is a new observation (`http://tinyurl.com/ycqkx9mu`) about protein folding process. During folding some proteins hold single building blocks in shapes that were thought to be impossible to find in stable form. Stable shapes contained some parts, which were trapped like mosquitos in amber.

A concrete TGD based model relies on the general ideas of TGD inspired quantum biology.

1. Biomolecules containing aromatic rings play a fundamental role. All DNA nucleotides contain them and there are 4 proteins, which also have them. trp and phe are of special importance and form a pair structurally analogous to a base pair in DNA strand. The rings are assumed to carry the analog of supra current and be in or at least be able to make transition to a state with large $h_{eff} = n \times h$. The delocalization of electron pairs in aromatic ring could be a signature of $h_{eff}/h > 1$.

2. trp-phe pairing would be responsible for information molecule-receptor pairing. Information molecule and receptor would be at the ends of flux tubes serving as communication lines, and the attachment of info molecule to receptor would fuse the two flux tubes to longer one. After that communication would become possible as dark photon signals and dark supra currents. Formation of info molecule-receptor complex would be like clicking icon generating a connection between computers in net. Info molecules would generate the communication channels - they would not be the signals. This is the distinction from standard neuroscience.

3. All quantum critical phenomena involve generation of large h_{eff} phases. Folding emerges or disappears at quantum criticality (QC) possible in certain temperature range of width about 40 K and depending on pH. The flux tubes associated with phe and trp containing aromatic rings carrying "supra current" would become dark (either $h \to h_{eff}$ or $h_{eff} > h$ increases) and thus much longer and reconnect temporarily and force phe and trp in a close contact after the reverse transition inducing shortening. This is a general mechanism making biomolecules able to find each other in what looks like molecular soup in the eyes of standard biochemist. The contacts between amino-acids phe and trp formed in this manner are structurally identical with the hydrogen bonding between members of DNA base pairs and they would fix the final folding pattern to high degree.

There was also a very interesting article (`http://tinyurl.com/y8foh93b`) about possible topological phenomena related to protein folding. Authors are Henrik and Jakob Bohr (akin to Niels Bohr?) and Sören Brunak.

The article explains the basic topological concepts like winding possible involved in protein folding in a simple manner. The proposal is that the excitation of so called wringing modes of proteins are involved in the generation and disappearance of the protein folding. Excitation of wringing modes twisting the protein (think about how one wrings water from a wetted cloth) would make the protein folding state *cold denatured* (CD) unstable and transform in to a stable

folded (F) state. In the same manner their excitation would transform *hot denatured* (HD) stable state to a *folded* (F) state. Wringing modes could be excited by radiation.

In TGD framework the folding phase diagram CD-F-HD could be understood also in terms of QC. Perhaps the simplest option is that the transitions CD-F and HD-F involve a generation of critical states leading to a generation of long range correlations (large h_{eff}) inducing the folding pattern. Absorption of photons to wringing modes would induce the criticality and the folding would proceed by the mechanism discussed above.

Relationship to DNA as topological quantum computer hypothesis

DNA as topological quantum computer (TQC) hypothesis [K17, K53] emerged roughly decade ago. The basic idea is that DNA and lipid layer of nuclear membrane are connected by magnetic flux tubes. Also connections to cell membrane and membranes of the other cells are in principle possible. The braiding of the flux tubes induced by the flow of lipid layer in liquid crystal (LC) state makes possible topological quantum computations. Similar topological quantum computations could be associated with the system formed by microtubules and axonal membranes.

A more general idea is that flux tubes are analogous to coordinate lines of 3-D coordinate grid forming a backbone of the organism [K62] implying that the morphogenesis of magnetic body would induce that of visible part of organism. For instance, each DNA codon could be accompanied by flux tubes parallel to DNA plus flux tubes in two orthogonal directions perhaps connecting DNA to the lipid layers of nuclear membrane. The orthogonal flux tubes could emanate from the dark protons associated with the phosphates of the strands.

One can imagine several identifications for the particles involved with the topological quantum computation. The basic condition is that DNA codons or codewords are represented in terms of dark variants of some particles.

1. If one assumes that individual nucleotides (A,T,C,G) are involved, it is natural to assume that the particles involves correspond to these in 1-1 manner. The realization discussed in [K17] assume that the codons correspond to the 2+2=4 spin states of u and d quarks and anticodons to corresponding states for antiquarks. The quarks would be of course dark to avoid annihilation. One can also imagine realizations in terms of $3+1 = 4$ spin states of pairs electrons associated with a pair of flux tubes connecting DNA nucleotide and lipid layer.

2. If the codewords of the genetic code formed by three codons are taken as basic units then the states of the particles used must correspond to 64 DNA codons. RNA nucleotides and amino-acids could also involve analogous flux tubes beginning from the paired dark protons. The obvious choice at DNA end are those dark proton states, which correspond to 64 DNAs. At the lipid end the dark proton state would be fixed by base pairing condition.

   An interesting question is whether phospholipid states can be said to be coded by DNA codons (surjective many-to-1 map of DNAs to lipid states). This question is quite general: is the possible DNA dark proton-biomolecule correspondence surjective so that genetic code would be much more general than thought.

   Hu and Wu [J20] have observed that proton pairs with members at opposite sides of cell membrane have spin-spin interaction frequencies in ELF scale. The TGD inspired the proposal [K66] was that the protons are dark and form sequence at both sides of the lipid layer.

7.4 Some Phenomena Discussed By Geesink From TGD View Point

In the sequel some of the numerous phenomena discussed by Geesink are considered from TGD point of view with emphasis on phyllosilicates and possible mechanism behind their positive health effects.

7.4.1 What Phyllosilicates Are?

Silicate minerals (`http://tinyurl.com/y9pb2hrs`) constitute approximately 90 per cent of the crust of Earth. Quite generally, these minerals contain Si, O and almost any other element typically

serving the role of cation in covalent bond. One can get an idea about the valence bond structure of the silicate mineral by using the familiar octet rule demanding full shells for anions. Typically one has SiO_4^{-4} tetrahedra as basic anion connected to 4 cations - in particular Si which can serve as both cation and anion. Note that for purely geometric reasons tetrahedra cannot form an infinite sized regular crystal. Quartz obeying chemical formula SiO_2 is the most well-known and simplest silicate mineral. There exist 6 different groups of silicate minerals and phyllosilicates are one of them.

Phyllosilicates (`http://tinyurl.com/y9enuwfs`) are sheet silicates formed from parallel sheets of silicate tetrahedra with Si_2O_5. All phyllosilicate minerals are hydrated with either water or hydroxyl (O=COH)groups attached. This makes them biologically especially interesting. There are four groups of them: serpentines, clays, micas, and chlorites ("chlorite" has nothing do with Cl). The characteristic property is -O-H group and is expected to be of special interest biologically. There are also other silicate minerals which can contain -O-H groups but only phyllosilicates contain them always.

One highly interesting property of phyllosilicates is that they are natural semiconductors. Semiconductors or even semi-superconductors are highly interesting biologically: consider only the pioneering work of Becker with DC currents [J6] discussed in [K42] and the recent work of Bandyophyay's group with microtubular semiconduction [J17, J4]- or maybe even "semi-superconduction") discussed in [K44, K62].

Geesink et all have used various dopands on silicate semiconductors and have found that the dopand ions have characteristic biological roles. Frequency mapping of the silicate semiconductors is carried out, and even storing frequencies to semiconductor materials has been found to be possible. This brings strongly in mind the work of Cyril Smith [I65] and the notion of water memory based on frequency storage discussed in [K24]. Also the presence of cyclotron frequencies associated with the "endogenous" magnetic field $B_{end} = .2$ Gauss first discovered by Blackman [J8] and other pioneers of bio-electromagnetism (discussed in [K38]) has been found and also evidences for multiples of basic frequencies coming as powers of 2 and 3 suggesting that the Pythagorean scale coming as quints (powers of 3/2 projected to the basic octave) might be fundamental in biology as proposed in the model of harmony in 12-note scale generalizing to a model of genetic code and suggesting that the 3-chords of so called bioharmonies with 64 basic chords are fundamental in living matter and realized also in terms of dark photons [L12] [K43].

7.4.2 Some Effects

Many of the effects listed by Geesink have not caught my attention and it is interesting to look whether they might allow to sharpen TGD based vision discussed above.

1. Phyllosilicates are natural semiconductors and reported to be able to store frequencies, which brings in mind water memory [K24]. Cyclotron frequencies assignable to magnetic field strength .2 Gauss are assigned with them and Geesink claims evidence for a Pythagorean spectrum of frequencies coming as power of 2 and 3 multiples of the fundamental frequency.

2. Phyllosilicates generate also THz/microwave radiation having biological effects. Frequency matters instead of amplitude, which is very weak. Thus the effect looks quantal. There are both frequency, temperature, and amplitude windows. The energies of this radiation are below thermal energy so that one encounters what might be called kT - paradox if one wants to understand the effects quantally.

3. Phyllosilicates are used in a form of cation exchanged silicate sheets as catalysts, which suggests that they might act also as prebiotic catalysts. They are also used in nano-technology as nano-materials, nano-wires and patterned surfaces in nano-biological devices. Andrew Adamatsky has developed a model of cellular automation based on oscillators in phyllosilicate excitable automata [I58] (`http://tinyurl.com/y7kbszgj`).

This dark irradiation could induce plasma oscillations with electron density of one electron per volume with scale of about 1 Angstrom perhaps applying in the case of EZs giving frequency $\succeq$ 9 THz, which corresponds to .03 eV slightly below the thermal energy and the energy of cell mambrane Josephson junction. It could also induce transitions between Rydberg states possibly

present in living matter. For hydrogen atom THz radiation would induced transitions between states with principal quantum numbers $n, n+1$ for $n \geq 10$, which corresponds to atomic radius about 10 nm, cell membrane thickness. THz/microwave radiation could also induce transitions of proteins and interaction with water clathrates.

TGD based explanation would be based on following basic ideas.

1. Quantum criticality occurs only for some critical ranges of parameters and could provide a generic explanation for the amplitude and temperature windows. Frequency windows in the case of cyclotron frequencies could be due to the windows for magnetic field strengths due to quantum criticality with respect to the generation of supra currents.

2. Large h_{eff} radiation with quanta having energies above thermal threshold and frequencies in THz/microwave range would induce classical coherence at the level of visible matter. Weak external em signal generates coherence - classical and perhaps even quantum mechanical. One can ask whether the emergence of coherence in mechanical systems could be induced in this manner.

3. Bose Einstein condensates and super-conductivity are speculated to be present. In TGD framework it would be enough to have BE condensates for cyclotron radiation and that in coherent oscillation modes proposed by Fröhlich would not be necessary. A storage of metabolic energy to cyclotron Bose-Einstein condensates could take place.

4. The EZs of Pollack would have natural description in TGD framework and would be analogs of electron plasmas. The coherence regions proposed by Del Giudice have much weaker experimental status. One should understand the formation of EZs and how the water molecules make coherently a transition from $2H_2O$ to $H_3O_2^-$ + dark proton in EZ, and how this state can be stable despite its large negative charge due to charge separation. If coherence regions exist it is natural to assume the they are precursors of EZs. To my opinion water clathrates are however more feasible candidates in this respect.

5. Phase transitions increasing h_{eff} by a power of 2 following by a compensating phase transition reducing h_{eff} back to 2 by increasing the p-adic length scale by the same power of 2 so that the expanded volume is not affected could create Rydberg states from states with low principal quantum number. The transition should respect rotational symmetries.

Davydov soliton propagating along protein as a kind of acoustic wave is classical candidate for biologically important excitation possibly coupling with THz/microwave radiation. Microwaves are strongly absorbed by atmosphere which would mean that they can be important only inside organisms whereas dark cyclotron radiation with EEG frequencies could have wave lengths of order Earth size scale or even large. Also the magnitude of quantum very small as compared to thermal energy.

7.4.3 Plasma Waves And Acoustic Oscillations

Geesink emphasizes the importance of plasma oscillations in THz/microwave range [L19]. Plasma frequency is analogous to cyclotron frequency in that it that it is purely classical notion. The fact that they are longitudinal oscillations suggets that they are not so fundamental as cyclotron radiation although also now energies would be proportional to h_{eff} and could be in bio-photon range. The plasma frequency is proportional to $e \times \sqrt{n/m}$ and cyclotron frequency to eB/m. Also the appearance of electron density also implies that plasma oscillations are not so fundamental as cyclotron radiation. Also the appearance of electron density also implies that plasma oscillations are not so fundamental as cyclotron radiation. For water with 1 electron per two water molecules (EZ) one would obtain 2.4 THz frequency assuming density of water.

Plasma oscillations require the presence of ionic lattice characterize ordinary biomatter. For dark matter at flux tubes only 1-D lattice structure can be imagined. Plasma oscillations might therefore belong to the classical part of the biophysics like biochemistry. They would be subject to control from magnetic body. Dark photons with energies above thermal threshold can induce plasma oscillations by inducing the plasma oscillations resonantly if h_{eff} has proper - rather small - value.

One of the open questions has been whether there are also the analogs of bio-photons in IR above thermal threshold. Cell membrane would radiate generalized dark Josephson photons with energies $E = \Delta E_c + E_J$. ΔE_c is difference between cyclotron frequencies associated with flux tubes at different sides of cell membrane and corresponds to an energy in visible-UV range if $h_{eff} = h_{gr}$ hypothesis [K76] holds true.

Typically the energy range would be that for cyclotron photons and in visible and UV but in special case one would obtain ordinary Josephson photons with energy spectrum $E = ZeV \sim Z \times .05$ eV just above thermal energy and frequencies about $(12 \times Z/h_{eff}$ THz. This is above THz/microwave region for ordinary value of Planck constant. Relatively small values of $h_{eff} = n \times h$ would give frequencies $f = E/h_{eff}$ in these regions. This part of the Josephson radiation from cell membranes acting as ordinary Josephson junctions and could induce plasma oscillations among other things.

Also the decay of dark photons to ordinary photons could be considered and is suggested by the n-sheeted covering of the space-time sheets associated with $h_{eff} = n \times h$. Therefore also energetic effects could below thermal energies could be achieved besides frequency based effects represented by the coupling with acoustic oscillations and plasma oscillations.

The description of plasmons in many-sheeted space-time of TGD Universe is a demanding challenge. Electrons of plasma wave correspond to different space-time sheets than the ionic lattice. Electrons experience the ionic em fields and the field created by electrons themselves at ionic space-time sheet through wormhole contacts to the space-time sheet of ions. Only the ions not screened by electrons contribute. The challenge is to understand how electrons are able move coherently. Does this require coherence in micron scale and is this coherence forced by the presence of dark matter? In any case, the fundamental description should be in terms of magnetic flux tubes and massless extremals (MEs, topological light rays). The usual description is an approximation obtained by lumping together the sheets of many-sheeted space-time to single sheet and describing the interaction of test particle with induced fields at space-time sheets using standard model.

7.4.4 The Transformation Of Dark Photons To Phonons And Plasma Oscillations

The transformation of dark photons to dark photons and plasma oscillations could take place and transform macroscopic quantum coherence to classical coherence at the level of visible matter.

1. The transformation of both ordinary dark photons to dark phonons and maybe even dark plasmons can be considered. The dispersion relations in the case of phonons are of same form but velocities differ dramatically. Energy and momentum conservation plus gauge invariance fixes the transformation amplitude essentially uniquely. Simplest process is 2 photon$\leftrightarrow$ 2 phonons such that phonons have in excellent accuracy opposite 3-momenta. The amplitude is in relativistic notation proportional to $k^1_\mu F^{\mu\beta}(a) F^\nu_\beta(b) k^2_\nu + (1 \leftrightarrow 2)$, here k^i denotes the momentum 4-vector of phonon and $F(a/b)$ denotes the electromagnetic field tensor assignable to the the photon a/b. Similar expression should apply in the case of plasmons.

2. Cyril Smith talks about what I see as different phenomenon in which low frequency em signal is transformed to high frequency signal with much lower frequency [I65] [K24]. A favored frequency ratio is reported to be $f_{high}/f_{low} = 2 \times 10^{11}$.

   I have considered a TGD based description based on the transformation of dark photons with low frequency but high energy $E = h_{eff} \times f_{low}$ to ordinary photons having $E = \times f_{high}$ [K24]. Smiths's findings suggest a favored value $h_{eff}/h = f_{high}/f_{low} = 2 \times 10^{11}$. Also bio-photons in visible and UV range would be ordinary photons resulting from dark photons in this manner. This suggests that the deeper description of the coherence is as quantum coherence induced by macroscopic coherence at the level of dark matter. Dark matter would control ordinary matter by forcing it to oscillate coherently.

3. Dark photons, phonons, plasmons, etc.. would appear at quantum criticality and this gives an important guideline in the attempts to construct models.

7.4.5 Why Do Phyllosilicates Have Positive Health Effects?

The article of Geesink contains a long list of positive health effects due to the presence of phyllosilicate minerals. Water clathrate structures are stabilized; formation of oligomers is catalyzed; silicate minerals have sequence-, regio-, and homochiral selectivity; they absorb nucleic acids on the mineral surfaces (prebiotic habitats); they catalyze vesicle formation; they protect DNA against X-ray and UV; they protect adenine exposed to gamma radiation.

1. The transformation of X-ray, UV, and maybe even gamma radiation (emitted in the possible formation of dark nuclear strings at magnetic flux tubes) to low frequency dark radiation at magnetic flux tubes and therefore having no direct interaction with DNA is one possible mechanism. Absorption of nuclei acids and catalysis of oligomers could be essential for the transfer of dark genetic code to ordinary RNA by pairing the flux tubes containing dark proton sequences with RNA sequence. This could be exchange of the dark proton flux tube. In the case of anionic structures this could be understood if fourth phase of water is involved as dark photons at the flux tubes of the magnetic body generated as the silicate mineral was formed.

2. The presence of say silicate minerals, also quartz, in living matter could strengthen the cyclotron resonances if weak for some reason - say by the interaction with man-made random radiation tending to destroy the effects of coherent behavior induced by dark photons. The magnetic body of the organism could be somehow damaged (health would be also health of magnetic body!) and unable to carry out the biocontrol. Phyllosilicates (for instance) would strengthen the dark photon radiation responsible for the control.

3. What about the positive biological effects of quartz crystals? Quartz does not have structural negative charge since it obeys effective chemical formula SiO_2. As found, charge neutralization at the boundary of quartz crystal is still needed and O^-:s at the surface could be replaced with -O-Hs. The presence of EZs could induce the transition back to O^- and generate dark proton so that also now dark magnetic body, dark cyclotron radiation, and even the analogs of bio-molecules as dark protons sequences could be present.

The picture becomes more attractive if one assumes that silicate minerals are accompanied magnetic flux tubes carrying dark nuclei and representing prebiotic phase. Ordinary DNA, etc could have emerged as a more faithful representation of dark genetic code by EZ mechanism generating also magnetic body for DNA. Ontogeny recapitulates phylogeny principle applied to silicates and bio-molecules would suggest that silicate minerals interact with DNA via dark matter.

7.5 Basic TGD Based Vision About Prebiotic Evolution

The fact that phyllosilicates generated in the interaction of water and silicate minerals have positive health effects suggests that they have played an important role in prebiotic evolution. There is indeed a lot of evidence to this direction coming from other sources: phyllosilicates allow adsorption of nucleotides and amino-acids, favour their polymerization, and induce the generation of lipid vesicles serving as predecessors of cell nucleus.

My own highly non-orthodox proposal [L45] is that prebiotic and even biotic lifeforms evolved in underground oceans, where UV radiation meteoric bombardment was absent. They were burst to the surface of Earth in Cambrian explosion in rapid expansion of Earth (cosmic expansion should take place as rapid phase transitions instead of smooth expansion - this is consistent with the fact the sizes of astrophysical objects are not observed to steadily increase). Basalt would have provided the silicate minerals having also dark magnetic bodies in presence of water and EZs. Chondrites from outer space contain basic bio-molecules and Earth has been formed from chondrites: therefore basic biomolecules would have also been present.

One prediction relates to the question about how oil and coal were formed (`http://tinyurl.com/dyjmmw2`. Two competing theories about the origin exist (`http://tinyurl.com/863hucw`).

1. The dominating theory assumes a biogenic origin of petroleum and coal (`http://tinyurl.com/dyjmmw2`, and states that they are produced from the organic material at the surface of

Earth. At the dry land peat is formed first and later transformed to coal under heavy pressure. Coal it is transformed to oil and transferred to towards surface of Earth. Analogous process process would have occurred at the bottom of ocean: organic material would have formed sediments and these lose gradually contact with oxygen. This would induce transformation to coal with a very slow rate. A strong support for biological origin is the presence of complex aromatic biomolecules such as porphyrins assignable to basic metabolic mechanisms - in particular photosynthesis.

2. Second theory assumes abiogenic (one might say geological) origin so that the term "fossil fuel" would not be appropriate. Methane and simple hydrocarbons would have been present inside the mantle. This kind of hydrocarbons are encountered in chondrites, which have probably served as building bricks of Earth. Methane appears also at other planets. The presence of complex biomolecules in oil is the problem of the abiogenic model, and one must assume that they appeared to the oil as it was in contact with ordinary biological matter.

   This model model however provides a more convincing explanation for the isotope ratios of oil than biotic theory. The ratios would correspond to those in magma and chondrites and also metallic and isotopic compositions are explained (at the surface of earth interaction with cosmic rays affects the ratios so that one can distinguish between the two models). Also the presence of He can be explained. The model also predicts that oil and coal fields are large scale structures and oil and cola should appear also in non-sedimentary rocks. These predictions are correct.

Both theories have strong and weak points and both mechanisms might be involved. TGD suggests a modification of the abiogenic theory. Petroleum and coal could be produced from prebiotic and even bacterial lifeforms living in the mantle and their presence could explain the origin of the oil and coal at least partially. This would resolve the problem of both options. Of course, both this and standard mechanism could be involved.

7.5.1 Basic Challenges

The concretization of this vision involves several challenges.

1. One must find whether the abundances of biologically important elements in Earth's mantle are consistent with those in living matter. This will be discussed later.

2. Electric discharges were present in Urey-Miller experiments. What could have been their function? The first guess is that they provided energy. Second guess is that they provided (also) magnetic flux tubes for dark protons to be transferred to form dark nuclei. Did lightnings serve the same function during prebiotic era? Did gel phase in Pollack's experiments perform the same function. Of course, lightnings could have provided also the UV light initiating the chain reaction generating EZ.

3. Ordinary solar radiation would have been absent. What served as the source of metabolic energy? How photosynthesis could have emerged? There are several options that one can consider.

   (a) The key observation is that the recent temperature in Earth's core is near to the metabolic energy quantum: .44 eV. The temperature of solar radiation about .58 eV! Could prebiotic life have emerged near the core and emerged to the surface in volcanic eruptions? Could dark photons from the core been able to propagate to underground oceans and provide the metabolic energy inducing the formation of EZs? Could highly developed lifeforms able to carry out photosynthesis have burst to the surface of Earth in Cambrian explosion?

   (b) Dolar radiation transformed to dark photons in the EZs associated with the water clathrates in atmosphere and propagated along dark flux tubes to the underground oceans.

   (c) If the generation dark nuclei liberated binding energy at bio-photon energy range, dark nuclear energy could have made prebiotic life independent of external energy sources.

4. Atmosphere would have been absent. This need not be a shortcoming: there would be no UV radiation and no meteoric bombardment. In the experiments of Miller utilizing simple precursors like NH_3,CH_3 in presence of water and simulated lightnings reducing atmosphere was essential for obtaining amino-acids in experiments (http://tinyurl.com/ycz6gtu8). Adenine, which is building brick of ATP, was formed when a system consisting of HCN and NH_4OH and montmorillonite was exposed to electric discharge. It is now however thought that the atmosphere was oxidizing, which supports the view that prebiotic life developed underground.

   Could an environment containing water and phyllosilicates have provided the counterpart of reducing atmosphere? Wikipedia tells that reducing molecule in reaction donates electrons and oxidizing molecule receives them. (http://tinyurl.com/q5g672s). Basic biologically important atoms (H,K,Na,Ca,Mg) are electron donors and reducers and Cl is oxidizer. In oxygen rich atmosphere Oxygen is oxidizer. For instance, montmorillonite contains all above mentioned reducing ions. Maybe phyllosilicates could provide the counterpart of reducing atmosphere their de-adsorbtion from the mineral surface in atomic form occurs with a considerable rate.

7.5.2 Are The Abundances Of Biologically Important Ions Consistent With Their Abundances In Earth's Mantle?

One possible objection is that the abundances of various biologically important molecules are different in the Earth's crust and in (say) human body (http://tinyurl.com/p3vse). The average abundances of carbon, nitrogen, carbon, sulphur, chlorine, phosphorus are considerably lower in the Earth's crust than in human body. These data are about Earth's crust. The problem disappears if the prebiotic evolution has taken place at special sites, perhaps even below crust.

1. Nitrogen is trace mineral in Earth's crust (3.3 per cent in human body). The low abundance is probably due to the degassing to the atmosphere. In mantle the concentration of nitrogen could have been much higher and in underground oceans a kind of nitrogen cycle might have been establishes. It is known that the N_2 in atmosphere originates from regions of the Earth where plates are converging. In Venus and Mars there is no plate tectonics and therefore a lack of N_2. The obvious guess is that the rapid expansion of Earth radius by factor two generated the plates during Cambrian explosion and the nitrogen which was in underground oceans aqueous ammonium NH_4^+ was degassed (http://tinyurl.com/ya36k9zl).

2. What about carbon (.03 per cent in crust and 18.5 per cent in human body), which is also a key element of life. The positive surprise is that the vast majority of carbon resides in the deep Earth, below the surface, maybe 90 per cent of it. http://tinyurl.com/cg83zv7. Most of carbon is in form of diamonds and not biologically interesting. There is however evidence that methane CH_4 is formed in the upper mantle 100-300 km below the 5-70 km thick crust (note that mantle is about 2900 km thick) (http://tinyurl.com/ybzgx325). This has inspired speculations about new sources of oil replacing the fossil fuels. To me the more interesting possibility is that the life could have develop below crust.

3. One can worry also about Cl^- (0.01 per cent in crust and .2 per cent in human body). The web search suggests that the situation about the content of Cl^- in mantle is not settled. I also understood that the abundance of Cl^- is not constant in mantle. What comes in mind that Cl^- is solved into the water reservoirs to form HCl. Cl abundance is higher in the oceans at the surface of Earth than elsewhere.

As already noticed, the proposed mechanism for the formation of EZs generates dark proton sequences having interpretation as dark nuclei. These could suffer dark beta decay to more complex nuclei and dark nuclei could transform to ordinary nuclei. There is evidence for bio-transmutations [C3, C9]. Could this allow the prebiotic life to generate some of the needed atomic nuclei artificially?

7.5.3 The Energetics Of Ezs

The above described mechanism for the generation of EZs involves the creation of dark nuclei as sequences of dark protons liberating nuclear energy compensating for the electronic Coulomb re-

pulsion can occur as a chain reaction if the distances of linear molecules containing -O-H structures have such distances that the dark nuclei can form. The liberated dark gamma rays should decay to bunches of ordinary photons inducing *hydrogen bonded* $2H_2O \rightarrow H_3O_2^-$ + *dark proton* and would care that the process continues as a chain reaction.

Contrary to the first guess, gel would not serve as an energy source but provide magnetic flux tubes at which the dark protons can condense. Also the electric discharges in Urey-Miller experiment would have this function. Lightnings are known to be accompanied by gamma rays and extremely energetic electrons. In TGD Universe this requires darkness and magnetic flux tubes. Same should be true also for electric discharges, which are indeed a critical phenomenon. Could the dark flux tubes associated with lightnings penetrate below the Earth's crust? There seems to be no obvious argument against this - the very definition of darkness suggests this.

The dark ionization of also other than -O-H bonds is possible in presence of EZ by the decay of dark gamma rays to ordinary photons and it is possible to generate dark variants of biologically important ions. One cannot however expect formation of the analogs of dark nuclei for sequences of heavier dark ions nor for dark electrons. They might be generated from phyllosilicates such as montmorillonite as dark ions. The presence of water could be enough for this.

7.5.4 The Role Of Phyllosilicates

Phyllosilicates are formed in the weathering of volcanic glass and rocks. Water in contact with volcanic glass and rocks produces clay minerals. This could also occur also in underground oceans without the presence of the atmosphere. How phyllosilicates in presence of water (and generated by the presence of water from simpler minerals) might help to achieve during prebiotic evolution? It is known that phyllosilicates adsorb amino-acids and RNA and induce their polymerization. Montmorillonite induces also the formation lipid miscelles serving as predecessors of cell membranes.

A TGD inspired vision about the role of phyllosicilicates

If TGD view is correct, phyllosilicates in presence of water and EZs plus metabolic energy source allowing their generation might have additional functions.

1. Phyllosilicates contain -O-H:s as a basic building brick and the transformation -O-H $\rightarrow$ -O^- plus dark proton is highly suggestive in the presence of EZs. This would help to generate dark proton sequences assignable to the boundaries of phyllosilicates providing the analogs of basic bio-molecules DNA, RNA, and amino-acids, and possibly realizing a very simple variant of genetic code in the sense that dark proton state correlates with the anion created.

   The dark proton sequences would be probably rather boring if the spin state of dark proton correlates strongly with the site, where it came from. This mechanism is attractive because it would allow to understand the emergence of immune system as will be found. For weak correlation so that the phyllosilicate analog of genetic code would be very many-to-one large number dark proton sequences would be generated. If RNA/DNA/amino-acid can condense around the dark proton templates with a 1-1 correlation between nucleotides/amino-acids a much more richer variety of these polymers are obtained.

2. The interaction of phyllosilicates with EZs could provide the dark variants of the biologically important ions. Montrorillonite contains almost all biologically important ions except anion Cl_- and can also doped by replacing -OH_- with Cl^-.

3. The layers of phyllosilicates could define kind of semi-super-conductors and there could be Josephson junctions between the layers so that primitive version of cell membrane might become possible generating dark photons at Josephson frequencies ZEV/h_{eff}.

4. If the lipid miscelles can surround EZs emerged from water clathrates, DNA or its predecessor could be stable inside them, and one would have a predecessor of cell nucleus and even cell. EZ could also stabilize the organic phosphate PO_4^{-3} containing O= and appearing in DNA (only diphosphate $P_2O_7^{-4}$ containing 2 O=:s is usually stable).

5. In TGD framework chiral selection can be explained in terms of large h_{eff} scaling up the weak scale from 10^{-17} meters to even cell length scale for the dark variants of weakly interacting

particles. This would allow to understand how the preferred chiralities of bio-molecules emerge. Quartz, which is the simplest silicate mineral is already chiral. Chirality might be transferred from the surface of the quartz crystal to that of dark DNA.

Adsorption of amino-acids and nucleic acids on phyllosilicates

One must take very cautiously the existing data about the adsorption of biomolecules on clay minerals. Probably water solutions are used but certainly not EZs of Pollack. Their use could change the situation completely. The experiments should be carried out in a situation in which coherence regions are generated (perhaps by electric discharges or spontaneously) and the analog of solar radiation provides the needed metabolic energy to generate EZs.

EZs could lead to the transformation -O-H$\rightarrow$ O^- + dark proton and assign dark proton sequences to phyllosilicate surfaces. After this DNA/RNA and amino-acid polymers could be formed through a kind of transcription process using dark proton sequences as template. One could say that dark proton sequence is "stolen". If dark proton sequences "code" for phyllosilicate molecules in 1-1 manner, the resulting sequences could be rather simple. If the code is many-to-one as in the case of the ordinary DNA-amino-acid code, rather complex polymers could be obtained.

Hideo Hashizume summarizes the existing ideas and experimental knowledge about the role of clay minerals in the evolution of life in in his book *Clay Minerals in Nature- Their Characterization, Modification, and Application*. The chapter *Role of Clay Minerals in Chemical Evolution and the Origins of Life* can be found in web (`http://tinyurl.com/qa8y5bs`).

Concerning adsorption of basic biomolecules montmorillonite (`http://tinyurl.com/ybbg7jf8`) and kaolinite (`http://tinyurl.com/mzeffyl`) $Al_2Si_2O_5(OH)_4$ are the most studied examples (`http://tinyurl.com/ycz6gtu8`).

Montromorillonite has 2 tetrahedral sheets sandwiching a central octahedral sheet. Plate shaped sheets have average diameter around 1 micrometer. Chemically montrorillonite is hydrated sodium calcium aluminium magnesium silicate hydroxide $(Na,Ca)_{1/3}(Al,Mg)_2(Si_4O_{10})(OH)_2\cdot nH_2O$ able to contain thus almost all biologically important ions. Cl^- is not included but can replace $(OH)^-$ in the hydroxyl site.

Adsorption of the free positively charged amino-acids aspartic acid, glutamic acid, and phenylalanine is reported to occur via cation exchange. Alanine, serine, leucine, aspartic acid, glutamic acid, phenylalanine adsorbed to H-montmorillonite occur by proton transfer. These amino-acids are either negatively charged or neutral. The adsorption of glycine and its oligomers occurred in Ca-montmorillonite Ca-illite and their adsorption increased with the length of oligomer.

Polymerization of bio-molecules

Thermal vents are promising places for prebiotic polymerization. Repeated wetting and drying at beach is known to promote polarization at the surface of Earth. Similar situation might be encountered also in underground oceans as a tidal effect.

What is known is about polymerization induced by phyllosilicates in absence of EZs?

1. The polymerization of peptides to give oligomers (same unit repeating) is observed. Also nucleotide polymers (RNA) are generated. In experiments leading to generation of RNA polymers a condensation of 5^{prime}-phosphorimidazolide obtained from RNA nucleotide by replacing O- in phosphor with carbon-5-cycle containing three nitrogens.

   RNA world as a model for prebiotic evolution requires 40 monomers theoretically. 6-14 are obtained. The reason is that hydrolysis competes with polymerization. A possible manner to overcome the problem would be formation of EZs preventing hydrolysis.

   Polymerization up to 55 units is however achieved in presence of montmorillonite using successive feedings of monomers as found by Ferris et al [I78] (`http://tinyurl.com/y7mfqc8t`). Note however that at the surface of Earth montrorillonite is formed by the weathering of volcanic ash (`http://tinyurl.com/y6uevvkj`): it is not clear whether it can be formed in underground oceans.

2. The polymerization of DNA has not been reported. The reason probably relates to the presence of high energy phosphate bond and to the instability of DNA in ordinary water. It

would be interesting to see if the presence of gel, water and irradiation with ligh could induce DNA polymerization.

3. Riboses are sugars and basic building bricks of DNA and RNA. Sugars have formaldehyde $O{=}CH_2$ as a precursor. Clay minerals can catalyze formation of formaldehyde and stabilize it.

Concerning the polymerization of biomolecules EZs provide an attractive mechanism. First dark proton sequence correlating loosely with the sequence of phyllosilicates at the boundary of a sheet is generated. This would represent "mineral life": something between mineral kingdom and living matter. After that the analog of transcription would occur: DNA-/RNA- or amino-acid sequence would be associated with this sequence. If the correspondence dark proton sequence $\rightarrow$ phyllosilicate unit is very many-to-one, this could give richly structured biopolymers.

DNA and RNA are accompanied by dark proton sequence at flux tube. Could it be that DNA and RNA could be generated from their dark analogs in presence of P_i or PP_i and coherence regions plus radiation at energy near metabolic energy quantum? The hydrolysis of DNA could be prevented inside EZ perhaps enclosed inside lipid miscelle formed in presence of montmorillonite.

These considerations are of course very naive. I have not even mentioned that in biology polymerization is catalyzed by enzymes, also by their RNA counterparts. What the precise function of catalyst could be if EZs and dark proton sequences are present and the relevant processes occur at the level of dark proton sequences? Could the reaction occur as reconnections of magnetic flux tubes associated with domains of reacting molecules forcing the reactants to re-organize around resulting new magnetic bodies. Could catalysis involve the generation of intermediate magnetic flux tubes structures allowing to overcome potential barriers? Phyllosilicates are of course excellent candidates for prebiotic catalysts.

About the origin of phosphate

The phosphate group is in many ways important in living things. It is a component of energy-rich molecules, such as ATP and without phosphates there would be no metabolism in the form as we know it. Phosphate is an important structural component of nucleotides, which are the basic structural units of DNA and RNA. It is bound to coenzymes like NADP/NADPH involved in anabolic reactions (such as photosynthesis in plants and lipid synthesis in animals). It also forms part of the hydrophilic head of phospholipids in biological membrane. Where there is life there is also phosphate, one might say.

Pyrophosphate $PP_i{=}P_2O_7^{-4}$ obtained from P-O-P by adding O= and two $-O^{-1}$:s to both phosphates. Pyrophosphate decays in presence of water to two HPO_4^{-2} so that O= disappears. How could (`http://tinyurl.com/y9eoxnop` be transformed to biologically two bioactive phosphates $O{=}(P\text{-}O\text{-}H))O_2^{-2}$ obtained by adding O= ,-O-H and to $-O^-$. This form of phosphate is needed to build up DNA/RNA, ATP and other phosphate compounds. Is the presence of EZ necessary to stabilize the double bond?

How high energy phosphate bond could be generated?

1. In presence of water $P_2O_7^{-4}$ suffers a hydrolysis to $2P_i$, where the standard notation $P_i = HPO_4^{-2}$ is used. What could happen in presence of EZ? The simplest guess is that the second -O-H loses its proton as dark proton and that what is usually called high energy phosphate bond is generated. High energy phosphate bond need not be the only bond of this kind also other "high energy bonds" are possible.

2. This picture is consistent with the fact that when ATP suffer hydrolysis to $ADP{+}P_i$ or $AMP{+}PP_i$ transforming O^{-1} to -O-H. The energy released - metabolic energy quantum - in ATP$\rightarrow$ $ADP{+}P_i$ is the energy liberated when e proton attaches back to O^-. The dark proton for single phosphate need not belong to a dark nucleus so that it is not at the bottom of potential well and dark proton can attach to O^-. In case of DNA only ordinary protons could be attache ti O^- if dark nucleus accompanies DNA polymer.

3. Phosphorylation and de-phosphorylation could be interpreted in terms of reconnection of flux tubes so that the dark proton associated with phosphate is transferred to the acceptor molecule. I have proposed that the deeper meaning of metabolism is transfer of negentropic

entanglement (NE). The reconnection of flux tubes would transfer NE between ATP and third party to NE between acceptor molecule and third party. There is a large number of alternative identifications for NE. It could be short range entanglement associated with $h_{eff} = h_{em}$ assignable to electron and nucleus of dark atoms, to pairs of atoms or molecules, or very long range entanglement between molecule and large scale structure with size scale of Earth or even galaxy and associated with $h_{eff} = h_{gr}$. Both forms of NE might be involved and distinguish between two evolutionary levels.

4. Short ranged NE could be associated with dark atoms for which the scale of binding energy behaves like $1/h_{eff}^2$ and is thus reduced for dark atoms [K75]. The creation of dark atoms would require metabolic energy. This metabolic energy could also be liberated as dark atoms transforms to ordinary atom. The dark atoms in nutrients transforming to ordinary atoms could provide the metabolic energy driving protons through the mitochondrial membrane against potential gradient and transforming ADP to ATP contains high energy phosphate bond, which would actually correspond to the presence of dark (say hydrogen -) atom. Phosphate containing the dark atom would carry the NE or be accompanied by dark magnetic flux tube. The transfer of NE would mean its disappearance followed by reappearance and it could happen that $h_{eff}/h = n$ is reduce in the process.

   The simplest view about photosynthesis would be that the absorption of solar photons excites some atoms to dark states and that nutrients contain these dark atoms as stable enough entities. The contamination of nutrients could mean the decay of these dark atoms to the normal states.

Some facts about phosphate in relation to geology are in order.

1. Phosphate minerals (`http://tinyurl.com/yatk23pu`) do not appear in crust. Apatite group consists of phosphate minerals having PO_4 and involves OH, Cl and F. It is one of the few minerals produced and used by biological systems and is used as fertilizer. Teeth and bones contain apatite. Apatite is not common in Earth's crust. Phosphosilicates exist but are very rare in crust.

2. Phosphate can appear also in igneous rocks. `http://tinyurl.com/y7c3kdr5` `http://tinyurl.com/y9j4u3tp` . Jukka Keinonen has written a book titled *Biological Role of Inorganic Pyrophosphate*. He proposes that volcanic magma could act as as a source of pyrophosphate PP_i. Which possesses the double bond and differs only that the protons lost in ionization are not dark.

The findings described by Keinonen raise the hope that water-phyllosilicate system could have utilized inorganic phosphate PP_i and other ions solved in underground oceans. The presence of EZs might have transformed the ordinary ionization of PP_i to dark ionization generating dark protons and perhaps inducing the transformation of PP_i to biologically active phosphate of DNA. The process would be essentially loading energy to give rise to the somewhat mysterious high energy phosphate bond characterizing ATP. In TGD picture also volcanoes could have made possible the bursts of life forms to the surface of Earth.

About the origin of cell membrane and cell

The presence of montmorillonite induces formation of lipid micelles - double layers assembling to vesicles. Hydrophobicity is the driving force and hydrophobic ends of the lipids in the bilayer are directed to the interior. The interior of vesicle would contain EZ generated from water clathrate, montrorillonite sheets, plus chemicals giving rise to the evolution of biomolecules. The stability of the fourth phase of water guaranteed by the cell membrane would prevent dehydration of DNA or of its predecessor.

During prebiotic evolution the DNA would have developed so that it would have correlated more and more strongly with the dark proton sequences defining the actual realization of genetic code. As already mentioned, the recent finding that so called knocked out genes are transcribed correctly [I98] (`http://tinyurl.com/y9849jkz`) supports this view [K76].

Also lattices of phyllosilicate molecules at the surface and linear sequences at the boundaries of sheets could develop symbolic representations in terms of dark proton sequences if the state

of dark proton correlates with phyllosilicate. These correlations could be also absent in which the random sequences of dark protons could serve as templates for the formation of complex DNA/RNA/amino-acid sequences. Same could happen also in the case of RNA and amino-acids. This could be seen as dark variant of ion exchange with ion now a dark proton. Phospholipid lattice of lipid miscell3 could be accompanied by flux tubes carrying dark protons perhaps forming dark nuclei and the liberated nuclear binding energy could have led to a chain reaction reactions the miscelles.

About the evolution of immune system

In [K24] I have considered a model for the evolution of immune system.

1. The prebiotic system can "direct attention" to invader molecule by forming reconnections with its magnetic body. The simplest manner to do this would be reconnection of U-shaped flux tubes serving as kind of tentacles to a pair of flux tubes connecting the it to the invader. The reconnection could form only if the magnetic field strengths are same so that prebiotic system should be able to vary the field strength by varying the flux tube thickness - kind of motor action of the magnetic body. This would allow for the prebiotic system to get information about the magnetic body of the invader molecule.

2. Dark proton sequences at the flux tubes associated with the invader would give rise to a representation about the negative ionic structure of the invader molecule if there is a correlation between ion and corresponding dark proton.

3. Suppose that the prebiotic system can learn this code by the mechanism of directed attention discussed - say by stealing pieces of the dark proton sequences in the magnetic body of the invader molecule! This would make possible to associated to this dark proton sequence an amino-acid sequence by a generalization of translation process proton sequences.

4. These proteins could attack the invader innocuous by attaching to it. Attaching would be the reverse form the transformation of say amino-acid to active state: -O-H$\rightarrow$ O^- + dark proton. Protein would attach to invader molecule in this manner.

The processes -O-H$\rightarrow$ O^- + dark proton and its reversal would be fundamental processes making bio-molecules active in presence of EZs and would give to genetic code and translation and transcription processes realized at the level of dark proton sequences. The analog of ion change reaction for magnetic flux tubes would make it possible to "steal" the dark protons sequences and make the invader molecule innocuous and this would give rise to the development of immune system.

7.5.5 Viruses as fragments of topological quantum computer code?

I was listening a highly interesting talk about viruses in Helsinki by Dr. Matti Jalasvuori, a molecular biologist working in the University of Jyväskylä as a researcher (for information about him and his publications see `http://tinyurl.com/hnj2k2s`). Jalasvuori has published a book about viruses in finnish titled "Virus. Elämän synnyttäjä, kuoleman kylväjä, ajatusten tartuttaja" (see `http://tinyurl.com/zvpvl2f`).

I learned an extremely interesting new-to-me fact about viruses. They might be far from a mere nuisance, In TGD Universe they could be quantum memes, short pieces of a code of quantum computer code, wandering around and attaching to the existing quantum computer code represented by DNA! Replication of viruses would be replication of memes. If the infected organism survives the virus attack by taming the virus and making it part of its non-coding DNA, it will gain more strength! If my computer survives the updating of the operating system, it works better!

Some basic facts

Viruses are very small, few nanometers is the size scale. Virus contains short pieces of RNA or DNA coding for the virus, in particular the protein shell around it, which virus must have in the "non-living" state outside the host cell to which it can penerate. Inside its host this shell melts

and virus attaches to DNA and is able to to replicate. The copies of virus leave the host cell to search for their own host cells.

Usually viruses are regarded as a nuisance. But a new more holistic vision is evolving about viruses and their actual role. Viruses have been present perhaps even before the cell was present in its recent form, they might have been crucial for the emergence of life as we know it and would be also now. The system would consist of various kinds of cells, not necesary those of single organism. The contain several kinds of DNA and RNA: cell nucleus and mitochondria contain their own genomes; there are circular plasmids, and also viruses.

There is a continual exchange of information between cells including viruses as form form of information exchange. In this framework virus represents a meme represented by its DNA ,which does not code for protein shell. This meme wants to replicate and must use the genetic machinery to achieve this. But does virus do this to only replicate and produce more nuisance?

The organism manages to survive the virus attack if it is able to transform the virus so that it cannot replicate. One manner to achieve this would be transformation of the DNA portion due to the attached virus DNA (possible reverse transcribed from the RNA of virus) to a non-coding DNA often referred to as "junk" DNA. Non-coding DNA includes both intragenic regions - introns (see `http://tinyurl.com/j2onbu2`) - and intergenic regions containing for instance promoters and enhancers crucial for the control of gene expression as proteins (see `http://tinyurl.com/juvow7w`). Introns are portions of genes, whose contribution to mRNA is sliced away in translation to proteins. The decomposition to introns and translated regions is dynamical, which gives rise to a rich spectrum of different translations of the gene.

In fact, most of non-coding DNA might be due to viruses! The portion of non-coding DNA increases for speciei at higher evolutionary level. For our species it is estimated to be 98 percent! Most of our genome is "junk" as many biologists still would put it. But can this really be the case? On might think that immune system would have invented some mechanism to prevent the infection of DNA by junk DNA? The size of the trash bin cannot be a measure for evolutionary level! It is also known that virus infections force the organism to change and in some cases to become a better surviver. Viruses would drive evolution.

One can speculate that during the very early period in evolution there were only viruses and proto-cells. There is no need for them to be coded by genes. Self-organization can produce cell membrane like structures: soap films represent an example. The DNA fragments could survive inside these proto-cells but according to simulations done by the Jyäskyl group in which Matti Jalasvuori is working, eventually the evolution would lead to the emergence of parasitic DNA strands, which would soon begin to dominate and kill the protocell.

Viruses might solve the problem. Viruses would attract DNA fragments and replicate with themto build a protein wall around the fragment containg also a piece of DNA of proto-cell. Viruses would leave the proto cell before its death and find another protocell. Gradually genome would be formed as viruses would steal pieces of DNA fragments from protocells. One step in the later evolution could be the elimination of the part of virus coding for the protein shell and the use of the rest as protein coding DNA. For eukariotes the transformation to non-coding DNA including intronic and intergenic DNA becomes possible.

Viruses as pieces of quantum computer code?

Computational thinking would suggest that viruses might make possible the emergence of new biological program modules allowing to use existing program modules coding for proteins more effectively. The different slicings of mRNA dropping some pieces away would correspond to different manners to transform DNA sequences to proteins. But what about intragenic portions of DNA: are they just junk?

Could the non-coding DNA and viruses have a much deeper purpose of existence than mere replication? In TGD Universe this kind of purpose is easy to imagine if the system formed by DNA - say intragenic portions of DNA - and nuclear membrane (or cell membrane) system serves as a topological quantum computer. DNA codons would be connected to lipids of the lipid layer of cell nucleus by magnetic flux tubes carrying dark charged particles. These connections could be also to cell membrane and even to cell membranes of other cells.

The braiding of the flux tubes would define the space-time realization of a quantum computer program. This would represent a new expression of DNA and would explain why so small differences

between our DNA and that of our cousins give rise to so huge differences. What is important that genetic code would not be terribly important: it is braiding that matters now. The realization as quantum computer programs would give rise to cultural evolution, the realization as proteins to biological evolution. There would be a transition from the level of genes to that of memes.

Viruses would correspond to pieces of quantum computer code - memes. They would be wandering between cells and infecting them to get fused to the DNA. If DNA is able to transform them to introns it gets the code. Otherwise it dies. Infection is the necessary price for achieving meme replication. Living cells could be seen quantum computer programs updating them continually. Sounds somehow familiar!

7.6 About Evolution Before Cambrian Explosion

In the following I try to formulate a more detailed TGD inspired vision about how life might have evolved in TGD Universe during pre-Cambrian era before relatively rapid expansion of Earth size by a factor of 2 assumed in TGD versions of Expanding Earth model predicting that cosmic expansion takes place in given scale as rapid jerks rather than continuously as in ordinary cosmology. The key ingredients besides standard facts are TGD inspired interpretation for Cambrian Explosion (CE) [K15, L19], the vision about dark matter as large h_{eff} phases [K75], and the notion of magnetic flux tubes. These provide TGD view about Pollack's Exclusion Zones (EZs, [L15]) as key factors in the evolution of life.

I have gathered useful links from web to build a more detailed version of TGD vision and it is perhaps appropriate to give a list of some useful links - they appear also as references. These links might help reader considerably in getting touch about the problems involved and reader can easily find more.

1. Data related to Mars
   Two generations of windblown sediments on Mars:
   `http://tinyurl.com/y744q6rd`,
   Sedimentary Mars: `http://tinyurl.com/yc6s22ra` *Liquid flows in Mars today: NASA confirms evidence*:
   `http://tinyurl.com/nb4vxbp`

2. Metabolism
   Microbial metabolism: `http://tinyurl.com/ycywt4mj`
   Electron transport chain: `http://tinyurl.com/77zzmak`
   Metal-eating microbes in African lake could solve mystery of the planet's iron deposits:
   `http://tinyurl.com/y9jyodxl`

3. When did photosythesis emerge?
   Ancient rocks record first evidence for photosynthesis that made oxygen
   `http://tinyurl.com/oeu3p9w`
   Cyanobacteria: `http://tinyurl.com/z75nx99`

4. When did oxygenation really occur?
   Great Oxygenation Event: `http://tinyurl.com/q7qfd55`
   Mass-Independent Sulfur Isotopic Compositions in Stratospheric Volcanic Eruptions:
   `http://tinyurl.com/yd38hszw`
   Neoarchean carbonateassociated sulfate records positive $\Delta^{33}S$ *anomalies*
   `http://tinyurl.com/ya77zygs`
   Great Oxidation Event "a misnomer":
   `http://tinyurl.com/qhnhyw2`
   An Oxygen-poor "Boring" Ocean Challenged Evolution of Early Life
   `http://tinyurl.com/y7wavpom`

5. The role of iron
   Evidence for a persistently iron-rich ocean changes views on Earth's early history
   http://tinyurl.com/3uxr6sd

7.6.1 What Happened Before Cambrian Explosion?

The story about evolution of life is constructed from empirical findings based on certain geological, chemical, and isotope signatures. The study of sediment rocks makes possible reasonably reliable age determinations but involves assumptions about the rate of sedimentation. Water, ice, acids, salt, plants, animals, and changes in temperature contribute to weathering and cause erosion involves water, ice, snow, wind, waves and gravity as agents and leads to sedimentation. Also organic material forms sediments both on land and at ocean floors.

Isotope ratios serve as signatures since they are different in inanimate and living matter because those for living matter reflect those in atmosphere and are affected by cosmic rays. The concentrations of various elements are important signatures: mention only oxygen, nitrogen, sulphur compounds such as sulphide, hydrogen sulphide. and sulphate iron, and molybden.

The story involves great uncertainties and should not be taken only as a story. In the following TGD view about how life evolved before Cambrian Explosion (CE) about .6 gy ago is summarized. The Pre-Cambrian part of TGD inspired story differs dramatically from the official narrative since only lakes would have been present whereas official story assumes oceans and continents. Earth would have very much like Mars before CE - even its radius would have been essentially same (half of the recent radius of Earth). This suggests that Mars could teach us a lot about the period before CE **??**. The deviations seem to explain its paradoxical looking aspects of the standard story.

1. Life according to TGD evolved in underground oceans and at the surface of Earth containing lakes but no oceans. The lifeforms at the surface of Earth were prokaryotes whereas the life in underground oceans consisted of relatively complex photo-synthesizing eukaryotes.

2. The recent data from Mars **??** gives an idea what the situation at Earth was during CE since the radius of Earth at that time was very nearly same as that of Mars now. There is evidence for sedimentation (see http://tinyurl.com/yc6s22ra) and for water (see http://tinyurl.com/nb4vxbp) near to and even at the surface provided quite recently. The life at the surface of Earth before CE consisted mainly of prokaryotes and very simple mono-cellular eukaryotes and something like this is expected at the surface of Mars now.

3. Already around 3.5 gy ago prokaryotes using sulphate as energy metabolite were present. Photo-synthesizing cyanobacteria (see http://tinyurl.com/oeu3p9w) emerged about 3.2 gy ago **??**. They became later the plasmids of plant cells responsible for photo-synthesis. The problem of the standard story is that this did not lead to oxygenation of the hypothetic oceans and rapid evolution of eukaryotes and multi-cellulars.

   In standard vision one can explain the absence of oxygen based life in hypothetic oceans by the presence of oxygen sinks. It is known that the ancient oceans (shallow oceans, lakes, or ponds in TGD) were oxygen poor and iron rich. The data about Mars **??** - the red planet because of iron rusting - makes possible to test the feasibility of this hypothesis. The oxygen produced by the cyanobacteria was used to the formation of rusted iron layers giving rise to iron ores. For 1.8 gy ago the formation of rusted iron layers ceased. A possible explanation is that all iron was used. The ores could have been also generated by bacteria using iron as metabolite (see http://tinyurl.com/y9jyodxl) **??** and transforming it to iron oxide. There are however now iron ores after 1-8 gy: did these bacteria lose the fight for survival?

   In TGD Earth atmosphere remained oxygen poor since the small lakes could not produce enough oxygen to induce the oxygenation of the atmosphere. The lakes however gained gradually oxygen. First it went to the oxidation of iron.

4. A general belief has been that about 2.4 gy ago Great Oxidation Event (see http://tinyurl.com/y9jyodxl) (GOE) **??** occurred. The basic evidence for GEO is from volcano eruptions,

which seem to have produced anomalously small amount of sulphur after 2.4 gy. The reason would have been the formation of sulphate SO_4 from atmospheric oxygen and sulphur emanating from volcano.

This evidence has been however challenged by measuring sulphur anomalies for recent volcanic eruptions. Their sign varies in time scale of month changing from positive to negative (see `http://tinyurl.com/yd38hszw`) **??**. It is quite possible that GOE is an illusion (see `http://tinyurl.com/qhnhyw2`) .

5. There is also problem related to to the "boring period" (see `http://tinyurl.com/y7wavpom`) 1.8-.8 gy. It seems that the hypothetic oceans remained still oxygen poor and iron rich **??**. It has been also suggested that the boring period continued up to CE: the first animals after CE could have oxygenated Earth's oceans (see `http://tinyurl.com/3uxr6sd`) **??**. In TGD Universe GOE is indeed illusion for the simple reason that oceans did not exist! Life was boring at the surface of Earth from 3.5 gy to .6 gy.

6. Life would have evolved in underground seas containing oxygenated water, probably already 3.2 gy ago, and making possible photo-synthesis and cellular respiration. Animal cells formed by eukaryotes with nucleus carrying genome with prokaryotes, which later became mitochondria. Plant cells emerged when these eukaryotes engulfed also cyanobacteria, which made photo-synthesis possible. The highly developed eukaryotes were burst to the surface as the radius of Earth increased by a factor two in geologically short time scale. Oceans containing oxygen rich water were formed. CE can be equated with GOE in TGD picture.

   Plants (see `http://tinyurl.com/z75nx99`) are divided into green and red algae, a small group of fresh water monocellulars glaucophytes, and land plants. Land plants must have emerged after CE. Red algae are multi-cellulars (corals are representative example). Also green algae can be multi-cellulars and land plants are thought to have developed from them. An interesting question is whether multi-cellular plants and animals emerged already before CE as the findings would suggest.

The basic objection against this vision is that photo-synthesis is not possible underground. Did photo-synthesis occur in shallow lakes storing chemical energy transferred to the underground seas. This does not seem a plausible option but cannot be excluded. The volcanoes and hydrothermal vents bring water from underground. The water contains ground water and ordinary sea water, which ended underground in various manners, and also magmatic component. The geothermal vents and most volcanoes are however associated with the regions were tectonic plates meet and should not have existed before CE.

TGD inspired model [L19] for Pollack's EZs [L15] suggests a solution of the problem. The formation of these negatively charged regions of water is induced by solar radiation, IR radiation at energies which correspond to metabolic energy quantum, and also at energies corresponding to THz frequency. TGD based model proposes that the protons from EZ becomes large h_{eff} protons at magnetic flux tubes associated with EZ. These flux tubes could be quite long and extend to the underground oceans. Dark photons with energy spectrum containing that of bio-photons could travel along these flux tubes. This suggests that solar radiation transforms partially to dark photons, which travel along flux tubes to the underground sea and transform to ordinary photons caught by photo-synthesizing cells.

Interestingly, also the temperature of Earth is such that thermal radiation would be in visible region and one cannot exclude the possibility that dark photons emerge also from this source. This would make possible also cell respiration and oxygen rich water.

Skeptic is of course wondering whether the flux tubes were long enough.

1. The basic idea about dark matter residing at magnetic flux tubes emerged in TGD from Blackman's findings [J8] about quantal looking effects of ELF em fields on vertebrate brain by assigning them to cyclotron frequencies Ca^{++} ions in endogenous magnetic field $B_{end} = .2$ Gauss, which is by a factor 2/5 weaker than the recent magnetic field of Earth and assigning large non-standard value of Planck constant to the flux tubes so that the energies of ELF quanta are above thermal energies.

2. The value of magnetic field at flux tubes of "personal" magnetic bodies of organisms have B_{end} in its value spectrum. B_{end} could be conserved in evolution somewhat like the salinity of ancient (underground) ocean. The flux tubes of B_{end} would have transformed the photons of solar radiation to dark cyclotron photons allowing them to travel to underground sea and transform back to ordinary photons to be absorbed by pre-plant cells. I have proposed that a similar mechanism is at work in biological body and could explain the reported ability of some people to survive without any obvious metabolic energy feed.

7.6.2 How The Cellular Life Could Have Evolved Before Ce?

In the following I summarize what looks the most plausible view about evolution of life in TGD framework. I represent first basic classification to make reading easier.

Basic classification of lifeforms

Lifeforms are classified into prokarioties (no cell nucleus) and eukaryotes (cell nucleus).

1. Prokaryotes (see `http://tinyurl.com/yazsp5fz`) are mono-cellular and have no separate cell nucleus. They are divided into bacteria and archea. Bacteria do not have genome but only circular DNA strand and usually accompanied by an almost palindrome. Archea have also genes. Cyanobacteria are simplest photo-synthetizing cells: these prokaryotes have been engulfed by eukaryotes to form plant cells containing them as plasmids. Plant cells contain also mitochondria believed also to be ancient prokaryotes which have been "eaten" by eukaryotes. Plants cells contain both mitochondria and plastids whereas animal cells contain only mitochondria.

2. Eukaryotes (see `http://tinyurl.com/y9pzg6jq`) have cell nucleus containing the genome. Eukaryotes divide into three kingdoms: animals (see `http://tinyurl.com/l78hgf8`), plants (see `http://tinyurl.com/ya6fpfkk`), and fungi (see `http://tinyurl.com/ybjgonj7`). Fungi can be said to be between animals and plants: they do not perform photo-synthesis but have cell walls.

Prokaryote-eukaryote distinction

From the existing data one can conclude that during pre-Cambrian period only prokaryotes existed at the at surface of earth - presumably in small lakes in TGD Universe and ocean floors in standard Universe. The first photo-synthetizing prokaryotes - cyanobacteria - emerged about 3.2 gy ago and their predecessors where prokaryotes extracting metabolic energy from sulphate. Cyanobacteria (see `http://tinyurl.com/z75nx99`) **??** are able to survive in practically any imaginable environment:

Cyanobacteria are arguably the most successful group of microorganisms on earth. They are the most genetically diverse; they occupy a broad range of habitats across all latitudes, widespread in freshwater, marine, and terrestrial ecosystems, and they are found in the most extreme niches such as hot springs, salt works, and hypersaline bays. Photoautotrophic, oxygen-producing cyanobacteria created the conditions in the planet's early atmosphere that directed the evolution of aerobic metabolism and eukaryotic photo-synthesis. Cyanobacteria fulfil vital ecological functions in the world's oceans, being important contributors to global carbon and nitrogen budgets.

It is therefore natural to assume that cyanobacteria migrated to underground ocean through pores and fractures at the floor of lakes. They would have fused with pre-eukaryotes having only cell nucleus but no metabolic machinery to become chloroplasts. This would have given rise to the first eukaryotes able to perform photo-synthesis. The primitive cells prokaryotes defining pre-mitochondria would have also fused with these pre-eukaryotes so that both pre-plant and pre-animal cells wold have emerged. Why there is no evidence for the existence of pre-mitochondria as independent cells at the surface of Earth? Did they emerge first underground oceans, where photo-synthesis was not possible and disappeared in the fusion with pre-eukaryotes and therefore left no trace about their existence on the surface of Earth?

Both photo-synthesis and cell respiration involve so called electron transport chain (see `http://tinyurl.com/77zzmak`) (ETC **??**) as a basic structural element. It is associated with any

membrane structure and in photo-synthesis it captures the energy of photon and in cell respiration it catches the biochemical energy which could be emitted as photon so that the fundamental mechanism is the same. This suggests that cell respiration emerged as a modification of photo-synthesis a the level of prokaryotes first. Before the emergence of mitochondria and plastids ETC associated with pre-eukaryote membrane would have served the role of mitochondria or plastid. Using business language, mitochondria and plastids meant "outsourcing" of photosynthesis and cellular respiration.

7.7 About Possible Practical Implications

The predictions and practical implications of the proposed vision - if correct - are probably obvious to the reader but deserve to be stated clearly.

7.7.1 About Predictions And Implications

The proposed vision sounds certainly totally crazy from the viewpoint of standard physics. There are several new notions forced by TGD: the notion of many-sheeted space-time leading to the notion of field/magnetic body as an intentional agent controlling biological body and receiving sensory input from it; quantum criticality explaining dark matter as large h_{eff} phases; ZEO and NMP in (only) apparent conflict with second law predicting the evolution occurs spontaneously.

The most counterintuitive predictions of TGD inspired biology are involved in an essential manner. In accordance with the observation that astrophysical objects do not themselves expand although they participate in cosmic expansion as comoving objects, cosmic expansion is replaced by sequence of rapidly occurring quantum phase phase transitions increasing the size of system by some factor - say two. This justifies Expanding Earth hypothesis and leads to the vision that life could have evolved underground. Second equally counterintuitive prediction is that life emerge as dark nuclear fusion spontaneously and led to generation of both biopolymers and lipid layers.

The model has however testable predictions. The experimental arrangement leading to the formation of EZs can be modified by introducing phyllosilicates and other biologically important biomolecules to see whether the presence of EZs leads to generation of more complex bio-molecules. The claims about biofusion could be also tested. There are connections with large number of anomalous phenomena - free energy and Brown's gas, cold fusion, biological transmutations, boiling salt water, etc... and TGD based explanation could be tested. For instance, biofusion of various light elements could lead to problems with radioactive dating since the ages of samples would have tendency to be too short. In the case of radiocarbon (C_{14}) dating this problem is indeed encountered and one performs a correction (`http://tinyurl.com/p5msnh6`).

It is also easy to imagine far reaching technological implications.

1. Dark fusion followed by a phase transition to ordinary matter could make possible artificial generation of elements. The technological significance for the world in which various resources are rapidly depleting would be immense.

2. The possibility to generate artificial silicate-based intelligent lifeforms of course comes first in mind but involves rather obvious dangers.

7.7.2 But What If Silicate Based Life Takes The Lead?

I do not take seriously the claims of the proponents of strong AI that computers could take power over humans. Strictly classical computers are zombies and uncapable of any intentional behavior. Their real life variants could possess some kind of primitive awareness but this consciousness would probably have very little to do with the program running in the computer.

Of course, computerization can be a real danger to humankind even if computers are for all practical purposes intentionless zombies. Indeed, many leading AI professionals together with Hawking (`http://tinyurl.com/p27q2cn`) have signed an open letter warning about the dangers of military AI. The military applications of computers are developing rapidly and are rather frightening. Already now military professionals talk about information war and suggest that also Finland should take active attitude: not only defense but also attack. Many professionals believe

that systems attacking living targets will be realized within few years. Systems, which behave autonomously and can select their targets, could lead to catastrophe, when their control breaks down. This would be third revolution in warfare after gunpowder and nuclear weapons and those who know should do all that they can to prevent the AI arms race.

I understand that the fusion of biosystems and computers via interfaces consisting of phyllosilicates is also studied and this represent something, which is goes beyond the boundaries of AI. If the vision discussed in this work or some other vision has something to do with reality, they could lead to a development of artificial life forms with conscious intelligence. The recipe would be rather simple: water+ silicates+ something, which could be gels and visible radiation or electric discharges. Silicon would be only replaced with silicates.

These kind of systems could act as intelligent and conscious interfaces between humans and computers. AI specialist could give probably give a long list of other applications. It would be very handy if they could replicate and evolve (by NMP in TGD framework) and this would be one of the goals of R&D activity. They should be also capable of simple intentional behaviors - also by NMP. Presumably we would couple them to world wide web.

But what happens if these local intelligences manage to make a phase transition to a collective intelligence with world wide nervous system that we have generously built for them. NMP suggests that this kind of awakening could occur! What would this magnificient conscious intelligence think about us? Would it regard us as rather primitive carbon based pre-silicate life forms and treat us as we treat what we call "lower" lifeforms - convenient sources of negentropic entanglement, nutrients? Or can we hope that they would tolerate us - NMP is nice principle but it does not guarantee this since it leaves for self to choose between good and evil!

If the hypothesis about generation of dark nuclei is correct then there is also a real danger that nuclear explosion is generated.

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Chapter 8

Expanding Earth Model and Pre-Cambrian Evolution of Continents, Climate, and Life

8.1 Introduction

TGD inspired quantum cosmology [K46, K45] predicts that astrophysical objects do not follow cosmic expansion except in jerk-wise quantum leaps increasing the gigantic value of the gravitational Planck constant characterizing space-time mediating gravitational interactions between two masses or gravitational self interactions. This assumption provides explanation for the apparent cosmological constant.

Also planets are predicted to expand in a stepwise manner. This provides a new version of Expanding Earth theory originally postulated to explain the intriguing findings suggesting that continents have once formed a connected continent covering almost the entire surface of Earth but with radius which was one half of the recent one [K45].

This leads also to a rather fascinating vision about biology. The mysterious Cambrian Explosion [I7] in which a large number of new species emerged suddenly (realized already Darwin as the strongest objection against his theory) could be understood if the life would have gone to underground lakes and seas formed during the expansion period as fractures were formed and the underground cavities expanded and were filled with water. This would have allowed the life to escape cosmic radiation, meteoric bombardment, and the extremely cold climate during Proterozoic period preceding the Cambrian Explosion and migrate back as highly developed life forms as the period of glaciations ended.

Before the Proterozoic era the radius of Earth would have been one half of its recent value and started to grow with gradually accelerating rate. This forces to rewrite the entire geological and climate history of Earth during the Proterozoic period.

1. The postulated physically implausible cyclic appearance of single connected super-continent containing all land mass can be given up and replaced with a single continent containing large inland seas. There is no need to postulate the existence of series of super-oceans whose ocean floor would have subduced totally so that no direct information about them would exist nowadays. It is also possible that the underground oceans have burst into the surface during the phase transition.

   What is amusing that this kind of sea with water volume three times that in ordinary seas has been discovered quite recently (`http://time.com/2868283/subterranean-ocean-reservoir-core-ringwo`) at depth of about 600 km to be compared to the depth of core which is about 2900 km. Water is associated with a mineral known as ringwoodite and ordinary sea water could have originated from this water.

2. The dominating model for pre-Cambrian climate is so called Snowball Earth model [F31] inspired by the finding that signatures of glaciations have been found at regions of Earth,

which should have been near Equator during the Proterozoic. Snowball model has several difficulties: in particular, there is a lot of evidence that a series of ordinary glaciations was in question. For $R/2$ option the regions located to Equator would have actually been near North Pole so that the glaciations would have indeed been ordinary glaciations proceeding from the poles. A killer prediction is the existence of non-glaciated regions at apparent southern latitudes around about 45 degrees and there is evidence for these indeed exists [F53]! The model makes also testable paleomagnetic killer predictions. In particular, during periods when the magnetic dipole in the direction of rotation axis the directions of the magnetic fields for $R/2$ model are predicted to be same at South Pole and apparent Equator and opposite for the standard option.

The appendix of the book gives a summary about basic concepts of TGD with illustrations. Pdf representation of same files serving as a kind of glossary can be found at `http://tgdtheory.fi/tgdglossary.pdf` [L11].

8.2 Experimental Evidence For Accelerated Expansion Is Consistent With TGD based model

There are several pieces of evidence for accelerated expansion, which need not mean cosmological constant, although this is the interpretation adopted in [E4]. It is interesting to see whether this evidence is indeed consistent with TGD based interpretation.

8.2.1 The Four Pieces Of Evidence For Accelerated Expansion

Supernovas of type Ia

Supernovas of type Ia define standard candles since their luminosity varies in an oscillatory manner and the period is proportional to the luminosity. The period gives luminosity and from this the distance can be deduced by using Hubble's law: $d = cz/H_0$, H_0 Hubble's constant. The observation was that the farther the supernova was the more dimmer it was as it should have been. In other words, Hubble's constant increased with distance and the cosmic expansion was accelerating rather than decelerating as predicted by the standard matter dominated and radiation dominated cosmologies.

Mass density is critical and 3-space is flat

It is known that the contribution of ordinary and dark matter explaining the constant velocity of distance stars rotating around galaxy is about 25 per cent from the critical density. Could it be that total mass density is critical?

From the anisotropy of cosmic microwave background one can deduce that this is the case. What criticality means geometrically is that 3-space defined as surface with constant value of cosmic time is flat. This reflects in the spectrum of microwave radiation. The spots representing small anisotropies in the microwave background temperature is 1 degree and this correspond to flat 3-space. If one had dark matter instead of dark energy the size of spot would be.5 degrees!

Thus in a cosmology based on general relativity cosmological constant remains the only viable option. The situation is different in TGD based quantum cosmology based on sub-manifold gravity and hierarchy of gravitational Planck constants.

The energy density of vacuum is constant in the size scale of big voids

It was observed that the density of dark energy would be constant in the scale of 10^8 light years. This length scale corresponds to the size of big voids containing galaxies at their boundaries.

Integrated Sachs-Wolf effect

Also so called integrated Integrated Sachs-Wolf effect supports accelerated expansion. Very slow variations of mass density are considered. These correspond to gravitational potentials. Cosmic

expansion tends to flatten them but mass accretion to form structures compensates this effect so that gravitational potentials are unaffected and there is no effect of CMB. Situation changes if dark matter is replaced with dark energy the accelerated expansion flattening the gravitational potentials wins the tendency of mass accretion to make them deeper. Hence if photon passes by an over-dense region, it receives a little energy. Similarly, photon loses energy when passign by an under-dense region. This effect has been observed.

8.2.2 Comparison With TGD

The minimum TGD based explanation for accelerated expansion involves only the fact that the imbeddings of critical cosmologies correspond to accelerated expansion. A more detailed model allows to understand why the critical cosmology appears during some periods.

Accelerated expansion in classical TGD

The first observation is that critical cosmologies (flat 3-space) imbeddable to 8-D imbedding space H correspond to negative pressure cosmologies and thus to accelerating expansion. The negativity of the counterpart of pressure in Einstein tensor is due to the fact that space-time sheet is forced to be a 4-D surface in 8-D imbedding space. This condition is analogous to a force forcing a particle at the surface of 2-sphere and gives rise to what could be called constraint force. Gravitation in TGD is sub-manifold gravitation whereas in GRT it is manifold gravitation. This would be minimum interpretation involving no assumptions about what mechanism gives rise to the critical periods.

Accelerated expansion and hierarchy of Planck constants

One can go one step further and introduce the hierarchy of Planck constants. The basic difference between TGD and GRT based cosmologies is that TGD cosmology is quantum cosmology. Smooth cosmic expansion is replaced by an expansion occurring in discrete jerks corresponding to the increase of gravitational Planck constant. At space-time level this means the replacement of 8-D imbedding space H with a book like structure containing almost-copies of H with various values of Planck constant as pages glued together along critical manifold through which space-time sheet can leak between sectors with different values of $\hbar$. This process is the geometric correlate for the phase transition changing the value of Planck constant.

During these phase transition periods critical cosmology applies and predicts automatically accelerated expansion. Neither genuine negative pressure due to "quintessence" nor cosmological constant is needed. Note that quantum criticality replaces inflationary cosmology and predicts a unique cosmology apart from single parameter. Criticality also explains the fluctuations in microwave temperature as long range fluctuations characterizing criticality.

Accelerated expansion and flatness of 3-cosmology

Observations 1) and 2) about super-novae and critical cosmology (flat 3-space) are consistent with this cosmology. In TGD dark energy must be replaced with dark matter because the mass density is critical during the phase transition. This does not lead to wrong sized spots since it is the increase of Planck constant which induces the accelerated expansion understandable also as a constraint force due to imbedding to H.

The size of large voids is the characteristic scale

The TGD based model in its simplest form model assigns the critical periods of expansion to large voids of size 10^8 ly. Also larger and smaller regions can express similar periods and dark space-time sheets are expected to obey same universal "cosmology" apart from a parameter characterizing the duration of the phase transition. Observation 3) that just this length scale defines the scale below which dark energy density is constant is consistent with TGD based model.

The basic prediction is jerk-wise cosmic expansion with jerks analogous to quantum transitions between states of atom increasing the size of atom. The discovery of large voids with size of order 10^8 ly but age much longer than the age of galactic large voids conforms with this prediction.

One the other hand, it is known that the size of galactic clusters has not remained constant in very long time scale so that jerk-wise expansion indeed seems to occur.

Do cosmic strings with negative gravitational mass cause the phase transition inducing accelerated expansion

Quantum classical correspondence is the basic principle of quantum TGD and suggest that the effective antigravity manifested by accelerated expansion might have some kind of concrete space-time correlate. A possible correlate is super heavy cosmic string like objects at the center of large voids which have negative gravitational mass under very general assumptions. The repulsive gravitational force created by these objects would drive galaxies to the boundaries of large voids. At some state the pressure of galaxies would become too strong and induce a quantum phase transition forcing the increase of gravitational Planck constant and expansion of the void taking place much faster than the outward drift of the galaxies. This process would repeat itself. In the average sense the cosmic expansion would not be accelerating.

8.3 Quantum Version Of Expanding Earth Theory

TGD predicts that cosmic expansion at the level of individual astrophysical systems does not take place continuously as in classical gravitation but through discrete quantum phase transitions increasing gravitational Planck constant and thus various quantum length and time scales. The reason would be that stationary quantum states for dark matter in astrophysical length scales cannot expand. One would have the analog of atomic physics in cosmic scales. Increases of $\hbar$ by a power of two are favored in these transitions but also other scalings are possible.

This has quite far reaching implications.

1. These periods have a highly unique description in terms of a critical cosmology for the expanding space-time sheet. The expansion is accelerating. The accelerating cosmic expansion can be assigned to this kind of phase transition in some length scale (TGD Universe is fractal). There is no need to introduce cosmological constant and dark energy would be actually dark matter.

2. The recently observed void which has same size of about 10^8 light years as large voids having galaxies near their boundaries but having an age which is much higher than that of the large voids, would represent one example of jerk-wise expansion.

3. This picture applies also to solar system and planets might be perhaps seen as having once been parts of a more or less connected system, the primordial Sun. The Bohr orbits for inner and outer planets correspond to gravitational Planck constant which is 5 times larger for outer planets. This suggests that the space-time sheet of outer planets has suffered a phase transition increasing the size scale by a factor of 5. Earth can be regarded either as n=1 orbit for Planck constant associated with outer planets or n= 5 orbit for inner planetary system. This might have something to do with the very special position of Earth in planetary system. One could even consider the possibility that both orbits are present as dark matter structures. The phase transition would also explain why n=1 and n=2 Bohr orbits are absent and one only n=3, 4, and 5 are present.

4. Also planets should have experienced this kind of phase transitions increasing the radius: the increase by a factor two would be the simplest situation.

The obvious question - that I did not ask - is whether this kind of phase transition might have occurred for Earth and led from a completely granite covered Earth - Pangeia without seas - to the recent Earth. Neither it did not occur to me to check whether there is any support for a rapid expansion of Earth during some period of its history.

Situation changed when my son visited me and told me about a Youtube video [F51] by Neal Adams, an American comic book and commercial artist who has also produced animations for geologists. We looked the amazing video a couple of times and I looked it again yesterday. The video is very impressive artwork but in the lack of references skeptic probably cannot avoid

the feeling that Neal Adams might use his highly developed animation skills to cheat you. I found also a polemic article [F1] of Adams but again the references were lacking. Perhaps the reason of polemic tone was that the concrete animation models make the expanding Earth hypothesis very convincing but geologists refuse to consider seriously arguments by a layman without a formal academic background.

8.3.1 The Claims Of Adams

The basic claims of Adams were following.

1. The radius of Earth has increased during last 185 million years (dinosaurs [I13] appeared for about 230 million years ago) by about factor 2. If this is assumed all continents have formed at that time a single super-continent, Pangeia, filling the entire Earth surface rather than only 1/4 of it since the total area would have grown by a factor of 4. The basic argument was that it is very difficult to imagine Earth with 1/4 of surface containing granite and 3/4 covered by basalt. If the initial situation was covering by mere granite -as would look natural- it is very difficult for a believer in thermodynamics to imagine how the granite would have gathered to a single connected continent.

2. Adams claims that Earth has grown by keeping its density constant, rather than expanded, so that the mass of Earth has grown linearly with radius. Gravitational acceleration would have thus doubled and could provide a partial explanation for the disappearance of dinosaurs: it is difficult to cope in evolving environment when you get slower all the time.

3. Most of the sea floor is very young and the areas covered by the youngest basalt are the largest ones. This Adams interprets this by saying that the expansion of Earth is accelerating. The alternative interpretation is that the flow rate of the magma slows down as it recedes from the ridge where it erupts. The upper bound of 185 million years for the age of sea floor requires that the expansion period - if it is already over - lasted about 185 million years after which the flow increasing the area of the sea floor transformed to a convective flow with subduction so that the area is not increasing anymore.

4. The fact that the continents fit together - not only at the Atlantic side - but also at the Pacific side gives strong support for the idea that the entire planet was once covered by the super-continent. After the emergence of subduction theory this evidence as been dismissed.

5. I am not sure whether Adams mentions the following objections [F6]. Subduction only occurs on the other side of the subduction zone so that the other side should show evidence of being much older in the case that oceanic subduction zones are in question. This is definitely not the case. This is explained in plate tectonics as a change of the subduction direction. My explanation would be that by the symmetry of the situation both oceanic plates bend down so that this would represent new type of boundary not assumed in the tectonic plate theory.

6. As a master visualizer Adams notices that Africa and South-America do not actually fit together in absence of expansion unless one assumes that these continents have suffered a deformation. Continents are not easily deformable stuff. The assumption of expansion implies a perfect fit of *all* continents without deformation.

Knowing that the devil is in the details, I must admit that these arguments look rather convincing to me and what I learned from Wikipedia articles supports this picture.

8.3.2 The Critic Of Adams Of The Subduction Mechanism

The prevailing tectonic plate theory [F27] has been compared to the Copernican revolution in geology. The theory explains the young age of the seafloor in terms of the decomposition of the litosphere to tectonic plates and the convective flow of magma to which oceanic tectonic plates participate. The magma emerges from the crests of the mid ocean ridges representing a boundary of two plates and leads to the expansion of sea floor. The variations of the polarity of Earth's magnetic field coded in sea floor provide a strong support for the hypothesis that magma emerges from the crests.

The flow back to would take place at so called oceanic trenches [F20] near continents which represent the deepest parts of ocean. This process is known as subduction. In subduction oceanic tectonic plate bends and penetrates below the continental tectonic plate, the material in the oceanic plate gets denser and sinks into the magma. In this manner the oceanic tectonic plate suffers a metamorphosis returning back to the magma: everything which comes from Earth's interior returns back. Subduction mechanism explains elegantly formation of mountains [F21] (orogeny), earth quake zones, and associated zones of volcanic activity [F37] .

Adams is very polemic about the notion of subduction, in particular about the assumption that it generates steady convective cycle. The basic objections of Adams against subduction are following.

1. There are not enough subduction zones to allow a steady situation. According to Adams, the situation resembles that for a flow in a tube which becomes narrower. In a steady situation the flow should accelerate as it approaches subduction zones rather than slow down. Subduction zones should be surrounded by large areas of sea floor with constant age. Just the opposite is suggested by the fact that the youngest portion of sea-floor near the ridges is largest. The presence of zones at which both ocean plates bend down could improve the situation. Also jamming of the flow could occur so that the thickness of oceanic plate increases with the distance from the eruption ridge. Jamming could increase also the density of the oceanic plate and thus the effectiveness of subduction.

2. There is no clear evidence that subduction has occurred at other planets. The usual defense is that the presence of sea is essential for the subduction mechanism.

3. One can also wonder what is the mechanism that led to the formation of single super continent Pangeia covering 1/4 of Earth's surface. How probable the gathering of all separate continents to form single cluster is? The later events would suggest that just the opposite should have occurred from the beginning.

8.3.3 Expanding Earth Theories Are Not New

After I had decided to check the claims of Adams, the first thing that I learned is that Expanding Earth theory [F6], whose existence Adams actually mentions, is by no means new. There are actually many of them.

The general reason why these theories were rejected by the main stream community was the absence of a convincing physical mechanism of expansion or of growth in which the density of Earth remains constant.

1. 1888 Yarkovski postulated some sort of aether absorbed by Earth and transforming to chemical elements (TGD version of aether could be dark matter). 1909 Mantovani postulated thermal expansion but no growth of the Earth's mass [F50].

2. Paul Dirac's idea about changing Planck constant led Pascual Jordan in 1964 to a modification of general relativity predicting slow expansion of planets. The recent measurement of the gravitational constant imply that the upper bound for the relative change of gravitational constant is 10 time too small to produce large enough rate of expansion. Also many other theories have been proposed but they are in general conflict with modern physics.

3. The most modern version of Expanding Earth theory is by Australian geologist Samuel W. Carey. He calculated that in Cambrian period (about 500 million years ago) all continents were stuck together and covered the entire Earth. Deep seas began to evolve then.

8.3.4 Summary Of TGD Based Theory Of Expanding Earth

TGD based model differs from the tectonic plate model but allows subduction which cannot imply considerable back-flow of magma. Let us sum up the basic assumptions and implications.

1. The expansion is or was due to a quantum phase transition increasing the value of gravitational Planck constant and forced by the cosmic expansion in the average sense.

2. Tectonic plates do not participate to the expansion and therefore new plate must be formed and the flow of magma from the crests of mid ocean ridges is needed. The decomposition of a single plate covering the entire planet to plates to create the mid ocean ridges is necessary for the generation of new tectonic plate. The decomposition into tectonic plates is thus prediction rather than assumption.

3. The expansion forced the decomposition of Pangeia super-continent covering entire Earth for about 530 million years ago to split into tectonic plates which began to recede as new non-expanding tectonic plate was generated at the ridges creating expanding sea floor. The initiation of the phase transition generated formation of deep seas.

4. The eruption of plasma from the crests of ocean ridges generated oceanic tectonic plates which did not participate to the expansion by density reduction but by growing in size. This led to a reduction of density in the interior of the Earth roughly by a factor 1/8. From the upper bound for the age of the seafloor one can conclude that the period lasted for about 185 million years after which it transformed to convective flow in which the material returned back to the Earth interior. Subduction at continent-ocean floor boundaries and downwards double bending of tectonic plates at the boundaries between two ocean floors were the mechanisms. Thus tectonic plate theory would be more or less the correct description for the recent situation.

5. One can consider the possibility that the subducted tectonic plate does not transform to magma but is fused to the tectonic layer below continent so that it grows to an iceberg like structure. This need not lead to a loss of the successful predictions of plate tectonics explaining the generation of mountains, earthquake zones, zones of volcanic activity, etc...

6. From the video of Adams it becomes clear that the tectonic flow is East-West asymmetric in the sense that the western side is more irregular at large distances from the ocean ridge at the western side. If the magma rotates with slightly lower velocity than the surface of Earth (like liquid in a rotating vessel), the erupting magma would rotate slightly slower than the tectonic plate and asymmetry would be generated.

7. If the planet has not experienced a phase transition increasing the value of Planck constant, there is no need for the decomposition to tectonic plates and one can understand why there is no clear evidence for tectonic plates and subduction in other planets. The conductive flow of magma could occur below this plate and remain invisible.

The biological implications might provide a possibility to test the hypothesis.

1. Great steps of progress in biological evolution are associated with catastrophic geological events generating new evolutionary pressures forcing new solutions to cope in the new situation. Cambrian explosion indeed occurred about 530 years ago (the book "Wonderful Life" of Stephen Gould [I136] explains this revolution in detail) and led to the emergence of multicellular creatures, and generated huge number of new life forms living in seas. Later most of them suffered extinction: large number of phylae and groups emerged which are not present nowadays.

   Thus Cambrian explosion is completely exceptional as compared to all other dramatic events in the evolution in the sense that it created something totally new rather than only making more complex something which already existed. Gould also emphasizes the failure to identify any great change in the environment as a fundamental puzzle of Cambrian explosion. Cambrian explosion is also regarded in many quantum theories of consciousness (including TGD) as a revolution in the evolution of consciousness: for instance, micro-tubuli emerged at this time. The periods of expansion might be necessary for the emergence of multicellular life forms on planets and the fact that they unavoidably occur sooner or later suggests that also life develops unavoidably.

2. TGD predicts a decrease of the surface gravity by a factor 1/4 during this period. The reduction of the surface gravity would have naturally led to the emergence of dinosaurs 230 million years ago as a response coming 45 million years after the accelerated expansion

ceased. Other reasons led then to the decline and eventual catastrophic disappearance of the dinosaurs. The reduction of gravity might have had some gradually increasing effects on the shape of organisms also at microscopic level and manifest itself in the evolution of genome during expansion period.

3. A possibly testable prediction following from angular momentum conservation ($\omega R^2 = constant$) is that the duration of day has increased gradually and was four times shorter during the Cambrian era. For instance, genetically coded bio-clocks of simple organisms during the expansion period could have followed the increase of the length of day with certain lag or failed to follow it completely. The simplest known circadian clock is that of the prokaryotic cyanobacteria. Recent research has demonstrated that the circadian clock of Synechococcus elongatus can be reconstituted in vitro with just the three proteins of their central oscillator. This clock has been shown to sustain a 22 hour rhythm over several days upon the addition of ATP: the rhythm is indeed faster than the circadian rhythm. For humans the average innate circadian rhythm is however 24 hours 11 minutes and thus conforms with the fact that human genome has evolved much later than the expansion ceased.

4. Scientists have found a fossil of a sea scorpion with size of 2.5 meters [I62], which has lived for about 10 million years for 400 million years ago in Germany. The gigantic size would conform nicely with the much smaller value of surface gravity at that time. The finding would conform nicely with the much smaller value of surface gravity at that time. Also the emergence of trees could be understood in terms of a gradual growth of the maximum plant size as the surface gravity was reduced. The fact that the oldest known tree fossil is 385 million years old [I115] conforms with this picture.

8.3.5 Did Intra-Terrestrial Life Burst To The Surface Of Earth During Cambrian Expansion?

Intra-terrestrial hypothesis [K19] is one of the craziest TGD inspired ideas about the evolution of life and it is quite possible that in its strongest form the hypothesis is unrealistic. One can however try to find what one obtains from the combination of the IT hypothesis with the idea of pre-Cambrian granite Earth. Could the harsh pre-Cambrian conditions have allowed only intra-terrestrial multicellular life? Could the Cambrian explosion correspond to the moment of birth for this life in the very concrete sense that the magma flow brought it into the day-light?

1. Gould emphasizes the mysterious fact that very many life forms of Cambrian explosion looked like final products of a long evolutionary process. Could the eruption of magma from the Earth interior have induced a burst of intra-terrestrial life forms to the Earth's surface? This might make sense: the life forms living at the bottom of sea do not need direct solar light so that they could have had intra-terrestrial origin. It is quite possible that Earth's mantle contained low temperature water pockets, where the complex life forms might have evolved in an environment shielded from meteoric bombardment and UV radiation.

2. Sea water is salty. It is often claimed that the average salt concentration inside cell is that of the primordial sea: I do not know whether this claim can be really justified. If the claim is true, the cellular salt concentration should reflect the salt concentration of the water inside the pockets. The water inside water pockets could have been salty due to the diffusion of the salt from ground but need not have been same as that for the ocean water (higher than for cell interior and for obvious reasons). Indeed, the water in the underground reservoirs in arid regions such as Sahara is salty, which is the reason for why agriculture is absent in these regions. Note also that the cells of marine invertebrates are osmoconformers able to cope with the changing salinity of the environment so that the Cambrian revolutionaries could have survived the change in the salt concentration of environment.

3. What applies to Earth should apply also to other similar planets and Mars [E2] is very similar to Earth. The radius is .533 times that for Earth so that after quantum leap doubling the radius and thus Schumann frequency scale (7.8 Hz would be the lowest Schumann frequency) would be essentially same as for Earth now. Mass is.131 times that for Earth so that surface

gravity would be.532 of that for Earth now and would be reduced to.131 meaning quite big dinosaurs! have learned that Mars probably contains large water reservoirs in it's interior and that there is an un-identified source of methane gas usually assigned with the presence of life. Could it be that Mother Mars is pregnant and just waiting for the great quantum leap when it starts to expand and gives rise to a birth of multicellular life forms. Or expressing freely how Bible describes the moment of birth: in the beginning there was only darkness and water and then God saidLet the light come!

To sum up, TGD would not only provide the long sought mechanism of expansion of Earth but also a possible connection with the biological evolution. It would be indeed fascinating if Planck constant changing quantum phase transitions in planetary scale would have profoundly affected the biosphere.

8.4 Implications Of Expanding Earth Model For The Pre-Cambrian Evolution Of Continents, Of Climate, And Of Life

Expanding Earth hypothesis is by no means not new. It was proposed by Mantovani and I learned about it from the video animations of [F51, F1] demonstrating that the continents fit nicely to form a single continent covering entire Earth if the radius is one half of the recent radius. What TGD has to give is a new physics justification for Expanding Earth hypothesis: cosmic expansion is replaced with a sequence of fast expansion periods increasing the value of Planck constant and these transitions occur in all scales.

If Expanding Earth hypothesis is correct it forces to modify dramatically the view about pre-Cambrian period. The super-continent theory could be replaced by much simpler theory and it might be possible to give up the assumption about hypothetical super continents and super oceans. The view about glaciations [F8] must be modified dramatically. Concerning the evolution of life the natural hypothesis is that it escaped to the underground seas formed as a consequence of expansion during pre-Cambrian era and returned back to the surface in Cambrian Explosion. In this section super-continent and super-ocean theory is discussed from TGD point of view. A model for glaciations based on the assumption that the radius of Earth was in good approximation one half of the recent radius during pre-Cambrian era is developed and shown to reduce to a sequence of ordinary glaciations initiated at pole caps. Snowball theory serves as a convenient reference. Expanding Earth theory is discussed also from paleomagnetic point of view and some experimental signatures of $R/2$ scenario differentiating it from standard scenarios are developed. Finally the hypothesis about underground evolution is discussed.

8.4.1 Super-Continent Theory

Super-continent theory assumes a cyclic formation of hypothetical super continents [F32]. Rodinia [F29], Pannotia [F25], and Pangea [F24] might have preceded by earlier super-continents. The period would be roughly 250 Myr.

1. The super-continent Rodinia [F29] is assumed to have existed during interval: 1100-750 Myr. 750 Myr ago Rodinia rifted into three continents: Proto-Laurasia which broke up and eventually reformed to form Laurasia (North America and Asia), the continental craton of Congo (part of Africa), and Gondwana (now southern hemisphere plus India).

2. Pannotia [F25] existed during time interval 600-540 Myr. Pannotia rifted in the beginning of Cambrian era to Laurentia (North America), Baltica, Siberia and Gondwana. See the illustration of Pannotia at [F14].

3. Wegener [F3] ended up to postulate that super-continent Pangea should have existed about 250 Myr ago [F24]. The support for its existence is rather strong since tectonic plate model and paleo-magnetic methods allows to trace the drift of the tectonic plates.

One can criticize the cyclic model. The concentration of land mass to Southern Hemisphere during Rodinia period does not look very probable event. The cyclically occurring formation of connected land mass surrounded by much larger ocean looks even less probable unless one can develop some very good physical mechanism forcing this. The basic motivation for super-continent theory are various correlations between distant parts of Earth which would cannot be understood otherwise. In $R/2$ model the continents would have been quite near to each other during the expansion and the notion of cyclic formation of super-continents becomes un-necessary since land bridges between the continents could explain the correlations. There would have been just single super-continent all the time.

8.4.2 Standard View About Oceans

In the standard model the total area covered by oceans has reduced since pre-Cambrian era due to the increase of the continental cover, which is nowadays 29 per cent. Oceans cover the remaining 71 per cent with Antarctica and Arctica included. The evolution of Oceans in standard model requires the introduction of hypothetical oceans which left no trace about their existence (subduction mechanism provides perhaps too convenient trash bin for hypothetical theoretical constructs).

1. Proto-Atlantic Ocean was introduced to explain some contradictions with Wegener's Pangea model allowing to conclude which parts at opposite sides of Atlantic Ocean had been in contact. Proto-Atlantic Ocean closed as Pangea formed and opened again in slightly different manner to form Atlantic Ocean. This process implied mixing of older pieces of the continents and explained the contradictions. Large inland sea is a natural counterpart of the Proto-Atlantic Ocean in $R/2$ option.

2. Mirovia [F18] was the super-ocean surrounding Rodinia. It transformed to Pan-African Ocean surrounding Pannotia. Pan-African ocean was then closed so that the ocean floor of Mirovia disappeared by subduction and left no signs about its existence.

3. In the rifting [F28] of Pannotia Panthalassic ocean [F26] emerged and was the predecessor of the Pacific ocean.

The presence of super-oceans is forced by the assumption that the radius of Earth was the recent one during the pre-Cambrian era plus the local data related to the evolution of continents. The questionable aspect is that these oceans did not leave any direct trace about their existence. In $R/2$ model there is no need for these super-oceans except possibly the counterpart of Panthalassic Ocean [F26].

8.4.3 Glaciations During Neoproterozoic Period

Glaciations dominated the Neoproterozoic period [F19] between 1-.542 billion years. The period is divided into Tonian [F36], Cryogenian [F4], and Ediacaran periods [F5]. The most severe glaciations occurred during Cryogenian period.

It is believed that during Cryogenian period [F4] two worldwide glaciations -Sturtian and Marinoan glaciations- took place. This involves extrapolation of continental drift model and plate tectonics theory. Also hypothesis about hypothetical super-continents is needed so that one must take these beliefs with some skepticism. In $R/2$ model the world wide glaciations are replaced with ordinary glaciations proceeding from poles.

1. Sturtian glaciation occurred 750-700 Myr. The breakup of Rodinia is believed to have occurred at this time. One can wonder whether there is a correlation between these events. $R/2$ model suggest that the energy needed to compensate the reduction of gravitational energy in expansion could have caused the cooling.

2. Marinoan (Varanger) glaciation ended around 635 Myr ago.

Deposits of glacial tillites [F34] at low latitudes serve as support for the claim that these glaciations were world wide. In $R/2$ model Equator corresponds to North pole in TGD framework where Rodinia covered entire Earth and the interpretation would as ordinary glaciations.

After the end of Marinoan glaciation followed Ediacaran period during 635-542 Myr [F5]. The first multicellular fossils appeared at this time. Their relationship to Cambrian fossils is unclear. The standard interpretation for the small number of fossils in pre-Cambrian period is that hard shells needed for fossilization were not yet developed. The problem is that these shells should have developed almost instantaneously in Cambrian explosion.

8.4.4 Snowball Earth Model For The Glaciation During Pre-Cambrian Era

Snowball Earth [F49, F41, F31] is recently the leading model for the glaciations [F9] during Proterozoic era. The term is actually somewhat misleading: Iceball Earth would more to the point. Slushball earth [F44] is a variant of Snowball Earth which does not assume total freezing near equator.

The history behind the Snowball Earth concept is roughly following [F31].

1. Mawson studied the Neoproterozoic stratigraphy of South Australia and identified extensive glacial sediments and speculated with the possibility of global glaciation. He did not know anything about continental drift hypothesis and plate tectonic theory and thought that the ancient position of Australia was the same as it is today. Continent drifting hypothesis however explained the finding as sediments deposited at the higher latitudes the hypothesis was forgotten.

2. Later Harland suggested on basis of geomagnetic data that glacial tillites [F34] in Svalbard and Greenland were deposited at tropical latitudes. In TGD framework with with $R \to R/2$ these tillites would have been at higher latitudes towards North Pole.

3. The facts are that Sun was 6 per cent fainter at that time and glaciations are known to occur. The question is whether they were global and long-lasting or a sequence of short-lasting possibly local glaciations. The Russian climatologist Budyko constructed a model based on energy balance and found that it is possible to have a global glaciation if the ice sheets proceeded enough from polar regions (to about 30 degree latitude). The model was based on the increased reflectiveness (albedo) of the Earth's surface due to the ice covering giving rise to positive feedback loop. Budyko did not believe that global glaciation had occurred since the model offered no way to escape eternal glaciation.

4. Kirschwink introduced the term Snowball Earth, which is actually misleading. Iceball Earth would be more to to the point. He found that the so called banded iron formations are consistent with a global glaciation. He also proposed a mechanism for melting the snowball. The accumulation of CO_2 from volcanoes would have caused ultra-greenhouse effect causing warming of the atmosphere and melting of the ice.

5. Slushball Earth [F44] differs from Snowball Earth in that that only a thin ice cover or even its absence near equator is assumed. The model allows to explain various findings in conflict with Snowball Earth, such as the evidence for the presence of melt-water basins.

6. Zipper rift model [F43] assumes that there was a sequence of glaciations rather similar to the glaciations that have occurred later. The model assumes that the rifts [F28] of the super-continent Rodinia occurred simultaneously with glaciations. The associated tectonic uplift led to the formation of high plateaus hosting the glaciers. The iron band formation can be be assigned with inland seas allowing complex chemistries and anoxicity near the sea floor.

The basic ideas of the Snowball Earth model

Snowball Earth [F49, F41, F31] differs from ordinary glaciations in that only oceans are frozen whereas in the ordinary glaciation land mass is covered by ice. The basic ideas of the snowball Earth relate to the mechanism initiating the global freezing and melting.

1. The glaciation would have been initiated by some event, say a creation of super-volcano. Also astrophysical mechanism might be involved. Somewhat paradoxically, tropical continents

during cryogenian period [F4] are needed for the initiation because they reflect the solar radiation more effectively than tropical oceans.

2. The positive ice-albedo feedback is an essential concept: the more ice the larger the fraction of the radiation reflected back so that the more ice is generated. If the glaciation proceeds over a critical latitude about 30 degrees positive feedback forces a global glaciation.

3. The problem of the model is how to get rid of the glaciation. The proposal of Kirschvink was that the accumulation of CO_2 from volcanoes could have led to a global super-warming. The time scale for CO_2 emissions is measured in millions of years. The needed atmospheric concentration of CO_2 is by a factor 350 higher than the recent concentration. Due the ice cover the CO_2 could not be absorbed to the siliceous rocks and concentration would increase. The melting of the ice meant higher absorbtion of heat by uncovered land. Positive feedback loop was at work again but in different direction.

Evidence for and objections against Snowball Earth

Wikipedia article about Snowball Earth [F31] discusses both evidence for and objections against Snowball Earth. Low latitude sediments at tropical latitudes and tropical tillites at Equatorial latitudes provide strong piece of evidence for Snowball Earth. Calcium carbonate deposits having ^{13}C signature (per cent for the depletion of ^{13} isotope and large for organic material) consistent with that for mantle meaning abiotic origin is second evidence. Iridium anomaly located at the base of Calcium Carbonate deposits is third piece of evidence. The evidence for Snowball Earth will be discussed in more detail later since it is convenient to relate the evidence to $R/2$ model for glaciations.

1. Paleomagnetic data [F23] used to the dating of sediments assuming tectonic plane theory and super-continent drifting might be misleading. No pole wandering maps exist and the polarity of the magnetic field must be deduced by statistical methods. The primary magnetization could have been reset and the orientation of the magnetic minerals could have changed from the original one. It is also possible that magnetic field patterns were not dipolar. Also the assumption of hypothetical super-continents and oceans brings in uncertainties. In $R/2$ model of course the determination of the positions changes completely.

2. Carbon isotope ratios are not what they should be. There are rapid variations of $^{12}C/^{13}C$ ratio with organic origin. Suggests that freezing and melting followed each other in rapid succession. In standard framework this would suggest Slushball Earth meaning ice-free and ice-thin regions around the equator and hydrological cycles. In $R/2$ model the regions at Equator are near North Pole and the explanation would be in terms of ordinary glaciations.

3. The distribution of isotopes of element Boron suggest variations of pH of oceans. The explanation is in terms of buildup of carbon dioxide in atmosphere dissolved into oceans/seas. In $R/2$ model a sequence of glaciations would explain the findings.

4. Banded iron formations providing support for the model are actually rather rare and absent during Marinoan glaciation.

5. Wave-formed ripples, far-traveled ice-rafted debris and indicators of photosynthetic activity, can be found throughout sediments dating from the "Snowball Earth" periods. This serves a evidence open-water deposits. In snow-ball model these could be "oases" of melt-water but computer simulations suggest that large areas of oceans would have left ice-free. in $R/2$ model these would be signatures of ordinary glaciations.

6. Paleomagnetic data have led to the conclusion that Australia was at Equator. In $R/2$ model it would have been near North Pole. Namibia was also thought to be near Equator [F33]. Indirect arguments forced the conclusion that it at 75 degree Southern latitude. In $R/2$ model this corresponds to 60 degrees Southern latitude and ordinary glaciation proceeding from South Pole is a natural explanation and ordinary glaciation would be in question in both cases.

7. There is evidence for the continental ice cover does not fit with Snowball Earth predicts that there should be no continental ice-cover. The reason is that freezing of the ocean means that there is no evaporation from oceans and no water circulation so that ice-cover cannot develop on continents. There is considerable evidence that continents were covered by thick ice [F31]. This suggests ordinary glaciations possible in $R/2$ model.

8.4.5 TGD Point Of View About Pre-Cambrian Period

What is new in TGD based view about pre-Cambrian period is basically due to the $R/2$ hypothesis.

TGD view about evolution of continents

The hypothesis about the existence of the super-continent Pangea [F24] was inspired by the work of Wegener [F3]. The hypothesis about the existence of former super-continents were forced by the correlations with fossil records suggesting connected continent. This is not necessary if the gigantic ocean was absent during $R/2$ era. The continent Rodinia [F29] could look much like the Rodinia of standard geology except that they formed single connected region with radius $R/2$.

1. It is possible that there was only single super-continent with widening inland seas all the time until 250 billion Myr. The first option is R increased slowly and that inland lake formed. Rifts could have got wider gradually during this era. If there were land bridges between the continents there would be no need for postulating the cyclic re-formation of super-continent.

2. One can pose many questions about the character of the expansion.

   (a) What was the duration of the expansion? Could the expansion have occurred in the time period 750-100 Myr (100 Myr corresponds to the age of dinosaurs with large body size made possible by the reduced gravitation and oxygenation of the atmosphere)? Duration would have been about 650 Myr in this case. Or did it began already at the beginning of Neoproterozoic period [F19] when super-continent Rodinia began to break up? In this case the duration would be about 1 Myr. The estimate based on the quantum model of gravitational radiation predicts that the transition lasted for about 1.1 Gy so that the latter option would be more plausible in this framework.

   (b) Did the expansion accelerate as does also cosmic expansion in TGD based universal model for the expansion periods containing only the duration of the expansion period as a parameter [K46] and applying in alls scales? It seems that accelerated expansion is the only sensible option since around 540 Myr the size of Earth should have been rather near to $R/2$ (perhaps so even at the period of Pangea around 250 My) unless one assumes that super-continent re-formed again.

3. One can also consider the possibility that the continents indeed broke up and reformed again during Cambrian era. One should however have a good physical reason for why this happened. Something must have connected the pieces together and created correlations. Gravitational magnetic flux tubes and phase transitions increasing and reducing Planck constant? Or could it be that the bridges connecting the continents acted like strings inducing oscillation of the distance between continents so that Pangea was surrounded by a large ocean?

4. The formation of the rift [F28] feeding magma from core to the surface would be due to the expansion leading to the formation of fractures. The induced local elevations would be like mountains. As in zipper-rift model ice could have covered these plateaus because the temperature was lower. This is not however essential for TGD based model of glaciations.

5. TGD based variant of Expanding Earth allows subduction but its role could have been small before the Pangeia period if the expansion was accelerating and led only to a relatively small increase of the radius before the Mesozoic period [F17] and continued with an accelerating rate during Mesozoic from 250 Myr to 65 Myr. It is interesting that Mesozoic period begins with the most intensive known extinction of history- so called Permian-Triassic extinction event [I36] - known as Great Dying. About 95 of marine species and 70 percent of terrestrial species became extinct. Maybe genetically determined bio-rhythms could not follow the

rapidly changing circadian rhythm. Another explanation for the extinction is the warming of the climate. For this there is indeed support: there is evidence that Antarctica was climate refuge during the extinction [I133]. Perhaps both factors were involved and were not independent of each other since rapid expansion might have generated massive methane leakages from underground seas and lakes.

TGD based view about evolution of oceans

Continents would have covered most of the area during $R/2$ era and the covered fraction was slightly smaller than 1/4 of the recent area of Earth. This depends on the area taken by inland seas and polar caps. Nowadays the area covered by continents and inland seas is about 31 per cent so that continental area has increased and would be due to the expansion in vertical direction and deepening of the oceans. The area covered by oceans has increased from a small value to about 70 per cent. Only a small fraction of ocean floor would be subduced in Expanding Earth model. The Proto-Atlantic would have been only a small inland sea. Panthalassic Ocean was inland sea, which expanded to Pacific Ocean during expansion. Pacific Ocean could contain data about ancient ice ages if it was frozen. It however seems that data are consistent with the absence of global glaciation.

Model for glaciations

In TGD framework single super continent covering most of Earth becomes the counterpart of Rodinia [F29]. The hypothetical oceans are replaced with inland seas and polar caps. The supercontinent covering most of Earth absorbs less solar heat than tropical oceans so that glaciations become more probable. Snowball Earth is replaced with a series of ordinary glaciations proceeding from poles since the places at Equator were near North Pole. There is no need for the glaciations to progress to the equator. The rifting for the counterpart of Rodinia is consistent with the formation of fractures due to the expansion of Earth. The reduction of gravitational binding energy due to the increase of the radius requires feed of energy and this could be one reason for the cooling and initiation of the glaciation.

There are several questions which must be answered if one wants to gain a more detailed understanding.

1. How does $R/2$ model modify the view about glaciations? Very probably there was a frozen polar cap. Snowball Earth could be replaced with ordinary glaciations proceeding from North and South Pole.

2. How does the predicted 3+3 hour diurnal cycle modify the ordinary picture? Certainly 3-hour day reduces the amplitude of the diurnal temperature variations. Could this period have left genetic traces to the mono-cellulars, say biological clocks with this period?

3. How does the predicted four times stronger surface gravity affect the glaciation process? Could strong gravity leave detectable signatures such as anomalously strong effects on the shape of surface of Earth or deeper signatures about the motion of ice.

There are also questions related to the energetics of the expansion.

1. The expansion required energy and could have induce glaciations in this manner. Energy conservation would hold for the total mechanical and gravitational energy of Earth given by

$$E = \frac{L^2}{2I} - k\frac{GM^2}{R} < 0 \ . \tag{8.4.1}$$

Here L is the conserved angular momentum of order $L \simeq I\omega$ and ω increases from $1/4\omega_{now}$ to ω_{now} during the expansion. The moment of inertia I is of order of magnitude $I \sim MR^2$ and k is a numerical constant not too far from unity. The kinetic energy is actually negligible as compared to the gravitational potential energy. The reduction of the gravitational binding energy requires a compensating energy, which could come both from Earth interior or from the Earth's surface. Both effects would induce a cooling possibly inducing glaciations.

2. One expects that in the initial stages of the expansion there was just an expansion. This meant stretching requiring also energy. The formation of rifts leading to the formation of oceans as magma flowed out would have started already in the beginning of Proterozoic period. Eventually fractures were formed and in TGD framework one might expect that the distribution of fractures could have been fractal. A considerable fraction of fractures was probably volcanoes so that CO_2 begun to leak to the atmosphere and local "oasis" were formed. Also hot springs liberating heat energy from Earth crust could have been formed as in Island. The pockets inside Earth increased in size and were filled with water. Life started to escaped to the walls of the fractures and to the water pockets. Also the recent oceans can be seen as widened cracks which transformed to the expanding sea floors whereas continents did not expand. As the continental crust ceased to expand no heat was needed for the expansion and this together with increased CO_2 content of atmosphere would explain why there was no further glaciations and heating of the Earth. At this period the flow of the magma from Earth core provided the energy needed to compensate the reduction of gravitational energy.

3. It must be emphasized that TGD variant of Expanding Earth theory is not in conflict with tectonic plate theory. It explains the formation of tectonic plates and the formation of magma flow from rifts giving also rise to subduction and is therefore a natural extension of the tectonic plate theory to times before the expansion ceased.

Estimate for the duration of the transition changing gravitational Planck constant

The reader without background in quantum physics and TGD can skip this section developing an estimate for the duration of the transition changing Planck constant and inducing the scaling of the radius of Earth by a factor two. The estimate is about 1.1 Gy. It must be emphasized that the estimate is not first principle calculation and relies strongly on quantum classical correspondence.

The duration of the quantum transition inducing the expansion of the gravitational space-time sheet of Earth and thus of Earth itself by a factor two can be estimated by using the same general formula as used to estimate the power of gravitational radiation emitted in a transition in which gravitational Planck constant assignable to star-planet system is reduced [K37].

1. The value of gravitational Planck constant characterizing the gravitational field body of Earth is GM^2/v_0, where the velocity parameter $v_0 < 1$ ($c = 1$) is expected to be larger than $v_0 \simeq 2^{-11}$ characterizing Sun-Earth system.

2. Assuming a constant mass density for Earth the gravitational potential energy of Earth is given by

$$V = \frac{M}{2}\omega^2 r^2 \ , \ \omega = \sqrt{\frac{6GM}{R^3}} \ . \tag{8.4.2}$$

As far as radial oscillations are considered, the system is mathematically equivalent with a harmonic oscillator with mass M. The energies for the radial oscillations are quantized as $E = (n + 1/2)\hbar_{gr}\omega$.

3. The radii of Bohr quantized orbits for the harmonic oscillator scale like $\sqrt{\hbar}$ so that $\hbar \to 4\hbar$ is needed to obtain $R \to 2R$ rather than $\hbar \to 2\hbar$ as the naive Compton length argument would suggest. This requires the scaling $v_0 \to v_0/4$. The change of the ground state energy in this quantum transition is

$$\begin{aligned} \Delta E &= \frac{1}{2}(\hbar_{gr,f}\omega_f - \hbar_{gr,i}\omega_i) \ , \\ \hbar_{gr,f} &= 4\hbar_{gr,i} = \frac{4GMm}{v_{0,i}} \ , \\ \omega_i &= 2^{3/2}\omega_f = 2^{3/2}\sqrt{\frac{6GM}{R_f^3}} \ . \end{aligned} \tag{8.4.3}$$

$R_f = R$ denotes the recent radius of Earth.

4. From the estimate for the power of gravitational radiation in similar transition the estimate for the duration τ of the quantum transition is

$$\begin{aligned} \tau &= a(v_{0,i}v_{0f})^{-k/2} \times \frac{(\hbar_{gr,i} + \hbar_{gr,f})}{2\Delta_E} \ , \\ &= a2^{-k} v_{0f}^{-k} \times \frac{1+r}{r\omega_f - \omega_i} \ , \ r = \frac{\hbar_f}{\hbar_i} = 4 \ . \end{aligned} \tag{8.4.4}$$

The average of Planck constants associated with the initial and final states and geometric mean of the parameters v_{0i} and v_{0f} is dictated by time reversal invariance. The exponent k is chosen to be same as that obtained for from the condition that that the ratio of the power to the classical radiation power emitted in the transition between planetary Bohr orbits does not depend on v_0 (quantum classical correspondence). This gives $k = 5$. The condition that the power of gravitational radiation from Hulse-Taylor binary is same as the power predicted by the classical formula (quantum classical correspondence) gives $a = .75$.

5. The explicit expression for τ reads as

$$\begin{aligned} \tau &= K \times a v_{0,f}^{-5} \times (\frac{R}{2GM})^{1/2} \times \frac{R}{c} \ , \\ K &= \frac{5 \times 2^{-7} \times (2 + 2^{1/2})}{3^{1/2}} \ . \end{aligned} \tag{8.4.5}$$

6. The basic data are $M_{Sun} = 332900M$ (mass of Sun using Earth's mass as unit) and the mnemonic $r_{S,Sun} = 2GM_{Sun} = 2.95 \times 10^3$ m: together with $R = 6371 \times 10^3$ m these data allow a convenient estimation of $R/2GM$. For $k = 10$ and $a = .75$ this gives $\tau = 1.17$ Gyr. This is twice the estimate obtained by requiring that the transition begins at about 750 Myr (the beginning of Sturtian glaciation) and ends around 100 My (the age of gigantic animals whose evolution would be favored by the reduction of surface gravity). The estimate would suggest that the quantum transition began already around 1.1 Gyr, which in the accuracy used corresponds to the beginning of Neoproterozoic at 1 Gyr [F19]. The breaking of supercontinent Rodinia indeed began already at this time.

7. Note that the value of v_{0f} for the gravitational field body of Earth as it is now would be $v_{0f} = 2^{-10}$ to be compared with $v_0 \simeq 2^{-11}$ for Sun-Earth gravitational field body.

Snowball Earth from TGD point of view

In TGD framework the main justification for Snowball Earth disappears since the samples believed to be from Equator would be from North pole and glaciation could be initiated from pole caps. Consider next in more detail the evidence for Snowball Earth from TGD point of view.

1. Low latitude glacial deposits, glacial sediments at tropical latitudes, tropical tillites, etc. providing support for snowball Earth [F31] would be near North pole of at Northern latitudes. Ordinary glaciations proceeding from poles would explain the findings [F11]. If total glaciations were present, a rough scaling suggests that the evidence from them should be found from southern latitudes around 45 degrees in the standard model framework.

   The testable prediction is that the evidence for glaciations in ice-ball Earth framework should be found only below Equator and near South Pole. This finding would be of course extremely weird and would strongly favor $R/2$ option. Interestingly, in Southern Brasil all indicators for glaciations are absent (see [F53] and references therein). This region belonged to Godwana continent and there is evidence that its location was at middle latitudes at Southern Hemisphere.

2. Banded iron formations [F31] are regarded as evidence for Snowball Earth and occur at tropical levels (near North Pole in $R/2$ model). Iron dissolved in anoxic ocean would have become in a contact with photosynthetically produced oxygen and implied the formation of iron-oxide. The iron formation would have been produced at the tipping points of anoxic and oxygenated ocean. One can consider also an explanation in terms of deep inland seas, which become stagnant and anoxic near the sea floor.

   In TGD framework sea floor near North Pole could contain banded iron formations. This would explain also why the banded iron formations are rather rare. The oxygen could have come also from underground after the formation of cracks and led to the oxygenation of inland seas from bottom. The assumption that oxygenation took place already during the first glaciation, could explain why banded iron formations are absent during the second glaciation.

3. Calcium carbonate deposits [F31] have ^{13}C signature (per cent for the depletion of ^{13} isotope and large for organic material) is consistent with that for mantle meaning abiotic origin. The explanation of Calcium carbonate deposits in TGD framework could be the same as in Snowball Earth model. Atmospheric CO_2 could come from the volcanoes and react with the silicates during the ice-free periods to form calcium carbonate which then formed the deposits. CO_2 could have also biological origin and come from the underground life at the walls of the expanding fractures/volcanoes or in underground seas or lakes. In this case also methane is expected. This option would predict ^{13}C signature characteristic for organic matter. Also this kind of signatures have been observed and support ordinary glaciations. Also rapid fluctuations of the signature from positive to negative take place and might have signatures of temporary melting induced organic contribution to the calcium carbonate.

4. Iridium anomaly [F31] is located at the base of Calcium Carbonate deposits. In Snowball Earth model Iridium deposits derive from the Iridium of cosmic rays arriving at the frozen ice surface. As the ice melts, Iridium deposits are formed. In $R/2$ model the condensation of Iridium would proceed through the same mechanism. The possible problem is whether the time is long enough for the development of noticeable deposits. Near poles (Equator and South pole in standard model) this could be the case.

8.4.6 Paleo-Magnetic Data And Expanding Earth Model

Paleomagnetic data from pre-Cambrian period might allow to test $R/2$ hypothesis. This data could in principle help to trace out the time development $R(t)$ from $R/2$ to R if the non-dipole contribution to magnetic field depends on $R(t)$.

About paleo-magnetism

Paleomagnetism [F23] provides quantitative methods to determine the latitude at which the sample of sedimentary rock was originally. Magnetic longitude cannot be determined because of rotational symmetry so that other information sources must be used. There are several methods allowing to deduce the direction and also the magnitude of the local magnetic field and from this the position of the sample during the time the sample was formed.

1. Below the Curie point thermal remanent magnetization is preserved in basalts of the ocean crust and not affected by the later magnetic fields unless they are too strong. This allows to deduced detail maps from continental drifting and polar wander maps after 250 Myr (Pangea period). During pre-Cambrian period the ocean floors of hypothetical oceans would have disappeared by subduction. In $R/2$ model there are no oceans: only inland seas.

2. In the second process magnetic grains in sediments may align with the magnetic field during or soon after deposition; this is known as detrital remnant magnetization (DRM). If the magnetization is acquired as the grains are deposited, the result is a depositional detrital remnant magnetization (dDRM); if it is acquired soon after deposition, it is a post-depositional detrital remnant magnetization (pDRM).

3. In the third process magnetic grains may be deposited from a circulating solution, or be formed during chemical reactions, and may record the direction of the magnetic field at the time of mineral formation. The field is said to be recorded by chemical remnant magnetization (CRM). The mineral recording the field commonly is hematite, another iron oxide. Red-beds, clastic sedimentary rocks (such as sandstones) that are red primarily because of hematite formation during or after sedimentary diagenesis, may have useful CRM signatures, and magnetostratigraphy [F16] can be based on such signatures. Snowball model predicts that nothing came to the bottoms of big oceans! How can we know that they existed at all!

During pre-Cambrian era the application of paleomagnetic methods [F23] is much more difficult.

1. Reliable paleomagnetic data range up to 250 My, the period of Pangaea, and magnetization direction serves as a reliable information carrier allowing detailed polar wander maps. During pre-Cambrian era one cannot use polar wander maps and the polarity of the magnetic field is unknown. Therefore theoretical assumptions are needed including hypothetical super-continents, hypothetical oceans, and continental drift and plate tectonics. All this is on shaky grounds since no direct information about super-continents and ancient oceans exists. $R/2$ model suggests that continental drift and plate tectonics have not been significant factors before the expansion period when only inland seas and polar ice caps were present. Measurements have been however carried out about magnetization for pre-Cambrian sediments at continents recently and gives information about the strength of the magnetic field [F15]: the overall magnitude of the magnetic field is same as nowadays.

2. At Precambrian period the orientation of iron rich materials can serve as a record. The original records can be destroyed by various mechanisms (diagenesis). Also the orientations of the sediments can change in geological time scales.

3. Tens of thousands of reversals of the magnetic polarity [F7] have occurred during Earth's history. There have been long periods of stability and periods with a high frequency of reversals. The average duration of glaciation is around one Myr. The determination of the polarity of B possible by using samples from different points.

4. Mountain building orogeny [F22] releases hot water as a byproduct. This water can circulate in rocks thousands of kilometers and can reset the magnetic signature. The formation of fractures during the expansion of Earth could have released hot water having the same effect.

Could paleomagnetic data kill or prove $R/2$ model?

The first question is how one might kill $R/2$ model using data from pre-Cambrian era. Paleomagnetic data could do the job.

1. Remanent magnetization is proportional to the value of magnetic field causing it in weak magnetic fields. Therefore the magnetization in principle gives information about the magnetic fields that prevailed in early times.

2. Suppose that the currents generating the magnetic field can be idealized to conserved surface currents K around cylindrical surfaces of radius r and height h scaled down to to $r/2$ and $h/2$ and that the value of K is not affected in the process. With this assumptions the magnetic moment behaves $\mu \sim Ir^2h \to \mu/8$. A continuous current vortices with $j = k/\rho$, which is ir-rotational outside the symmetry axis, produce a similar result if the radius of the vortices scales as $r \to r/2$. Since dipole magnetic field scales as $1/r^3$ and is scaled up by a factor 8 in $R \to R/2$, the scalings compensate and the dipole magnetic fields at surface do not allow to distinguish between the two options. Non-dipole contributions might allow to make the distinction.

3. The group led by Lauri J. Pesonen in Helsinki University [F15] has studied paleomagnetic fields at pre-Cambrian era. The summary of results is a curve at the home page of the group

and shows that the scale of the magnetic during pre-Cambrian era is same as nowadays. On the other hand, the recent thesis by Johanna Salminen- one of the group members- reports abnormally high values of magnetization in Pre-Cambrian intrusions and impact structures in both Fennoscandia and South Africa [F48]. No explanation for these values has been found but it is probably not the large value of primary magnetization.

Another manner to do test the $R/2$ model is by comparing the signs of the magnetizations at magnetic equator and poles. They should be of opposite sign for dipole field. The polarity of magnetic field varies and there are no pre-Cambrian polar wander maps. One can deduce from the condition $B_r/rB_\theta = 2cot(\theta)$ holding true for dipole field the azimutal distance $\Delta\theta$ along the direction of the measured magnetic field to the pole along geodesic circle in the direction of the tangential component of B. One cannot however tell the sign of $\Delta\theta$, in other words whether a given pre-Cambrian sample belongs to Norther or Southern magnetic hemisphere. There are however statistical methods allowing to estimate the actual pole position using samples from several positions (for an excellent summary see [F48]).

For instance, if the magnetic field is in North-South direction during Rodinian period [F29], standard model would predict that the sign at the Equator is opposite to that at South Pole. In $R/2$ model the sample would be actually near North Pole and polarizations would have same sign. The sign of magnetization at apparent southern latitude around 45 degrees would have been opposite to that at South pole which is in conflict with dipole field character. Maybe the global study of magnetization directions when magnetic field was approximately in North-South direction could allow to find which option is correct. Also the dependence of the strength of the magnetic field as function of θ could reveal whether $R/2$ model works or not. The testing requires precise dating and position determination of the samples and a detailed model for the TGD counterpart of Rodinia and its construction requires a specialist.

If the expansion continued after 250 Myr with an accelerating rate and Earth radius was still considerably below its recent value, the comparison of pole wandering charts deduced from ocean floor paleomagnetic data at faraway locations might allow to show that the hypothesis about dipole field is not globally consistent for R option. Even information about the time evolution of the radius could be deduced from the requirement of global consistency.

8.4.7 Did Life Go Underground During Pre-Cambrian Glaciations?

The basic idea of Expanding Earth model is that the life developed in underground seas and emerged to the surface of Earth in Cambrian explosion. The series of pre-Cambrian glaciations explains why the life escaped underground and how the underground seas were formed.

1. If one believes that the reduction of gravitational binding energy was responsible the cooling, then the expansion of Earth could have begun at the same time as Sturtian glaciation [F4] . On the other hand, the TGD estimate for the duration of the expansion period giving 1.1 Gyr, suggests that the breakup of the Rodinia, which began in the beginning of Proterozoic period corresponds to the beginning of the expansion. The simplest assumption is that the radius of R at the beginning of Cambrian period was not yet much larger than $R/2$ and continued to increase during Cambrian period and ended up around 100 My, when dinosaurs and other big animals had emerged (possibly as a response to the reduction of gravity). This means that there were land bridges connecting the separate continents.

2. One must explain the scarcity of fossils during pre-Cambrian era. If the more primitive life forms at the surface of Earth did not have hard cells and left no fossils one can understand the absence of highly evolved fossils before Cambrian explosion [I7]. If life-forms emerged cracks and underground seas there would be no fossils at the surface of Earth. In the case of volcanoes dead organisms would have ended to gone to the bottom of the water containing volcano and burned away.

3. The expansion had formed the underground pockets and fractures made possible for the water to flow from the surface to the pockets. Life would have evolved in fractures and pockets. The first multicellular fossils appeared during Ediacaran period (segmented worms, fronds, disks, or immobile bags) [F5] and have little resemblance to recent life forms and

their relationship with Cambrian life forms is also unclear. Ediacaran life forms could have migrated from the fractures and Cambrian fossils from from the underground seas and lakes. The highly evolved life-forms in Cambrian explosion could have emerged from underground seas through fractures.

One can make also questions about the underground life.

1. The obvious question concerns the sources of metabolic energy in underground seas. In absence of solar radiation photosynthesis was not possible plants were absent. The lowest levels in the metabolic hierarchy would have received their metabolic energy from the thermal or chemical energy of Earth crust or from volcanoes. The basic distinction between plants and animals might be that the primitive forms of plants developed at the surface of Earth and those of animals in underground seas.

2. At first it seems strange that the Cambrian life-forms had eyes although there was no solar radiation in the underground seas. This is actually not a problem. These life-forms had excellent reasons for possessing eyes and in absence of sun-light the life forms had to invent lamp. Indeed, many life forms in deep sea and sea trenches produce their own light [I25]. It would be interesting to try to identify from Cambrian fossils the body parts which could have served as the light source.

8.4.8 Great Unconformity As A New Piece Of Support For Expanding Earth Model

I hope that this chapter demonstrates convincingly that single hypothesis - a sudden phase transition increasing the radius of Earth by a factor 2 natural in the many-sheeted space-time of TGD - explains Cambrian explosion in biology (a sudden emergence of huge number of life forms after very slow Precambrian evolution), and also provides a model for Precambrian evolution of continents, climate and life.

Already Darwin realized that the absence of fossils from Precambrian era (see `http://tinyurl.com/65zeh5`) is a deep problem for his theory and assumed that this is an artefact due to the incomplete fossil record. Fossils of Precambrian origin have been indeed found after Darwin's time but they are simple and very rare, and the conclusion is that Cambrian explosion (see `http://tinyurl.com/3flhcw`) [I7] meaning a huge diversification was real. Two mysteries therefore remain. Why the development of life was so slow during Precambrian era? Why the diversification was so incredibly fast during Cambrian explosion? Various explanations have been proposed. Did the oxygen content of the atmosphere reach a critical value and lead to the diversification? Or did predation pose the evolutionary pressure making the pace of evolution dramatically faster?

In New Scientist (see `http://tinyurl.com/nenk8nq`) [F46] geologists Robert Gaines and Shanan Peters describe a geological finding perhaps related to the Cambrian Explosion: the mysterious "Great Unconformity" (see `http://tinyurl.com/bqm9ndz`) [F10], which is a juxtaposition of two different types of rock of very different geological ages along a prominent surface of erosion. This surface represents a very long span of "missing" time. More than 1 billion years of geological record is missing in many places! From the figure (see `http://tinyurl.com/y8tnbneb`) of the Wikipedia article [F10] about Great Unconformity visible in Grand Canyon the thickness of the missing layer can be estimated to be about 12.6 km. Somehow before the Cambrian the uppermost rocks of the continents were stripped away exposing the underlying crystalline basement rocks. The cause of this gap remains a complete mystery so that we have three mysteries! Plus the mysteries related to the evolution of climate (problems of Snowball Earth model).

The authors suggest that the formation of Great Unconformity relates to the Cambrian explosion. Large scale erosion and chemical weathering of the the exposed crystalline rock caused mineralization of the sea water. The hypothesis is that this led to bio-mineralization: animal groups possessing mineral skeletons - such as silica shells and calcium carbonate shells - emerged. This hypothesis looks rather plausible but does not solve the three great mysteries.

The authors indeed leave open the question about the origin of Great Unconformity and of Cambrian explosion. The TGD based explanation of Cambrian explosion comes from the model realizing the old idea about Expanding Earth in terms of TGD inspired new physics. Already Wegener observed that continents can be fit together nicely and this led to the recent view about

plate tectonics. Wegener's model however fits only "half" of the continent boundaries together. One could however do much better: the observation is that the continents would fit nicely to cover the entire surface of Earth if the radius of Earth were 1/2 of its recent value! Expanding Earth model postulates that the radius of Earth grows slowly. Geologists have not taken Expanding Earth model seriously: one good reason is that there is no physics allowing it.

As has been found, TGD predicts a candidate for the needed new physics.

1. At given sheet of the many-sheeted space-time cosmic expansion is predicted to take place as sudden phase transitions in which the size of some space-time sheet suddenly increases. By p-adic length scale hypothesis the preferred scaling factors are powers of 2 and the most favored scaling factor is just two. The proposal is that during the Precambrian era life resided in underground seas being thus shielded from meteor bombardment and cosmic rays. This explains the scarcity of the fossil records and the simplicity of the fossils found. The sudden phase transition was a very violent process increasing the area of the Earth's surface by a factor of 4. The area of continents is 29.1 per cent from the recent area of the Earth's surface - not too far from the naively predicted fraction 1/4.

2. It is easy to imagine that the uppermost rocks of the continent covering the entire Earth were stripped away and correspond nowadays to 100 km thick continental tectonic plates consisting of mainly silicon and aluminium). This expansion created split first the topmost layer as continental plates and regions between them giving rise to oceans. The magma which was uncovered by the process cooled down and solidified and the continued expansion gave rise to ocean plates with different composition (mainly silicon and magnesium).

3. The expansion phase corresponds to criticality so that fractality of the expansion is expected. At least for continental plates this process could have been fractal occurring in various length scales characterizing the thickness and the area of the sub-plates generated in the process. p-Adic length scale hypothesis suggests that the scales involved should appear as powers of $\sqrt{2}$ or 2. Generation of Great Unconformity as a process in which the underlying crystalline basement rocks were uncovered could correspond to a splitting of a layer of the continental plates to pieces. The length scale characterizing the thickness is 12.6 km from the above estimate and with 1 per cent accuracy by a factor 1/8 shorter than 100 km length scale for tectonic plates. This conforms with p-adic fractality. If the process of expansion involved a cascade of scalings by factor 2, one can wonder whether it proceeded from long to short length scales or vice versa. In other words: did continental and oceanic tectonic plates form first and after than the smaller structures such as the Great Unconformity or vice versa?

4. Note that the Compton scale $L_e(237)$ corresponding $p \simeq 2^{237}$ is 88 km - ten per cent smaller than 100 km. Maybe thermal expansion could account the discrepancy if the original thickness was $L(237)$. Second interpretation could be that besides electron Compton scale $L_e(239)$ the p-adic scale $L(239) = L_e(239)/\sqrt{5} \simeq 78.7$ km matters. The importance of $L(k)$ does not implicate that of scaled up electron, and the following argument suggests that it is p-adic length scale rather than corresponding electron Compton scale that matters now. Remarkably, also M_{241} is Gaussian Mersenne and corresponding electronic Compton scale is $L_e(241) = 154.7$ km.

   Note that 88 km is rather precisely the thickness of the atmosphere above which there is ionosphere (see `http://tinyurl.com/lqr85j`) [F12]. The thickness of KennellyHeaviside layer (see `http://tinyurl.com/25ur2tl`) [F13] inside which radio waves used in terrestrial radio communications propagate, has thickness about 150 km which roughly corresponds to $L(239)$. Note that Continental litosphere (see `http://tinyurl.com/d96kw`) [F27] has typical thickness of 200 km ($L(239)$) whereas oceanic litosphere is 100 km thick ($L(237)$). This fits at least qualitatively with the proposed formation mechanism of continental tectonic plates.

   There is a nice fractal analogy with cell membrane and connection with Gaussian Mersennes (see `http://tinyurl.com/pptxe9c`) [A1] expected to be of special importance in TGD Universe. The scales $L(239)$ and $L(241)$ would be in the same relation as the thickness $L_e(149)$ of the lipid layer of cell membrane to the cell membrane thickness $L_e(151)$ characterized by Gaussian Mersenne $M_{151,G}$. The two kinds of tectonic plates (continental and oceanic) would be analogous to the lipid layers of cell membrane.

5. The rapid expansion process could have also brought in daylight the underground seas and the highly developed life in them so that Cambrian diversification would have been only apparent. Skeptic can of course ask whether it is necessary to assume that life resided in underground seas during Precambrian era. Could just the violent geological process be enough to induce extremely fast diversification? This might of course be true.

6. There is one further argument in favor of the Expanding Earth model. The fact that the solar constant was during proto Earth period (see `http://tinyurl.com/pc83uvt`) [F35] only 73 per cent from its recent value, is a problem for the models of the very early evolution of life. If the radius of Earth was 1/2 of its recent value the duration of day and night was from conservation of angular momentum only 1/4: th of the recent value and thus 3 hours. This could have made the environment much more favorable for the evolution of life even at the surface of the Earth since the range for the temperature variation would have been much narrower.

8.4.9 Where Did The Oceans Come From?

TGD based vision about life has been developing rapidly thanks to the realization that hierarchy of Planck constants and dark matter could relate directly to criticality: consider only long range correlations, phase separation, and classical non-determinism near critical point as common aspects [K75]. The article "Half of the Earth's water formed before the sun was born" (`http://news.sciencemag.org/earth/2014/09/half-earths-water-formed-sun-was-born`) describes research results proving additional support for the TGD inspired idea about the occurrence of prebiotic evolution in underground water reservoirs shielded from meteorites and cosmic rays. The idea relies on TGD inspired variant of Expanding Earth hypothesis [K37, L45].

1. Article represents first a standard argument in favor of late formation of oceans. The collisions by astreroids and meteorites could have evaporated the water or blown off it in to space. Hence surface water at Earth should have emerged much later. Note that one can replace "water" with "life" in the argument.

2. The researchers end up to propose that the water emerged already before Sun, and also oceans did so rather early. Carbonaceous chondrites (`http://tinyurl.com/75fh74p`), which formed at the same time as Sun and well before the planets, could have served as a source of water. These meteorites were formed very early, already earlier than Sun. Their composition resembles that of bulk solar system composition. By studying basaltic meteorites from asteroid Vesta, which is known to be formed in the same region as Earth, the reaserachers found that they contain same hydrogen isotopic composition as carbonaeous chondrites.

   This motivates the proposal that chondrites contained the water. A further proposal is that the water reservoirs formed at the surface of Earth as it formed. Here I beg to disagree: the objection represented in the beginning is difficult to circumvent!

The article stimulates several interestig questions in TGD based conceptual framework.

1. Why not to assume formation of underground water reservoir? Here meteorites and UV radiation did not form a problem. And there is indeed recent evidence for the previous existence of large underground reservoirs (`http://tinyurl.com/k2d2ttj`). The formation process for Earth could have naturally led to the evaporation of of chondrite water from the interior of Earth and its transfer nearer to surface and getting caught inside reservoirs.

   Also prebiotic life could have evolved in the underground water reservoirs and already in chondrites (DNA, RNA, aminoacids, tRNA represented as dark proton sequences at flux tubes) and transformed to the life as we know. Mother Gaia's womb was nice place: no meteorite bombardment, no cosmic rays, and metabolic energy provided by Mother Gaia as dark photons. Cambrian explosion as Earth's radius increased by a factor of two was the birthday of the life as we identify it, the (child) water burst to the surface and seas were formed and life began to evolve at the surface of Earth.

   Recall that in TGD continous cosmological expansion at level of space-time sheets is at quantum level replaced with a sequence of phase transitions increasing $h_{eff} = n \times h$ and/or

p-adic length scale of the space-time sheet - by p-adic length scale hypothesis most naturally by a factor of two. This kind of transition explains why the continents of Earth fit nicely together to cover entire Earth if the radius is half of its recent value, the emergence of gigantic life forms, etc... [L45].

2. The basic objection relates to the basic mechanisms of metabolism. What replaced plants receiving metabolic energy from solar light as source of metabolic energy? What replaced Sun? Did the dark photon radiation generated by Earth - or maybe also Sun - and penetrating ordinary matter as dark radiation, replace sun light? Any critical system could generate this radiation and it should not be difficult to identify this kind of system: the boundary between core and mantle is the most obvious candidate for a critical system as also for a rapid self-organization process). I proposed for more than decade ago this option half-jokingly as metabolic sources of IT (intraterrestrial) life as I called it.

3. Dark photon radiation would have had a universal energy spectrum - the spectrum of biophotons in visible and UV range. Part of it would have transformed to biophotons (`http://tinyurl.com/yb9hnmu7`) taking the role of solar radiation as a metabolic energy source. An interesting question is whether the life at the bottom of oceans could give some hints about the counterpart of photosynthesis based on bio-photons? The discovery that the metabolic reactions thought to require complex catalytic maschinery can take place in the environment simulating ocean bottom (`http://tinyurl.com/ydc8g7r4`) supports the idea about the evolution of life from prebiotic life forms in the womb of Mother Gaia. In TGD framework these prebiotic life forms could correspond to dark proton sequences (dark nuclei) at magnetic flux tubes associated with the negatively charged exclusion zones discovered by Pollack [L15] (`http://tinyurl.com/oyhstc2`).

8.5 What about other planets?

8.5.1 How Was Ancient Mars Warm Enough for Liquid Water?

The popular article "Mars Mystery: How Was Ancient Red Planet Warm Enough for Liquid Water?" (see `http://tinyurl.com/gsbwyhe`) tells about a mystery related to the ancient presence of water at the surface of Mars. It is now known that the surface of Mars was once covered with rivers, streams, ponds, lakes and perhaps even seas and oceans. This forces to consider the possibility there was once also life in Mars and might be still. There is however a problem. The atmosphere probably contained hundreds of times less carbon dioxide than needed to keep it warm enought for liquid water to last. There are how these signature of flowing water there. Here is one more mystery to resolve.

The TGD version of Expanding Earth Hypothesis states that Earth has experienced a geologically fast expansion period in its past. The radius of the Earth's space-time sheet would have increased by a factor of two from its earlier value. Either the p-adic length scale or effective value of Planck constant $h_{eff}/h = n$ for the space-time sheet of Earth or both would have increased by factor 2.

This violent event led to the burst of underground seas of Earth to the surface with the consequence that the rather highly developed lifeforms evolved in these reservoirs shielded from cosmic rays and UV radiation burst to the surface: the outcome was what is known as Cambrian explosion. This apparent popping of advanced lifeforms out of nowhere explains why the earlier less developed forms of these complex organisms have not been found as fossile. I have discussed the model for how life could have evolved in underground water reservoirs [L19].

The geologically fast weakening of the gravitational force by factor 1/4 at surface explains the emergence of gigantic life forms like sauri and even ciant crabs. Continents were formed: before this the crust was like the surface of Mars now. The original motivation of EEH indeed was that the observation that the continents of recent Earth seem to fit nicely together if the radius were smaller by factor 1/2. This is just a step further than Wegener went at his time. The model explains many other difficult to understand facts and forces to give up the Snowball Earth model. The recent view about Earth before Cambrian Explosion is very different from that provided by EEH. The period of rotation of Earth was 4 times shorter than now - 6 hours - and this would

be visible of physiology of organisms of that time. Whether it could have left remnants to the physiology and behavior of recently living organisms is an interesting question.

What about Mars? Mars now is very similar to Earth before expansion. The radius is one half of Earth now and therefore same as the radius of Earth before the Cambrian Explosion! Mars is near Earth so that its distance from Sun is not very different. Could also recent Mars contain complex life forms in water reservoirs in its interior. Could Mother Mars (or perhaps Martina, if the red planet is not the masculine warrior but pregnant mother) give rise to their birth? The water that has appeared at the surface of Mars could have been a temporarily leakage. An interesting question is whether the appearance of water might correspond to the same event that increased the radius of Earth by factor two.

Magnetism is important for life in TGD based quantum biology. A possible problem is posed by the very weak recent value of the magnetic field of Mars. The value of the dark magnetic field $B_{end} = .2$ Gauss of Earth deduced from the findings of Blackman about effects of ELF em fields on vertebrate brain has strength, which is 2/5 of the nominal value of B_E. Hence the dark MBs of living organisms perhaps integrating to dark MB of Earth seem to be entities distinct from MB of Earth. Could also Mars have dark magnetic fields?

Schumann resonances might be important for collective aspects of consciousness. In the simplest model for Schumann resonances the frequencies are determined solely by the radius of Mars and would be 2 times those in Earth now. The frequency of the lowest Schumann resonance would be 15.6 Hz.

8.5.2 New Horizons About Pluto

ew Horizons (see `http://tinyurl.com/cjdzsk9`) is a space probe that has just been passing by Pluto and has taken pictures about the surface of Pluto and its Moon Kharon. The accuracy of the pictures is at best measured in tens of meters. Pluto has lost its status as a genuine planet and is now regarded as dwarf planet in the Kuiper belt - a ring of bodies beyond Neptune. Using Earthly unis its radius, mass (from New Horizons data), and distance from Sun are $R = .18R_E$, $M = .0022 \times M_E$ and $d = 40d_E$.

Pictures have yielded a lot of surprises. Pluto is not the geologically dead planet it was though to be. The following summarizes what I learned by reading a nice popular article by Markku Hotakainen in finnish weekly journal ("Suomen Kuvalehti") and also represents a TGD based interpretation of the findings.

1. Surprisingly, the surface of the Pluto is geologically young: the youngest surface shapes have age about 10^8 that is .1 billion years. This is strange since the temperature is about -240 °C at the cold side and it receives from Sun only 1/1000 of the energy received by Earth. Textbook wisdom tells that everything should have been geologically totally frozen for billions of years.

2. There is a large champaign - one guess is that it has born as an asteroid or comet has collided with the surface of Pluto. The region is now officially called Tombaugh Regio. The reader can Google the reason for this. The flat region does not seem to have any craters so that it should be rather young. The boundary of this lowland area is surrounded by high (up to 3.5 km) mountains. Also these formations seem to be young. Nitrogen, methane and CO-ice cannot form so high formations.

   Several explanations have been imagined for the absence of craters: maybe there are active processes destroying the craters very effectively. Maybe there is tectonic activity. This however requires energy source. Radioactivity inside Pluto? Underground seas liberating heat? Or maybe tidal forces: the motions of Pluto and its moon Kharon are locked and they turn always the same side towards each other. There is a small variation in the distance of Kharon causing tidal forces. Could this libration deform Pluto and force the liberation of heat produced by frictional forces?

3. The flat region decomposes to large polygons with diameter of 20-30 km. The mechanism producing the polygons is a mystery. Also their presence tells that the surface is geologically young: at some places only .1 billion years old.

4. The atmosphere of Pluto has also yielded a surprise. About 90 per cent of atmosphere (78 per cent at Earth) is nitrogen but it is estimated to leak with a rate of 500 tons per hour since the small gravitational acceleration (6 per cent of that on Earth) cannot prevent the gas molecules from leaking out. How Pluto manages to keep so much nitrogen in its atmosphere?

5. Kharon - the largest moon of Pluto - has radius which is half of that for Pluto. Also the surface texture of Kharon exhibits signs about upheavals and has similarities to that in Pluto. Craters seem to be lacking. North Pole has great dark region - maybe crater. Equator is surrounded by precipices with depths of hundreds of meters, maybe up to kilometers. If they are torn away so should have been also the precipices.

Can one understand the surface texture of Pluto and Kharon? For years I proposed a model for the finding that the continents of Earth seem to fit nicely to form a single supercontinent if the radius of Earth is taken to be one half of its recent radius. This led to a TGD variant of Expanding Earth theory [L45].

1. It is known that cosmic expansion does not occur locally. In many-sheeted space-time of TGD this could mean that the space-time sheets of astrophysical objects comove at the the large space-time sheet representing expanding background but do not themselves expand. Another possibility is that they expand in rapid jerks by phase transitions increasing the radius. p-Adic length scale hypothesis suggests that scaling of the radius by two is the simplest possibility.

2. If this kind of quantum phase transition occurred for the space-time sheet of Earth about .54 billion years ago it can explain the weird things associated with Cambrian explosion (see `http://tinyurl.com/ntvx38e`). Suddenly totally new life forms appeared as from nowhere to only disappear soon in fight for survival. Could highly evolved life in underground seas shielded from UV radiation and meteoric bombardment have burst to the surface. The process would have also reduced the value of the gravitational acceleration by factor 1/4 and increased the length of the day by factor 4. The reduction of the surface gravity might have led to emergence of various gigantic lifeforms such as dinosauri, which later lost the evolutionary battle because of their small brains. Climate would have changed dramatically also and the Snowball Earth model is replaced by a new view.

If these sudden quantum phase transitions at the level of dark matter ($h_{eff} = n \times h$ phases of ordinary matter) is the manner how cosmic expansion universally happens then also Pluto might so the signs of this mechanism.

1. The surface of Pluto is indeed geologically young: the age is measured in hundreds of millions of years. Could the sudden jerkwise expansion have occurred - not only for Earth but - for objects in some region surrounding Earth and containing also Pluto?

2. The polygonal structure could be understood as a ripping of the surface of Pluto in the sudden expansion involving also cooling of magma and its compression (the analogy is what happens to the wet clay as it dries and becomes solid). The lowland region could correspond to the magma burst out from the interior of Pluto being analogous to the magma at the bottom of oceans at Earth. The young geological age of this region would explain the absence of craters. Also the surface texture of Kharon could be understood in the similar manner.

Could one understand the presence of nitrogen?

1. If the gravitational acceleration was 4 times larger (24 percent of that in Earth) before the explosion, the leakage would have been slower before it. Could this make it easier to understand why Pluto has so much nitrogen? Could the burst of material from the interior have increased the amount of nitrogen in the atmosphere? Geochemist could probably answer these questions.

2. A more radical explanation is that primitive life forms have prevented the leakage by binding the nitrogen to organic compounds like methane. If underground oceans indeed existed (and

maybe still exist) in Pluto as they seem to exist in Mars, one can wonder whether life has been evolving as an underground phenomenon also in Pluto - as so many nice things in this Universe must do;-). Could these lifeforms have erupted to the surface of Pluto in the sudden expansion from underground seas and could some of them - maybe primitive bacteria - have survived. Nitrogen (see `http://tinyurl.com/yb3yexsu`) is essential for life and binds the nitrogen to heavier chemical compounds so that its leakage slows down. Could there exist an analog of nitrogen cycle (see `http://tinyurl.com/yc4r39o8`) meaning that underground life bind the nitrogen from the atmosphere of Pluto and slow down its leakage?

8.6 Expanding Earth hypothesis, Platonic solids, and plate tectonics as symplectic flow

A FB discussion inspired by the evidence reported by Nasa for the existence of life in Mars coming from a generation of methane (see `http://tinyurl.com/y735g9kn`) (thanks to Nikolina Bedenikovic for the link). It seems that it must originate below the surface of Mars - possibly from underground oceans. The emission of methane is periodic having the year of Mars as a period and has maximum during summer time. This suggests that solar radiation somehow serves as a source of metabolic energy. The TGD based explanation might be in terms of dark photons able to propagate through the crust to the underground oceans.

The finding provides support for TGD based Expanding Earth model [L45] explaining Cambrian explosion, which is one of the mysteries of recent day biology. According to this model life would have evolved in underground oceans where it was shielded from UV light, cosmic rays, and meteor bombardment, and burst to the surface of Earth during the period when Earth expanded and the crust developed cracks.

One can wonder whether Expanding Earth model is consistent with plate tectonics and with the motivating claim of Adams that the continents fit together nicely to cover the entire surface of Earth if its radius were one half of the recent radius. The outcome was what one might call Platonic plate tectonics.

1. The expansion would have started from or generated decomposition of the Earth's crust to an icosahedral lattice with 20 faces, which contain analogs of what is known as cratons and having a total area equal to that of Earth before expansion. The prediction for the recent land area fraction is 25 per cent is 4.1 per cent too low. The cause could be sedimentation or expansion continuing still very slowly.

2. Craton like objects (in the sequence briefly cratons) would move like 2-D rigid bodies and would fuse to form continents.

3. The memory about the initial state should be preserved: otherwise there would exist no simple manner to reproduce the observation of Adams by simple motions of continents combined with downwards scaling. This might be achieved if cratons are connected by flux tubes to form a network. For maximal connectivity given triangular face is connected by flux tube to to all 3 nearest neighbour faces. Minimal connectivity corresponds to an essentially unique dodecahedral Hamiltonian cycle connecting cratons to single closed string. At least for maximal connectivity this memory would allow to understand the claim of Adams stating that the reduction of radius by factor 1/2 plus simple motions for the continents allow to transform the continents to single continent covering the entire surface of the scaled down Earth.

4. The dynamics in scales longer than that of craton would be naturally a generalization of an incompressible liquid flow to area preserving dynamics defined by symplectic flow. The assumption that Hamilton satisfies Laplace equation and is thus a real or imaginary part of analytic function implies additional symmetry: the area preserving flow has dual. The flow has vanishing divergence and curl. Sources and sinks and rotation are however possible in topological sense if the tectonic plate has holes.

8.6.1 Summary of the model

Expanding Earth hypothesis in TGD framework

The TGD variant of Expanding Earth hypothesis [L45] (see `http://tinyurl.com/y75hku4x`) can be motivated by both cosmological and biological considerations.

1. The basic observation is that astrophysical objects seem to not take part of cosmic expansion but only to co-move. This leads to the idea that the corresponding space-time sheets experience cosmic expansion as relatively rapid jerks and have constant size between these jerks. Second motivation comes from the claim of Adams [F1] (see `http://tinyurl.com/fxsve`) that the continents would fit nicely together to form a single continent covering the entire surface of Earth if the radius of Earth were 1/2 its recent radius.

2. There is also a connection with biology. Cambrian explosion (see `http://tinyurl.com/ntvx38e`) is a poorly understood period in the history of life at Earth. Suddenly a burst of highly developed life forms emerged from some unknown source. TGD explanation would be in terms of rather rapid increase of the radius of Earth by factor of two from the recent size $R_{Mars} \simeq R_E/2$ of Mars to the recent size R_E of Earth with the consequences that the stretching developed cracks. Since the radial scaling caused similar stretching everywhere, the decomposition to a lattice at some critical value of the scale parameter λ would have generated the cracks. The generation of a lattice in drying clay serves as an analogy.

   The relatively highly developed underground life would had evolved below the surface of Earth, where it was shielded from the bombardment by meteors, cosmic rays, and UV radiation and was burst to the surface as the oceans were formed on the cracks.

   The increase of the radius of Earth by factor 2 increased the duration of day by factor 4 and reduced the surface gravity by a factor 1/4. The genetically conserved features preceding the expansion would be still seen in biology. For instance, there might exist a 3 hour bio-rhythm if the underground life received solar radiation somehow. The reduction of gravity could explain the emergence of giant sized organisms such as dinosaurs.

   Underground life must have some source of metabolic energy and photosynthesis should have developed already before the Cambrian expansion. This suggests that visible light from some source must have been present. I have considered possible sources in [L19]. The most science fictive proposal is that part of the photons of solar radiation transform to dark photons identified as a phase of ordinary photons residing at magnetic flux tubes. They would have had a non-standard value of Planck constant $h_{eff} = n \times h_0$ and in absence of direct interactions with the ordinary manner would have managed to penetrate through the crust to the underground oceans.

   In the recent biology bio-photons with energies in visible and UV range would emerge as energy conserving transformations of large h_{eff} photons to ordinary photons. The value of h_{eff} for charged particle of mass m would be by a generalization of Nottale's proposal equal to $\hbar_{eff} = n \times \hbar_0 = h_{gr}GMm/v_0$, where M could correspond to a dark mass assignable to Earth and v_0 is a parameter having dimensions of velocity. This hypothesis implies that cyclotron energies of charged particles do not depend at all on the mass of the charged particle so that cyclotron photons can induce transitions of bio-molecules [K75, K76].

   Remark: h_0 is the minimal value of h_{eff}: the best guess for the ordinary Planck constant corresponds to $n = 6$ [L23, L42].

   This mechanism for the transfer of solar energy under the surface of Mars could explain the annual periodicity of the methane production in Mars. Magnetic fields serve as a shield against UV radiation and cosmic rays in the case of Earth. Mars has only weak and local magnetic fields above its surface. This gives a good reason why for the Martian life to stay below the surface. The strengthening of the Earth's magnetic field might have preceded or accompanied the proposed expansion of Earth.

3. This vision profoundly modifies the ideas about what happened before Cambrian explosion. In particular, Snowball Earth hypothesis (see `http://tinyurl.com/prem7nj`) about the the climate evolution must be given up. The magnetic history of Earth allows to test the model.

Basic ideas of Platonic plate tectonics

The FB discussion raised the question whether the TGD based Expanding Earth model [L45] is consistent with plate tectonics and with the motivating claim of Adams that the continents fit nicely to cover the entire surface of Earth if its radius were one half of the recent radius. The outcome was what one might call Platonic plate tectonics.

1. The expansion would have started from or generated decomposition of the Earth's crust to an icosahedral lattice with 20 faces, which contain what could be identified as cratons (see `http://tinyurl.com/y8juty2q`) having a total area equal to that of Earth before expansion. Cratons represent the stable part of the continental litosphere and are found in the interiors of the tectonic plates. They consist of ancient crystalline basement rock and maybe be covered by younger sedimentary rock. They have a thick crust and deep litospheric roots. The prediction 25 per cent for the recent land area is 4.1 per cent too low. The simplest explanation is that expansion still continues but very slowly. Also the formation of sedimentary rocks could have increased the area.

2. The cratons would move like 2-D rigid bodies and would fuse to form continents.

3. The memory about the initial state should be preserved: otherwise there would exist no simple manner to reproduce the observation of Adams by simple motions of continents combined with downwards scaling. This could be achieved if cratons are connected by flux tubes to form a network (for tensor networks in TGD Universe see [L22]). For maximal connectivity given triangular face is connected by flux tube to to all 3 nearest neighbour faces. Minimal connectivity corresponds to an essentially unique dodecahedral Hamilton's cycle [A14] (see `http://tinyurl.com/pf33vkt`) connecting cratons to single closed string. At least for maximal connectivity this memory would allow to understand the claim of Adams stating that the reduction of radius by factor 1/2 plus simple motions for the continents allow to transform the continents to single continent covering the entire surface of the scaled down Earth.

4. The dynamics in scales longer than that of craton would be naturally a generalization of an incompressible liquid flow to area preserving dynamics defined by symplectic flow. The assumption that Hamilton satisfies Laplace equation and is thus a real or imaginary part of analytic function implies additional symmetry: the area preserving flow has dual. The flow has vanishing divergence and curl. Sources and sinks and rotation are however possible in topological sense if the tectonic plate has holes. This would suggest conformal invariance.

The proposal is that the expansion of Earth taking place as discrete jerkes is basically a quantum phenomenon in astrophysical scales.

1. In TGD framework magnetic flux tubes are carriers of dark matter identified as phases of ordinary matter with non-standard value of Planck constant. As explained, the value of gravitational Planck constant h_{gr} would be enormous and imply quantum coherence in the size scale of Earth at the magnetic body forcing coherence at the level of ordinary matter [K76]. The transitions changing the value of h_{eff} would change the length of flux tubes and these transitions would be crucial for the dynamics of water [L49] (see `http://tinyurl.com/ydhknc2c`).

2. Also the ability of biomolecules to find each other in molecular soup would rely on the same mechanism. In biology also the formation of organs and organelles from cells would involve the shortening of flux tubes [L47] (see `http://tinyurl.com/y9pxr9dx`). In brain synchronously firing neuron groups would form dynamical networks. An interesting question inspired by the huge value of h_{gr} is whether cratons could be seen as analogs of cells and continents as analogs of organs of Mother Gaia. Note that the magnetic bodies of living systems with EEG would have layers with size scale of Earth [K15].

What happened in the expansion of Earth and after that?

One can try to imagine what happened during and after the expansion of Earth.

1. The spherical crust developed at least one hole as the radius increased by factor 2: $R_f = 2R_i$. The crust free regions became frozen magma covered by ocean. The total area of crust was preserved. A stronger condition is that only some minimal stretching required by the increase of the radius occurred. Too large a stretching would have generated the cracks.

   The experimentation with toy models leads to the conclusion that minimal stretching is achieved if the crust decomposes into a spherical lattice - regular tesselation- having maximal number of cells. Platonic solids are the only regular tesselations of sphere. The dual P_D of platonic solid P has as its vertices the faces of P and vice versa. The list of Platonic solids (see `http://tinyurl.com/p4rwc76`) is short.

   - Self-dual tetrahedron (4 faces and 4 vertices).
   - Cube with 6 faces and 8 vertices faces and its dual octahedron.
   - Icosahedron and its dual dodecahedron with 20 and 12 faces respectively. For icosahedron the number of faces is maximal and the size of the face minimal and the local stretching is therefore minimal. The faces of icosahedron correspond to the vertices of the dual dodecahedron and icosahedral tesselation is the best candidate to begin with. Note however that the 6 faces of cube could correspond to the 6 continents. One can of course image that the moving cratons later evolved to form an approximate cubical tessselation.

   Remark: Surfaces with flat metric (plane and cylinder) allow warpings (see `http://tinyurl.com/ycyregve`) for which the induced metric remains flat so that the deformation can be regarded as an isometry with no stretching but non-trivial bending. For instance, for the surface $z(x, y) = z_0$ one can have warping $z = z_0 + f(x)$. The dynamics for the page of book provides a good example of this kind of warping. Could this kind of warpings leading to one-dimensional deformations of the surface of Earth happen for continents in sufficiently short scales?

2. During subsequent evolution radius R_f remains (approxmately) constant and the pieces of crust move along the surface of Earth. No stretching condition prevents the change of shape. If changes of shape are allowed, the first guess is that this evolution was area preserving and thus generated as by a Hamiltonian flow. This would be just classical Hamiltonian mechanics in 2-D phase phase associated with the piece of crust.

   If distances inside cratons were preserved (no stretching and change of shapce), the dynamics for small enough plates would reduce in a reasonable approximation to a rigid body rotation in the tangent plane at the center of mass of the plate and movement along a geodesic line along the Earth's surface plus collisions. If one accepts that the initial state was a tesselation defined by a Platonic solid, in particular icosahedron, the symplectic evolution trivializes in this manner. The faces contain cratons with area scaled down by factor 1/4. If craton like object is a disk with radius d one would have $d = (1/2\sqrt{20})R_E \simeq .11R_E$. Using $R_E = 6371$ km this gives $d = 1425$ km.

3. The first guess is that the expansion period is over now and one has $R_f = 2 \times R_i$ exactly. As found, the predicted fraction of land area for $R_f = 2 \times R_i$ is 4.1 per cent smaller than the actual value about 29.1 per cent. A possible explanation for 4.1 per cent is the generation of sedimentary rocks. This would give a probably testable prediction for the fractional area due to sedimentation. Subduction would increase this estimate.

   One can also ask whether the expansion still continues slowly so that the radius is not yet quite equal to $R_f = 2 \times R_i$ so that the fraction of land area is larger than 25 per cent. One would have $R_f = 2xR_i$, $x = .93$. Subduction tends to increase and sedimentation to reduce the value of x. The separation of expansion period from the period during, which R_f stays constant would be a good approximation if the time scales for tectonics are considerably shorter than for the expansion.

Could flux tube network reproduce the claims of Adams?

The triangular faces can move around and can scale down their size scale by factor 1/2 to the size of craton so that a fusion of cratons to larger units forming continents becomes possible. If one takes the claim of Adams [F1] (see `http://tinyurl.com/fxsve`) seriously, the subsequent dynamics for the faces containing the cratons must be such that it is easy to see how to move continents in the scaling down of the radius of Earth to achieve the gluing together without overlaps and holes (the mere scaling down does not allow to achieve this since the distances between scaled down continents would be 1/2 of the recent distances).

The dynamics must remember the initial regular icosahedral tesselation at S_i^2. In the ideal situation every face must "remember" its former nearest neighbours at S_i^2 even when some of them can be faraway at S_f^2. This requires a network connecting the faces. If the faces are connected by a large enough number of flux tubes able to change their lengths this can be realized and as the radius is imagined to decrease by a factor 1/2, all faces combine to form a spherical crust without overlaps. One can consider two extreme situations.

1. Maximal connectedness requires that every face of icosahedron is connected to each of its 3 nearest neighbours. In this case the dynamics can only involve condensation of the cratons/faces of the network to form continents and for this option the claim of Adams seems trivial.

2. The minimally connected network would correspond to a string connecting the 20 faces to single non-self-intersecting closed string identifiable as a Hamiltonian cycle at dodecahedron. One identifies cycles differing only by an isometry of dodecahedron and already Hamilton discovered that dodecahedron allows only single cycle if one identifies cycles differing only by an isometry of dodecahedron. Given triangle would be connected by flux tube to 2 (rather than 3) nearest neighbors.

   Remark: Hamilton's cycles at icosahedron [A14, A3, A9, A2, A8] with 12 vertices play fundamental role in TGD inspired model for music harmony lead to a model of genetic code and of bio-harmony. In this case there is large number of harmonies [L12] [L50].

   Whether this option is consistent with the claim of Adams is not clear. One can argue that without additional assumptions the dynamics of the Hamiltonian cycle can destroy the information about the initial icosahedral tesselation by permuting the faces. Could the condition that no self intersections of the flux tubes (strings) of the cycle take place, be enough to preserve the information about initial configuration? The (unique apart from isometries) Hamiltonian cycle can have a fold so that it turns back. The cratons of the antiparallel nearby portions of string can fuse together. The pairing induced by the folding can take place in several manners: say ...(1,6)-(2,5)-(3,4) or ...(-1,6)-(0,5)-(1,4)-(2,3). Here (a,b) corresponding fusion of cratons and - for the Hamiltonian link between neighbouring faces. The increase of the land area by 4.1 percent forces some overlap in the final state if the expansion period has ceased.

8.6.2 Plate tectonics as a symplectic flow in scales longer than the size of craton?

For the icosahedral model the short scale dynamics reduces to much simpler dynamics of 2-D rigid bodies at S^2 having collisions leading to subductions. Cratons however fuse together to form continents having plate tectonics as their dynamics. Tectonic dynamics applies in length scales longer than craton size and cratons could be idealized as point like objects analogous to lipids in cell membrane.

The first guess for the dynamics after the expansion period is symplectic flow preserving the signed area of the continent defining an area preserving map for each value of the time parameter. The area preserving flow is analogous to an incompressible liquid flow in 3 dimensions and serves as a natural model for liquid crystals. For instance, cell membrane is liquid crystal. In this case lipids are idealized as point like objects with symplectic dynamics making sense in length scales longer than the thickness of lipid.

Symplectic flow would be therefore a natural model for plate tectonics (see `http://tinyurl.com/hmby9d4`), and the idealization of cratons as pointlike entities would allow to overcome the objection due to stretching. Symplectic flows could be also used to model the emergence of cracks using Hamiltonians discontinuous along cuts and to model "self-subductions" as flows, which become non-injective and generate mountains.

Remark: Symplectic flows could also be used to model the liquid magma in the outer core idealized as 2-D layer analogous to liquid crystal.

What conditions could one pose on the Hamiltonian defining the symplectic flow? The observation that Hamiltonians identified as real or imaginary parts of analytic functions have additional symmetry implying the existence of a dual flow for which flow lines are orthogonal to those for the flow. A good guess therefore that the local tectonics for a continent is defined by a Hamiltonian satisfying Laplace equation. There would be a nice connection between analytic functions and symplectic flows.

A model for the continuous time evolution of tectonic plate

The simplest model for a continuous local evolution of given tectonic plate in length scales longer than the size of craton after the expansion period and formation of continents assumes the conservation of signed area meaning that the evolution is symplectic flow generated by some Hamiltonian defined in the region defined by the continent. The symplectic flow would be a 2-D variant of incompressible hydrodynamics.

1. The dynamics would be dictated by the conservation of signed area element $dS = R^2 sin(\theta) d\theta \wedge d\phi$ defined by the symplectic form of $J = J_{kl} ds^k \wedge ds^l$ of S^2. Symplectic transformations preserve the local area form and are generated by the exponentiation of Hamiltonian function H giving models for time evolutions as exponentiation of H defining a flow along the continent.

2. A model for the generation of cracks could be based on Hamiltonian function, which has line discontinuities completely analogous to discontinuities of imaginary or real part of an analytic function. The Hamiltonian flow would take the two sides of the cut to opposite directions in the Hamiltonian flow and crack would develop. The cracks would be filled with water and become oceans.

3. Hamiltonian time evolution defines symplectic map for each value of the time parameter t, which can cease to be injection at some moment of time at some point and give rise to growing regions into which two different regions of the continent are mapped. Cusp catastrophe with 3 sheets gives a standard topological description for what would have happened. The folding would have 3 plates above each other in the fold region. This "self-subduction" would produce regions analogous to those formed in subduction in which two continents drifting at the surface of magma collide and subduce. Also this process can generate mountains.

   The signed area of the middle sheet of the cusp is negative if the area of the other sheets is positive. The formation of the cusp seems therefore to reduce the land area since the middle sheet and lowest sheet of the cusp are invisible. When plate subduces another plate visible land area is also lost. One can imagine two explanations for the missing 4.1 per cent: sedimentation has generated new land area or the expansion period has not yet ended.

One can formulate this picture in more detail as follows.

1. The area preserving symplectic time evolution obeys in general coordinates s^k for S^2 the formula

$$\frac{ds^k}{dt} = j^k = J^{kl}\partial_l H \quad , \quad J_k{}^r J^r{}_l = -s_{kl} \quad . \tag{8.6.1}$$

   where J_{kl} and s_{kl} are the symplectic form and standard metric of S^2. In spherical coordinates (θ, ϕ) one has $J_{\theta\phi} = -J_{\phi\theta} = sin(\theta)$. $H = H(\theta, \phi)$ is the function defining the Hamiltonian and subject to physical constraints. j^k has vanishing divergence:

$$D_k j^k = 0 \ . \tag{8.6.2}$$

This equation codes for the local conservation of area.

2. The real or imaginary part of an analytic function having cut along curve can serve as a Hamiltonian in this case. Analyticity would give strong additional constraints on the discontinuity since Laplace equation would be satisfied meaning that not only the current j^k but also the dual current $j_D = g^{kl} H_l$ is conserved:

$$D_k j_D^k = 0 \ . \tag{8.6.3}$$

j_D^k and j^k are orthogonal and correspond to real and imaginary parts of an analytic function. Also j_D^k defines an area preserving flow. This connection between conformal symmetries and symplectic symmetries for Hamiltonians satisfying Laplace equation does not seem to be very familiar to physicists. As a consequence the flow has vanishing divergence and curl. Sources and sinks and global rotation are possible in topological sense if the tectonic plate has holes. This would suggest conformal invariance in some sense.

The absence of sinks implies that one can express j_D^k as a curl of vector field orthogonal to S^2. A possible interpretation is as induced Kähler magnetic field or Z^0 magnetic field. One of the first ideas related to the applications of TGD to condensed matter was that hydrodynamic flow could give rise to Z^0 magnetic fields just like em currents give rise to magnetic fields and that vortices of the flow correspond to magnetic flux tubes. This picture makes sense for Kähler magnetic field as well - an option that seems more natural now. The different directions of rotational axis and magnetic dipole axis of Earth would correspond to different directions of the ordinary magnetic field and Z^0 or Kähler magnetic field. These magnetic fields would be effective magnetic fields identified as sums of magnetic fields considered at different space-time sheets at quantum field theory limit of TGD. The flow dynamics could be essentially that of induced Kähler magnetic field orthogonal to S^2.

Remark: At fundamental level only the effects of classical fields on test particle touching several space-time sheets sum up, not the fields. At QFT limit induced fields from different space-time sheets sum up.

The equation for the flow can be integrated for a given flow line as

$$s^k(t) = exp(tj^r \partial_r) s^k(0) \ . \tag{8.6.4}$$

3. The model for the emergence of a crack requires Hamiltonian discontinuous along a 1-D cut. One has $H = H_\pm$ at the two sides of the cut. The expression of $s^k(t)$ for the flow lines beginning from the point $s^k(0) = s_\pm^k(0)$ of the cut and continuing to the side $\pm$ is given by

$$s_\pm^k(t) = exp(tJ^{rl} \partial_l H_\pm) \partial_r) s^k(0) \ . \tag{8.6.5}$$

The model for the emergence of "self-subductions" and generation of mountains can be constructed using non-injective Hamiltonian evolutions in which regions having as pre-images two regions appear. These regions correspond to two continent plates above each other. Both self-subduction and subduction reduce the land area.

8.6.3 Appendix: Some mathematical details

The icosahedral model for the generation of continents was an outcome of experimentation. I started with a model inspired by the idea that an analog of super-continent Gondwana was generated as single cap during the expansion period but realized soon that it requires quite too large stretching unless one allows generation of cracks. Also a model with two gaps seemed non-realistic. Homogenous upwards scaling of the Earth's radius suggests strongly lattice like structure and the minimization of stretching led to icosahedral model. I however decided to include these attempts as Appendix - a kind of confession. Hasty reader can skip these parts of the Appendix.

Generation of one or two caps requires too much stretching

The basic objection against single cap model is that the proposed model for expansion requires quite much stretching, which requires large energy. It is also clear that too much stretching leads to a generation of cracks. The following argument is more precise formulation of this observation in terms of a toy model.

1. The first option is that supercontinent analogous to Gondwana (see `http://tinyurl.com/hcgjnrb`) was generated as an expanding hole hole in the crust of S_i^2 emerged somewhere in what became Pasific Ocean - call this place "South pole". Gondwana hypothesis is consistent with Wegener's construction.

2. This period corresponds to a total area preserving map taking the spherical surface (crust) of S_i^2 to a cap of S_f^2 with the same area. The area of the cap should have been thus fraction $S_f/S_i = R_i^2/R_f^2 = 1/4$ of the total area: this corresponds to 25 per cent of the area of Earth. The actual portion of continents from total area is 29.1 per cent. 4 per cent of new land area should have been generated later by some mechanism.

3. The expansion would take the crust covering entire S_i^2 to a supercontinent covering part of S_f^2. The simplest map of this kind maps the surface of S_i^2 to a cap of S_f^2 defined by the condition $\theta_f \in [0, \pi/3]$: this corresponds to $[0, 60]$ degrees. $\theta_f = 0$ would correspond to the "North Pole". This model is certainly non-realistic since it requires large stretching at the bottom of the gap. The stretching is expected to cause cracks mainly in the direction of the coordinate lines of θ_f.

   For the cap at "North pole" the stretching along the coordinate circles of ϕ_f would be very large near the bottom of the cap. One possibility is that cracks in direction of θ_f were generated or that the boundary of cap or that the boundary was "wavy".

A slightly more plausible option reducing the stretching along coordinate circles of ϕ_f would assume generation of 2 caps located at "South pole" and "North pole" as a crack along equator was generated. Also now a wavy crack would allow to minimize the stretching along the coordinate circles of ϕ_f. There would be also stretching along coordinate lines of θ_f. In this case one would have two separate super-continents from the beginning and fitting together along their boundaries of the gaps.

Cap models for the expansion period

The expansion period as generation of one or two caps is unrealistic since it produces too much stretching. In the following however the details of the model are given.

1. There exists no isometry between the crust associated with S_i^2 and connected crust associated with S_f^2. Isometry would require that curvature scalars are same and this is impossible since the radii of S_i^2 and S_f^2 are different.

2. The conservation of total area in the map $S_i^2 \to S_f^2$ taking spherical crust to cap $0 \leq \theta_f \leq \theta_{max}$ with same area: $S_f = S_i$.

3. If the expansion begins from an icosahedral lattice the dynamics of expansion period could reduces to simple scaling in a reasonable approximation. The fraction of land area is however

29.1 per cent rather than 25 per cent however that the expansion is still occurring albeit very slowly. Therefore one cannot separate expansion period completely from the tectonic dynamics. One can however think of time dependent scaling combined with the motion and collisions of cratons leading to their fusion.

Consider a more detailed definition of the cap models.

1. In the case of single-cap model the simplest manner to guarantee this is to require $cos(\theta_{f,max}) = cos(\theta_{i,max})/4 + 3/4 = 1/2$ giving $cos(\theta_{f,max}) = 1/2$ and $\theta_{f,max} = \pi/3$, which corresponds to 60 degrees. As mentioned the large strength in ϕ_f direction requires either a wavy boundary of generations of cracks in θ_f direction.

2. For the two-cap model the hemispheres $\theta_i < \pi/2$ and $\theta_i > \pi/2$ are contracted to caps when the crack at $\theta_i = \pi/2$ is generated. The condition that no stretching occurs along the coordinate circles of ϕ_f is guaranteed if one has

$$2sin(\theta_f) = sin(\theta_i) \quad . \tag{8.6.6}$$

For small values of $sin(\theta_f)$ near poles this condition reduces approximately to the condition $2\theta_f = \theta_i$, which guarantees that the distances along coordinate lines of θ_f are same as along those of θ_i so that stretching is minimal also along this direction near poles.

This correspondence is well-defined only for $sin(\theta_f) \leq 1/2$, which corresponds to $|cos(\theta_f)| \geq \sqrt{3}/2$. On the other hand, the condition that the sum of the areas of the caps equals the area of S_i^2 gives $|cos(\theta_f)| \geq 3/4 < \sqrt{3}/2$ so that one must have larger gaps than allowed by no-stretching condition along coordinate circles of ϕ_f. A possible manner to solve the problem is to assume that the boundaries of the gaps are wave or that cracks are generated mainly in θ_f direction.

One can model the expansion period $t = (0, T)$ as a homotopy $R = R(t)$, $[R(0) = R_i = R, R(T) = R_f = 2R]$. During this period the cap develops and $\theta_{f,max}$ satisfies the formulas guaranteeing the conservation of distances along coordinate circles of ϕ_i and of total area.

1. For single-cap case one has

$$\frac{R(t)}{R_i} sin(\theta_f) = sin(\theta_i) \quad , \quad (\frac{R(t)}{R_i})^2 (1 - cos(\theta_{f,max}) = 2 \quad . \tag{8.6.7}$$

The first condition can be satisfied only for $cos(\theta_f) \geq \sqrt{1 - (R_i/R(t))^2}$. This lower limit should be smaller than the limit given by the latter condition: $R_i/R(t) \leq \sqrt{7}/4$. For $R(t)/R_i > 4/\sqrt{7} < 2$ the conditions are consistent with each other.

2. The 2-gap case gives

$$\frac{R(t)}{R_i} sin(\theta_f) = sin(\theta_i) \quad , \quad (\frac{R(t)}{R_i})^2 (1 - cos(\theta_{f,max})) = 1 \quad . \tag{8.6.8}$$

Also for this option one must have $cos(\theta_f) \geq \sqrt{1 - (R_i/R(t))^2}$. The condition $cos(\theta f, max) = 1 - (R_i/R(t))^2$ implies that the first condition cannot be satisfied for all values of $cos(\theta_f)$.

8.7 New support for the view about Cambrian explosion being caused by rapid increase of Earth radius

There was an interesting popular article in Quanta Magazine titled "*Oxygen and Stem Cells May Have Reshaped Early Complex Animals*" (see `http://tinyurl.com/y86ta45l`).

The article dicusses the work of geobiologist Emma Hammarlund and tumor biologist Sven Påhlman: their interdisciplinary hypothesis is published as article in Nature [I111] with title "*Refined control of cell stemness allowed animal evolution in the oxic realm*" (see `http://tinyurl.com/y85ufngz`).

Here is the abstract of their article.

Animal diversification on Earth has long been presumed to be associated with the increasing extent of oxic niches. Here, we challenge that view. We start with the fact that hypoxia ($\leq 1-3$ per cent O_2) maintains cellular immaturity (stemness), whereas adult stem cells continuously - and paradoxically- regenerate animal tissue in oxygenated settings. Novel insights from tumour biology illuminate how cell stemness nevertheless can be achieved through the action of oxygen-sensing transcription factors in oxygenated, regenerating tissue. We suggest that these hypoxia-inducible transcription factors provided animals with unprecedented control over cell stemness that allowed them to cope with fluctuating oxygen concentrations. Thus, a refinement of the cellular hypoxia-response machinery enabled cell stemness at oxic conditions and, then, animals to evolve into the oxic realm. This view on the onset of animal diversification is consistent with geological evidence and provides a new perspective on the challenges and evolution of multicellular life.

8.7.1 The proposal of Hammarlund and Påhlman

Cambrian explosion (see `http://tinyurl.com/ntvx38e`) during which highly advanced lifeforms suddenly emerged - prolifiration and diversification of animal life are the terms used about this - is one of the mysteries of biology. For most of its 4.5-billion-year history, Earth has sustained life but that life was largely limited to microbial organisms: bacteria, plankton, algae. For about 540 million years ago did larger, more complex species are assumed to dominate the oceans, but within just a few tens of millions of years (very short time on the evolutionary timescale), the planet had filled up with all kinds of animals. The fossil record from that period shows the beginnings of almost all modern animal lineages: animals with shells and animals with spines, animals that swam and animals that burrowed, animals that could hunt and animals that could defend themselves from predators. Also many lineages that disappeared were present as one learns from the book of Stephen Jay Gould describing in detail the Burgess Shale finding that revolutionized the picture about evolutionary biology and remains still a puzzle (see `http://tinyurl.com/y9orfy43`).

The belief is that the environment became considerable more oxic - that is contained oxygen - and lifeforms had to cope with this change. Before the change the animals in seas (believed to exist!) were anaerobic. The shifting to aerobic respiration was however an enormous metabolic advantage since the effectiveness of metabolic energy gain become roughly 20-fold. Increased metabolic feed in turn made possible the emergence of complexity during Cambrian period.

1. The proposal of the authors is that the evolution of the capacity to maintain stem cells even in an oxic environment allowed the animals to keep stocks of stem cells needed for tissue growth and repair for that this required at gene level new genes coding for so called HIFs.

2. Stem cells require low oxygen levels to preserve their stemness. Heightened oxygen levels cause them to differentiate abruptly. This explains why stems cells are often located in hypoxic regions of the body (say bone marrow) having low oxygen levels. There are however exceptions to this rule: stem cells can also survive in ocix regions such as skin or retina. Cancers also utilize stem cells to achieve growth.

3. Hammarlund and Påhlman turned their attention to HIFs (hypoxia-inducible transcription factors), which are proteins, which for hypoxic environment shift the metabolism from aerobic to an-aerobic. For oxic environment they are not needed.

   HIF-2α remains however active also in oxic environment and make the cells behave as if the environment were hypoxic. This would allow the stem cells to survive. HIF-2α would

however keep the stem cells in immature state also in the case of cancer. The hypothesis of Hammarlund and Påhlman was that HIF-2α functions similarly in normal animal tissues. They have seen some preliminary evidence for the hypothesis but further work is needed.

4. HIFs could have helped the animals to survive in oxic environment. Consider an organism as a blob of cells. Before the oxygenation the stem cells would have been forced to the deep interior of the blob, where oxygen concentration was especially low. When oxygenation took place, and oxygen level varied, this trick did not work anymore and HIFs had to be invented.

5. Hammarlund and Påhman postulate what they call HIF-1, which would have helped stem cells to behave as if the environment were hypoxic. Later HIF-2α unique to vertebrates emerged and improved the situation further. Vertebrates are bigger and have longer time spans that invertebrates and they can live in oxygenated environments. Inveratebrates such as insects live most of their life as larvae under low-oxygen conditions and they cannot regenerate tissues as vertebrates can.

6. Cancer would be the price paid for this evolutionary advance since cancer cells can proliferate because HIF-2 keeps the stem cells alive. OH present in oxygen rich environment is an oxidant causing cancer.

What caused the oxygenation? So called Great Oxygenation Event (GOE,see `http://tinyurl.com/q7qfd55`) is believed to have occurred about about 2.25 billion years ago and thus preceded Cambrian explosion that occured about .5 billion years ago.The time lapse between these events is about 1.75 billion years and much longer than the duration of Cambrian period, which was only tens of millions years. Thus GOE was not the reason for the Cambrian explosion. What caused a further oxygenation or were the effects of GOE somehow postponed (wink-wink!)?

8.7.2 TGD view

My own proposal is that life evolved in underground oceans and entered to the surface of Earth in Cambrian explosion (see `http://tinyurl.com/ntvx38e`) when oceans were formed at the surface of Eearth from cracks formed when Earth expanded rapidly in geological time scale. Before the explosion Earth did not have oceans and continents and was like Mars nowadays: even its radius was that of Mars. This picture follows from TGD based variant of Expanding Earth hypothesis [L45, L44] (see `http://tinyurl.com/yc4rgkco` and `http://tinyurl.com/yb68uo3y`) .

The habitat changed in the rapid expansion of Earth from hypoxic to oxic and the emergence of the hypothetical HIF-1 transcription factor would have been forced by this evolutionary pressure and made it possible for the lifeforms to adapt oxygen based metabolism. This would have led to a rapid evolution of animals and emergence of vertebrates. One can of course think that oxygenation developed already in the underground oceans as cracks caused in the crust by the expansion of Earth began to develop and provided oxygen. The alternative - not so plausible sounding - option is that the highly developed organisms developed underground slowly and only bursted to the surface of Earth in the explosion.

1. Chemical markers (see `http://tinyurl.com/ntvx38e`) indeed indicate dramatic change in the environment at the start of the Cambrian period. The markers are consistent with a massive warming due to the release of methane ice (clathrate hydrate, see `http://tinyurl.com/peq9gmw`) trapped within the crystal structure of water. Methane clathrate is found deep under the sediments at the ocean floors. Methane hydrates are believed to form by migration of gas from deep along geological faults (the cracks produced by rapid expansion of Earth [L44]!).

2. During the period before Cambrian explosion Earth would have been very much like in recent Mars. Even its radius would have been that of recent Mars! One can ask whether GOE forced the existing primitive lifeforms underground or saved only those already living underground. Situation would have been be very much like in the recent Mars, which also seems to possess undergound life.

The development of HIF proteins (hypoxia inducing factor) making possible for stem cells to survive in environments with varying and thus temporarily higher oxygen content would have been a natural reaction to the dramatic changes in habitat.

What can one say about the emergence of animal life in TGD framework?

1. The rapid evolution leading to the emergence of animals - if it was present - would relate to the quantum criticality associated with the increase of the effective Planck constant $h_{eff}/h_0 = n$ by factor 2 increasing the size scale of Earth. The increase of $h_{eff}/h_0 = n$ might have occurred at several levels of dark matter hierarchy, also at biological relevant scales and led to an increase of biological "IQ" (note that evolution corresponds in TGD to gradual increase of number theoretical complexity and n characterizes the dimension of extension of rationals characterizing the complexity [L35, L34]).

2. Animals use oxygen for breathing and are multicellular eukaryotes having cell membrane enclosing nucleus and other membrane bound organelles. The quantum critical period could have led to the emergence of a kind of symbiosis of various kind of organelles within cell membrane bounded volume. The p-adic length scale $L(k)$ determined by the value of n assignable to the outer membrane of organelles could correspond to the prime $k = 163$ (or 167). Inside plant cells having no cell membrane these organelles correspond to vacuoles (see `http://tinyurl.com/yd879b2d`). The outer membrane that emerged in the transition increasing h_{eff}/h_0 meant increase of the scale of quantum coherence to a longer p-adic length scale - say $k = 167$ (or $k = 169 = 13^2$ if doubling took place).

3. Mitochondria would have emerged and made possible oxygen based respiration whereas plant like organisms preceding them utilized anaerobic respiration. Methanogenesis (see `http://tinyurl.com/y97gkym8`) utilizing carbon instead of oxygen and producing carbon-dioxide and methane CH_4(water in O_2 based respiration) is the most natural option. The large methane storages underground would be due to methanogenesis.

   The recent findings (see `http://tinyurl.com/y735g9kn`) indicate that there is life in Mars: methane emissions occurring periodically with a period of Martian year have been detected. This suggests that solar radiation is somehow able to enter to the interior of Mars or that it heats the underground Oceans. In TGD one can consider also the possibility that some part of solar photons transforms to dark photons and is able to propagate to the underground oceans through the Martian crust [L44].

4. What was the primary source of metabolic energy? Direct solar radiation was absent in underground oceans. The immediate source of metabolic energy for the plant like organisms might have been dark nuclei consisting of dark proton sequences and liberating energy in the transitions reducing of $h_{eff}/h_0 = n$. Dark proton triplets give rise to dark variants of DNA, RNA, tRNA, and amino-acids [L21, L19, L46]. These dark proton sequences could have formed by Pollack effect at the surface of Earth possibly containing some water and could have propagated along dark flux tubes to the interior: also in "cold fusion" dark nuclei would be formed. Some fraction of them would transform to ordinary nuclei and liberate practically all the nuclear binding energy. Also transitions to dark nuclei with a smaller value of h_{eff}/h_0 is possible and liberates energy usable as metabolic energy. Most dark nuclei could leak out along magnetic flux tubes [L29]. The hen-egg problem - which came first, metabolism or genetic code - would trivialize in this framework.

   For p-adic length scale $L(k = 149) = 5$ nm - thickness of cell membrane - the typical dark nuclear excitation energy was about .5 eV, the nominal value of metabolic energy quantum. For $L(151) = 10$ nm (thickness of neuronal membrane and DNA double strand its value is .25 eV. These estimates are based on the scaling of the typical nuclear excitation energy taken to be 1 MeV and are uncertain by a factor of 2 at least. One of course expects also higher excitation energies - even so high that they correspond to visible ordinary photons. Metabolic energy could have been liberated as dark photons in dark nuclear transitions transforming to ordinary photons and absorbed by the photosynthetic machinery.

   The (rough) estimate for the typical value of the dark photon energy is considerably lower than in ordinary photosynthesis. Pollack effect [L15] occurring in presence of gel phase

bounding water volume suggests that for $k = 149$ the transformation of dark proton sequences to ordinary ones: this mechanism would liberate energy per proton ~ 1.5 eV [L37], which corresponds to infrared photon. The small value of the metabolic energy quantum need not be a problem: there is recent evidence that IR light with energy 1.76 eV can be used in photosynthesis (see `http://tinyurl.com/yc6pqjed`).

Part II

TGD INSPIRED MODELS FOR GENETIC CODE

Chapter 9

Three new physics realizations of the genetic code and the role of dark matter in bio-systems

9.1 Introduction

This chapter represents an attempt to integrate three different models of genetic code [K17, K51, K56] with each other and with DNA as topological quantum computer (TQC) hypothesis [**?**] as well as the general ideas behind the model of protein folding and bio-catalysis [K2]. The considerations lead to a modification of the earlier model of protein folding.

9.1.1 The Notions Of Dark Matter And Magnetic Body

The generalization of the imbedding space to a book like structure (see Appendix) with pages labeled by two non-negative integers (n_a, n_b) characterizing the singular coverings of M^4 (or actually of causal diamond of M^4 defined as intersection of future and past directed light-cones) and of CP_2 together with pages representing singular coverings and represented similarly by a pair of integers (or equivalently inverses of non-negative integers) provides a possible mathematical realization of dark matter hierarchy. Dark matter is interpreted as phases of ordinary matter at various pages of the book like structure. The pages of the book are partially characterized by a hierarchy of Planck constants. The notion of darkness is only a relative concept in this picture. The phase having $(n_a, n_b) = (1, 1)$ can be identified as ordinary visible matter.

Magnetic body is second key concept in TGD based model of quantum biology. Magnetic body has onion like structure with layers characterized by a spectrum of values of (n_a, n_b) identifiable as orders of the cyclic groups Z_{n_a} *resp.* Z_{n_b} acting in the fiber of singular covering space or factor space assignable M^4 *resp.* CP_2 degrees of freedom. Also the extensions of these groups obtained by adding reflection can be considered. Phase transitions changing the values of (n_a, n_b) and thus also the length of magnetic tubes correspond to a tunnelling between two pages of the book and in general change the value of Planck constant. The basic selection rule is familiar from the sub-group rule for phase transitions and means that either n_{a_1} (n_{b_1}) divides n_{a_2} (n_{b_2}) or vice versa. These phase transitions are in a key role in TGD inspired model of bio-catalysis.

The reconnections of flux tubes represents second basic mechanism of bio-catalysis. Together these two mechanisms could be at least partially responsible for the amazing aspects of bio-catalysis such as extreme selectivity and the ability of distant bio-molecules to find each other in the dense soup of bio-molecules.

9.1.2 Realizations Of Genetic Code

I have proposed several realization of the genetic code during past 15 years. There are three realizations which are especially interesting physically.

1. The first realization is based on the map of G,C *resp.* A,T codons to quarks u,d *resp.* their anti-quarks. This code was proposed to realize DNA as TQC with braid strands represented as flux tubes connecting nucleotides with the lipids of cell membrane [**?**]. The quantum states at the ends of braid strands -would be represented by many particle states of quarks and anti-quarks in this model and entanglement of quarks and anti-quarks would be essential for TQC and affected by the braiding induced by the 2-D liquid flow of the lipids.

2. Second realization is based on the observation that the neutral states of dark baryons consisting of u and d quarks in nuclear string model can be regarded as counterparts of DNA, RNA, amino-acids and perhaps even tRNA [K24, K51]. Nuclear strings would represent DNA and other polymers at the level of dark matter.

3. Third realization is based on the interpretation of divisor code discovered by Khrennikov and Nilsson [A30] in terms of the sub-group rule for phase transitions [K51]. Second realization and this one are in 1-1 correspondence under certain prerequisites. The magnetic- interaction energy of the dark baryon depends on the projections of the total quark spin and total color flux tube spin to the direction of the magnetic field labeling both DNA codons and amino-acids. This interaction energy is a function of (n_a, n_b) and minimized for some pair (n_a, n_b). This gives 1-1 correspondence the states of dark baryon and page of the book and since the page numbering allows to interpret physically the divisor code, one might hope that this correspondence is consistent with both codes.

4. Proposals for two further realizations are inspired by the observation that the number of vertices of icosahedron is 12 - the number of notes in 12-note scale - and that of vertices is 20 - the number of amino-acids. This suggests a connection between music and genetic code. The second model allows to "understand" the degeneracies of the genetic code in terms of representations for discrete subgroups if icosahedral group and involves imbedding of 12-note scale as a Hamiltonian cycle to icosahedron.

5. I have also proposed number theory based thermodynamical models for the genetic code [K11, K56] discussed also by others [A18, A12]. and a suitable modification of this kind of model could allow to model the thermodynamics based on magnetic interaction energy.

I have also suggested realizations of the genetic code in terms of electromagnetic field patterns and computer metaphor encourages to think that standard genetic code is just one possible realization among many.

9.1.3 Questions

These ideas raise a bundle of questions.

1. There are severa candidates for the realization of the genetic code. Are all these realizations needed? Are the realizations based on dark baryons and divisor code equivalent?

2. The realization based on correspondence with DNA nucleotides and quarks and anti-quarks works nicely for DNA as TQC hypothesis. Can one consider also a realization of DNA as TQC in terms of dark baryons?

3. How dark baryon realization relates with ordinary chemical realizations and to evolution of pre-biotic life forms? Could it be that the life based on nuclear string genetic code gradually moved from the dark pages of the book to the page containing visible matter as chemical realizations of the analogs of DNA, RNA, amino-acids and even tRNA gradually developed? Note that the process bears formal similarity to the transition of life from sea to land. Is it possible to transcribe the counterparts of DNA,RNA, and amino-acids to their real counterparts? Is pre-biotic era continuing still inside dark magnetic flux tubes and could it make possible genetic engineering?

The appendix of the book gives a summary about basic concepts of TGD with illustrations. Pdf representation of same files serving as a kind of glossary can be found at `http://tgdtheory.fi/tgdglossary.pdf` [L11].

9.2 A Vision About Evolution And Codes

The fact is that the only thing we really know about dark matter is that 95 percent of matter is dark (matter or dark matter and energy depending on theoretical framework used). Therefore the ideas about dark baryon code are necessarily speculative. One can however base the speculations to some vision in order achieve internal consistency if nothing else.

9.2.1 Basic Insights

The idea that biological life was preceded by dark life with subset for the counterparts of DNA, RNA, amino-acids and tRNA dominating the scene looks like a plausible starting point. Second attractive assumption is that this era still continues at magnetic bodies and makes possible genetic engineering based on experimentation and transcription of at least dark baryon analog of DNA to ordinary DNA.

The transformations for RNA and amino-acids to dark matter and vice versa seems necessary if the experimentation with new variants of genes is to be carried out unless one is satisfied with the testing of the modified genes in a small scale. Reconnection and $\hbar$ changing phase transitions of flux tubes would serve as the basic mechanism of bio-catalysis in TGD Universe. One can imagine two basic mechanisms involving reconnection of flux tube and transforming dark nuclear strings to polymers (see **Figs.** `http://tgdtheory.fi/appfigures/manysheetd.jpg`, `http://tgdtheory.fi/appfigures/field.jpg`, `http://tgdtheory.fi/appfigures/fluxquant.jpg`, `http://tgdtheory.fi/appfigures/reconnect1.jpg`, `http://tgdtheory.fi/appfigures/reconnect2.jpg`, `http://tgdtheory.fi/appfigures/fluxtubedynamics.jpg`, which can be also found in the appendix of this book).

1. Given bio-molecule could be accompanied by a closed flux tube of the magnetic field containing dark matter and extending to some page of the book characterized by two numbers x_a *resp.* x_b, which are integers for singular coverings of M^4 *resp.* CP_2 and inverse integers for singular factor spaces of M^4 *resp.* CP_2. For bio-molecules for which x_a and x_b are identical these closed loops could reconnect to form a pair of flux tubes connecting bio-molecules (see **Fig. ??**). A phase transition reducing Planck constant would bring the molecules close to each other. This would provide a general recognition mechanism central in the reactions of bio-molecules.

2. These flux tube connections between two molecules could also involve only single *permanently* existing flux tube (this is a rather strong prediction which might be used to kill this option). In this case the reconnection for the flux tubes connecting molecules X and Y *resp.* U and V would give rise to connections $X-U$ and $Y-V$ for instance. The general recipe for achieving these transformations is based on the assumption that molecule and its dark conjugate connected by flux tubes can be present and that reconnection process given exchange of particles describable in terms of diagrams analogous to stringy diagrams is possible. This means that pairings $X-dY$ and $U-dV$ can be transformed to pairings $X-U$ and $dY-dV$ and $X-dV$ and $U-dY$ (see **Fig. ??**). This process would extend the variety of possible transcription like processes to allow also transcription of dark variants of DNA, RNA and amino-acids to visible ones and vice versa.

Genetic engineering would be possible by the fact that the dark nuclear string variants of genes could be easily transferred around the biological body unlike modified DNAs. In particular, modified dark genes could be transferred to the nuclei of germ cells. Essentially the TGD inspired mechanism of homeopathy would be in question [K24].

There is analogy with the evolution of language. Both DNA codons and representation of nucleotides in terms of quarks and anti quarks (perhaps accompanying the intronic portions of DNA) mean a representation of codons as three-letter sequences. Since dark baryons represent genetic codons as indecomposable structures in terms of quantum entanglement, the emergence of both representations would be analogous to the emergence of written language when spoken words forming indecomposable units decomposed into letters having no meaning as such. The findings that there are major differences between the genomes of blood and tissue cells [I87] and that the

genetic variation due to jumping genes is highest in brain and germ cells [I56] is consistent with the view about dark evolution modifying at least intron portion of the genome.

RNA world [I113, I142, I63] represents a dominating vision about pre-biotic evolution. The idea is RNA era was first and that somehow DNA and amino-acids emerged in some later stage. It has not been possible yet to reproduce replicating RNA sequences in laboratory so that there is still room for alternatives. Dark baryon realization of the genetic code predicts that the analogs of DNA, RNA, amino-acids and even tRNA anticodons might have been there all the time. This might apply also to the primitive chemical representations of DNA, RNA, tRNA, and amino-acids. It is of course possible that the chemical representation of RNA evolved first. This era could still continue inside cell nuclei and make possible genetic engineering as experimentation with dark baryon genes producing amino-acids and RNA and then possibly transforming the resulting RNAs to DNA by reverse transcription. Also a direct transcription to DNA could take place.

9.2.2 The Simplest Scenario

The evolution could might have proceed as a gradual transition of life from dark pages to the visible page allowing chemical realization of the genetic code.

1. Dark matter era would replace RNA and already this era involved at least the dark counterparts of DNA, RNA, amino-acids and perhaps even $64-40 \to 40-20$ two-step realization of the genetic code with tRNA anticodons representing a particular example of 40-D realization intermediate between DNA and amino-acids. Maximum number of different tRNA codons is indeed around 40 [I50]. Without further assumptions the pairing of all dark DNA and RNA codons coding for the same amino-acid was possible. The situation changes if one assumes 1-1 correspondence between dark baryon realization and the realization of the divisor code in terms of dark magnetic flux tubes to be discussed later. This era could still continue at magnetic bodies and make genetic experimentation and genetic engineering possible.

2. Dark nuclear strings became gradually associated with the magnetic bodies of DNA, RNA and amino-acids and a machinery transforming DNA to mRNA to tRNA to amino-acids developed. Flux tube connections could have formed between nuclear strings and the magnetic bodies of the bio-molecules. A stronger condition is that dark nuclear strings became part of the magnetic bodies of DNA, RNA and amino-acids forming helical structures running parallel to the corresponding molecular structures. For this option base pairing could have made the dark counterparts of DNA-DNA and DNA-mRNA pairings unique (also the equivalence of dark baryon and divisor codes could have guaranteed this). mRNA-tRNA base is pairing is not unique but wobble base pairing made possible for all mRNA codons except stopping codons to pair to tRNA anticodons. Whether RNA appeared first or whether the counterparts of the basic bio-molecules were present from the beginning remains an open question.

3. Topological quantum computation based on the map of A, G *resp.* T, C to quarks *resp.* anti-quarks emerged later as something analogous to written language and would naturally correspond to the intron portions of genome for which the decomposition into triplets is not essential and the nucleotide composition is not too essential since it is braiding which defines topological quantum computation (the 4 different colors of the braid strands are not necessary).

9.2.3 How Dark Baryon Code Could Be Involved With Transcription And Translation Mechanisms?

In the following it is assumed that one can talk about magnetic flux tubes containing dark nucleon strings as independent objects and therefore not identified as a helical string parallel to DNA, RNA or amino-acid sequence as one might also imagine. Therefore it is not necessary to assume that dark baryons have the same size scale as corresponding molecular units. One can also assume that one can connect flux tubes associated with nuclear strings by magnetic flux tubes.

Genetic engineering makes sense if the transcription of nuclear string counterparts of DNA, RNA, tRNA, and amino-acids to their chemical counterparts is possible.

1. One can classify flux tube connections by introducing the notion of order of flux tube connection expected to characterize the probability of flux tube connection. First order means a flux tube entirely in given page of the book like structure defined by the generalized imbedding space, second order to a flux tube between two different pages, third order a flux tube traversing through an intermediate page between two pages, and so on. Reconnection of the magnetic flux tubes provides a general mechanism for this transformations and as already explained there are two general recipes for the formation of reconnection.

2. **Option I** - the simpler one - involves a reconnection of the closed flux tubes associated with the molecules to be paired. This mechanism would make it possible for a bio-molecule X to catch a partner Y if the corresponding closed flux tubes reside at same page of the book s(see **Fig. ??**). This mechanism provides a straightforward description of replication, transcription and translation as well as their generalizations allowing to transform dark nuclear strings to their molecular counterparts and vice.

3. **Option II** is more complex (see **Fig. ??**) and can be formulated in terms of two stringy diagrams with two strings connecting objects X and Y *resp.* U and V at their ends touch and transform to strings with X and V *resp.* U and V or X and U *resp.* Y and V at their ends. The process can be visualized as exchange of half strings and stringy diagrams represent various processes. Denote by dX the dark matter counterpart of X which can be DNA, RNA, or amino-acid and assume that all combinations obtained by the reconnection process are possible so that one would has pairings $X-Y, X-dY, dX-Y$, and $dX-dY$ defined by flux tube connections. All these variants present and $X-Y$ and $dX-dY$ can be first order connections whereas $X-dY$ and $dX-Y$ are second or higher order connections. This option requires permanent flux tube connections.

4. These are the simplest options. One can wonder whether the hydrogen bonds associated with base pairs correspond to a pair $(A-T)$ or triplet $(G-C)$ of contracted flux tubes. It is of course possible to have more than two flux tubes. If the third hydrogen bond for $G-C$ corresponds to a flux tube a permanent flux tube connection between G and C nucleotides would exist.

One could think that only few bio-molecules can have flux tubes at the page at which the particular dark nuclear string typically resides (minimization of the magnetic interaction energy could fix the most probable candidate for this page and imply connection between dark baryon code and divisor code) and that bio-molecules are gradually selected from these particular molecules. The process would be still in progress. Vertebrate nuclear code would be however identical with the dark baryon code. For tRNA anti-codons the situation would be far from ideal.

Replication

In the following "$\circ$" means one or two bonds depending on whether Option I or II is in question.

Option I: Let $(X \circ Y)$ denote DNA double helix with two flux tubes connecting them and U a V DNA nucleotides. The opening of DNA double strand means reconnection of these flux tubes so that two closed loops are obtained. These flux tubes transform to dark flux tubes and reconnect with dark flux tubes associated with U and V respectively and a phase transition reducing $\hbar$ brings U and V near sequences X and Y where they combine with already existing new sequence.

Option II: Let $(X \circ Y)$ denote DNA double helix and $(U \circ V)$ to a pair of codon and anticodon assumed to be connected by a long flux tube (this should be a testable prediction). Replication of DNA would correspond to $(X \circ Y) + (U \circ V) \to X \circ U \to Y \circ V$ with reconnection taking place for the flux tubes.

With the same conventions the transcription of dark DNA to ordinary DNA and vice versa would correspond to a process $dX \circ dY + U + V \to dX \circ U \to V \circ dY$ giving rise to ordinary-dark DNA double strand. This process would be followed by $(dX \circ U) + (dV \circ Y) \to dX \circ dV \to U \circ Y$ proceeding like DNA replication.

$DNA \to mRNA$ **transcription**

Let $X \circ Y$ denote DNA double helix in the sequel. For Option I the transcription process would occur in straightforward manner by the transformation of double connection between X and Y to loops and the reconnection of loop associated with Y with that assignable to $mRNA$ codon followed by $\hbar$ reducing phase transition leading to a generation of DNA and mRNA sequences with nucleotides connected by flux tube pairs. The third step would be reconnection transforming double flux tube bonds between DNA and mRNA nucleotides to loops.

Consider next Option II:

1. Let $U \circ V$ denote mRNA-cmRNA that is pair of mRNA codon and its conjugate assumed to be connected by a long flux tube. Ordinary transcription $DNA \to mRNA$ could correspond to the $(X \circ Y) + (U \circ V) \to X \circ U \to Y \circ V$ followed by its reversal but mRNAs arranged to a sequence. Note that every mRNA would have long flux tube connection with the conjugate mRNA.

2. Let $U \circ V$ could denote mRNA-dcmRNA. The same process would give mRNA sequence with each codon connected by a long flux tube to dcmRNA codon.

3. For a third realization $U - V$ would denote the pair $mRNA - dtRNA$. The same process as above would give mRNA sequence with each mRNA codon connected by a long flux tube to $dtRNA$ anticodon.

This process has also variants allowing to assign mRNA to dDNA and to DNA dmRNA.

Translation as a sequence of reconnections

For Option I the description of translation should be obvious on basis of previous examples. For Option II translation could be realized as a sequence of reconnections in several manners. The basic idea is that the reconnections and their reversals transform the tRNA_1-AA pairs with $tRNA_1$ denotes $tRNA$ without amino-acid AA to a sequence of them but $tRNA_1$ connected to amino-acid by a long flux tube. In the decay of the amino-acid this long tRNA would reduce to ordinary tRNA: this serves as a killer prediction.

For instance, let $X - Y = mRNA - dmRNA$ mRNA sequence with dark mRNA codons connected to mRNA codons and let $U - V = tRNA_1 - AA$ denote tRNA. Reconnection would allow to arrange tRNAs to sequence of "long" tRNAs while keeping $X - Y$ as such. One could also replace Y by $dtRNA$. Obviously the process has several variants. When amino-acid sequence decays ordinary "short" tRNAs are formed again. Also the translation of dark mRNA to ordinary amino-acid sequence with long flux tubes to either dark tRNA or ordinary tRNA.

9.3 DNA As Topological Quantum Computer: Realization Of The Genetic Code In Terms Of Quarks And Anti-Quarks

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Large values of Planck constant allow to imagine all kinds of quantum computations [B1, B19, B5, B17]. What makes topological quantum computation (TQC) [B11, B16, B13, B2], [C5] so attractive is that the computational operations are very robust and there are hopes that external perturbations do not spoil the quantum coherence in this case. The basic problem is how to create, detect, and control the dark matter with large $\hbar$. The natural looking strategy would be to assume that living matter, say a system consisting of DNA and cell membranes, performs TQC and to look for consequences.

There are many questions. How the TQC could be performed? Could TQC hypothesis might allow to understand the structure of living cell at a deeper level? What does this hypothesis predict about DNA itself? One of the challenges is to fuse the vision about living system as a conscious hologram with the DNA as TQC vision. The experimental findings of Peter Gariaev [I81, I105] might provide a breakthrough in this respect. In particular, the very simple experiment in which

one irradiates DNA sample using ordinary light in UV-IR range and photographs the scattered light seems to allow an interpretation as providing a photograph of magnetic flux tubes containing dark matter. If this is really the case, then the bottle neck problem of how to make dark matter visible and how to manipulate it would have been resolved in principle. The experiment of Gariaev and collaborators [I105] also show that the photographs are obtained only in the presence of DNA sample. This leaves open the question whether the magnetic flux tubes associated with instruments are there in absence of DNA and only made visible by DNA or generated by the presence of DNA.

9.3.1 Basic Ideas Of TQC

The basic idea of topological quantum computation (TQC) is to code TQC programs to braiding patterns (analogous to linking and knotting). A nice metaphor for TQC is as dance. Dancing pattern in time direction defines the TQC program. This kind of patterns are defined by any objects moving around so that the Universe might be performing topological quantum computation like activities in all scales.

One assigns to the strands of the braid elementary particles. The S-matrix coding for TQC is determined by purely topological consideration as a representation for braiding operation. It is essential that the particles are in anyonic phase: this means in TGD framework that the value of Planck constant differs from its standard value. Tqc as any quantum computation halts in state function reduction which corresponds to the measurement of say spins of the particles involved.

As in the case of ordinary computers one can reduce the hardware to basic gates. The basic 2-gate is represented by a purely topological operation in which two neighboring braid strands are twisted by π. 1-particle gate corresponds to a phase multiplication of the quantum state associated with braid strand. This operation is not purely topological and requires large Planck constant to overcome the effects of thermal noise.

In TGD framework TQC differs somewhat from the ordinary one.

1. Zero energy ontology means that physical states decompose into pairs of positive and negative energy states at boundaries of causal diamond formed by future and past directed light-cones containing the particles at their light-like boundaries. In positive energy ontology the interpretation is as an event, say particle scattering. The time like entanglement coefficients define S-matrix, or more precisely M-matrix, and this matrix can be interpreted as coding for physical laws in the structure of physical state as quantum superposition of statements "A implies B" with A and B represented as positive and negative energy parts of quantum state. The halting of topological quantum computation would select this kind of statement.

2. The new view about quantum state as essentially 4-D notion implies that the outcome of TQC is expressed as a four-dimensional pattern at space-time sheet rather than as time=constant final state. All kinds of patterns would provide a representation of this kind. In particular, holograms formed by large $\hbar$ photons emitted by Josephson currents, including EEG as a special case, would define particular kind of representation of outcome.

9.3.2 Identification Of Hardware Of TQC And TQC Programs

One challenge is to identify the hardware of TQC and realization of TQC programs.

1. Living cell is an excellent candidate in this respect. The lipid layers of the cell membrane is 2-D liquid crystal and the 2-D motion of lipids would define naturally the braiding if the lipids are connected to DNA nucleotides. This motion might be induced by the self organization patterns of metabolically driven liquid flow in the vicinity of lipid layer both in interior and exterior of cell membrane and thus self-organization patters of the water flow would define the TQC programs.

2. This identification of braiding implies that TQC as dancing pattern is coded automatically to memory in the sense that lipids connected to nucleotides are like dancers whose feet are connected to the wall of the dancing hall define automatically space-like braiding as the threads connected to their feet get braided. This braiding would define universal memory realized not only as tissue memory but related also to water memory [K19].

3. It is natural to require that the genetic code is somehow represented as property of braids strands. This is achieved if strands are "colored" so that A, T, C, G correspond to four different "colors". This leads to the hypothesis that flux tubes assignable to nucleotides are wormhole magnetic flux tubes such that the ends of the two sheets carry quark and anti-quark *resp.* anti-quark and quark) quantum numbers. This gives mapping A, T, C, G to u, u_c, d, d_c. These quarks are not ordinary quarks but their scaled variants predicted by the fractal hierarchy of color and electro-weak physics. Chiral selection in living matter could be explained by the hierarchy of weak physics. The findings of topologist Barbara Shipman about mathematical structure of honeybee dance led her to proposed that the color symmetries of quarks are in some mysterious manner involved with honeybee cognition and this model would justify her intuition [A15].

4. One should identify the representation of qubit. Ordinary spin is not optimal since the representation of 1-gates would require a modification of direction of magnetic field in turn requiring modification of direction of flux tubes. A more elegant representation is based on quark color which means effectively 3-valued logic: true, false, and undefined, also used in ordinary computers and is natural in a situation in which information is only partial. In this case 1-gates would correspond to color rotations for space-time sheets requiring no rotation of the magnetic field.

In this framework genes define the hardware of TQC rather than genetic programs. This means that the evolution takes place also at the level of TQC programs meaning that strict genetic determinism fails. There are also good reasons to believe that these TQC programs can be inherited to some degree. This could explain the huge differences between us and our cousins in spite of almost the identical genetic codes and explains also cultural evolution and the observation that our children seem to learn more easily those things that we have already learned [I128]. It must be added that DNA as TQC paradigm seems to generalizedDNA, lipids, proteins, water molecules, ... can have flux tubes connecting them together and this is enough to generate braidings and TQC programs. Even water could be performing simple TQC or at least building memory representations based on braiding of flux tubes connecting water molecules.

Comment:

1. Some years after writing this it became clear that elementary particles correspond to wormhole magnetic fields carrying monopole flux. By stability requirement the wormhole magnetic flux tubes associated with TQC could therefore correspond to elementary particles with large value of Planck constant or more generally, to meson like states having at both ends of the wormhole magnetic flux tube fermion or fermion pair. Both leptons and quarks could be associated with the ends, and the condition that braid colors realize genetic code poses additional conditions on the model.

2. It has also turned that genetic code allows a realisation in terms of dark nucleons [K24, L2]. Note that the assignment of genetic code with braid coloring is not necessary for TQC.

9.3.3 How Much TQC Resembles Ordinary Computation?

If God made us to his own image one can ask whether we made computers images of ourselves in some respects. Taking this seriously one ends up asking whether facts familiar to us from ordinary computers and world wide web might have counterparts in DNA as TQC paradigm.

1. Can one identify program files as space-like braiding patterns. Can one differentiate between program files and data files?

2. In ordinary computers electromagnetic signalling is in key role. The vision about living matter as conscious holograms suggests that this is the case also now. In particular, the idea that entire biosphere forms a TQC web communicating electromagnetically information and control signals, looks natural. Topological light rays (MEs) make possible precisely targeted communications with light velocity without any change in pulse shape. Gariaev's findings [I81] that the irradiation of DNA by laser light induces emission of radio wave photons having biological effects on living matter at distances of tens of kilometers supports this kind

Table 9.1: Table show four possible options for em charge as sum of quark charges.

$$\begin{aligned} Q_a &= [n(A)-n(T)]\tfrac{2}{3} - [n(G)-n(C)]\tfrac{1}{3} \ , \\ Q_a &= -[n(A)-n(T)]\tfrac{1}{3} + [n(G)-n(C)]\tfrac{2}{3} \ , \\ Q_a &= -[n(A)-n(T)]\tfrac{2}{3} + [n(G)-n(C)]\tfrac{1}{3} \ , \\ Q_a &= [n(A)-n(T)]\tfrac{1}{3} - [n(G)-n(C)]\tfrac{2}{3} \ . \end{aligned} \tag{9.3.2}$$

of picture. Also the model of EEG in which the magnetic body controls the biological body also from astrophysical distances conforms with this picture.

3. The calling of computer programs by simply clicking the icon or typing the name of program followed by return is an extremely economic manner to initiate complex computer programs. This also means that one can construct arbitrarily complex combinations from given basic modules and call this complex by a single name if the modules are able to call each other. This kind of program call mechanism could be realized at the level of TQC by DNA. Since the intronic portion of genome increases with the evolutionary level and is about 98 per cent for humans, one can ask whether introns would contain representations for names of program modules. If so, introns would express themselves electromagnetically by transcribing the nucleotide to a temporal pattern of electromagnetic radiation activating desired subprogram call, presumably the conjugate of intronic portion as DNA sequence. A hierarchical sequence of subprogram calls proceeding downwards at intronic level and eventually activating the TQC program leading to gene expression is suggestive. Note that the repetitive nature of introns is not a problem from the point of TQC.

   Gariaev [I81] has found that laser radiation scattering from given DNA activates only genomes which contain an address coded as temporal pattern for the direction of polarization plane. If flux tubes are super-conducting and there is strong parity breaking (chiral selection) then Faraday rotation for photons traveling through the wormhole flux tube code nucleotide to an angle characterizing the rotation of polarization plane. User id and password would define kind of immune system against externally induced gene expression.

4. Could nerve pulses establish only the connection between receiver and sender neurons as long magnetic flux tubes? Real communication would take place by electromagnetic signals along the flux tube, using topological light ray (ME) attached to flux tube, and by entanglement. Could neural transmitters specify which parts of genomes are in contact and thus serve as a kind of directory address inside the receiving genome?

9.3.4 Some Predictions Related To The Representation Of Braid Color

Even in the rudimentary form discussed above the model makes predictions. In particular, the hypothesis that neutral quark pairs represent braid color is easily testable.

Anomalous em charge of DNA as a basic prediction

The basic prediction is anomalous charge of DNA. Also integer valued anomalous charge for the structural units of genome is highly suggestive.

The selection of the working option - if any such exists - is indeed experimentally possible. The anomalous charge coupling to the *difference* of the gauge potentials at the two space-time sheets defines the signature of the wormhole contact at the DNA end of braid strand. The effective (or anomalous) em charge is given as sum of quark charges associated with DNA space-time sheet:

$$Q_a \quad = \quad [n(A)-n(T)]Q(q_A) + [n(G)-n(C)]Q(q_G) \tag{9.3.1}$$

is predicted. The four possible options for charge are given explicitly in **Table 9.1**.

Second option is obtained from the first option $(A,T,G,C) \to (u,\overline{u},d,\overline{d})$ by permuting u and d quark in the correspondence and the last two options by performing charge conjugation for quarks in the first two options.

The anomalous charge is experimentally visible only if the external electromagnetic fields at the two sheets are different. The negative charge of DNA due to the presence of phosphate groups implies that the first sheet carries different em field so that this is indeed the case.

The presence effective em charge depending on the details of DNA sequence means that electromagnetism differentiates between different DNA: s strands and some strands might be more favored dynamically than others. It is interesting to look basic features of DNA from this view point. Vertebral mitochondrial code has full $A \leftrightarrow G$ and $C \leftrightarrow T$ symmetries with respect to the third nucleotide of the codon and for the nuclear code the symmetry is almost exact. In the above scenario A and C *resp.* G and T would have different signs and magnitudes of em charge but they would correspond to different weak isospin states for the third quark so that this symmetry would be mathematically equivalent to the isospin symmetry of strong interactions.

The average gauge potential due to the anomalous charge per length at space-time sheet containing ordinary em field of a straight portion of DNA strand is predicted to be proportional to

$$\frac{dQ_a}{dl} = [p(A)-p(T)]Q(q_A) + [p(G)-p(C)]Q(q_G)\frac{1}{\Delta L} \quad ,$$

where ΔL corresponds to the length increment corresponding to single nucleotide and $p(X)$ represents the frequency for nucleotide X to appear in the sequence. Hence the strength of the anomalous scalar potential would depend on DNA and vanish for DNA for which A and T *resp.* G and C appear with the same frequency.

Chargaff's second parity rule and the vanishing of net anomalous charge

Chargaff's second parity rule states that the frequencies of nucleotides for single DNA strand satisfy the conditions $p(A) \simeq p(T)$ and $p(C) \simeq p(G)$ (I am grateful for Faramarz Faghihi for mentioning this rule and the related [H2] [I144] to me). This rule holds true in a good approximation. In the recent context the interpretation would be as the vanishing of the net anomalous charge of the DNA strand and thus charge conjugation invariance. Stability of DNA might explain the rule and the poly-A tail in the untranslated mRNA could relate stabilization of DNA and mRNA strands.

Together with $p(A)+p(T)+p(G)+p(C)=1$ Chargaff's rule implies the conditions

$$\begin{array}{ll} p(A)+p(C) \simeq 1/2 \ , & p(A)+p(G) \simeq 1/2 \ , \\ p(T)+p(C) \simeq 1/2 \ , & p(T)+p(G) \simeq 1/2 \ . \end{array} \tag{9.3.3}$$

An interesting empirical finding [I144] is that only some points at the line $p(A)+p(C) \simeq 1/2$ are realized in the case of human genome and that these points are in a good accuracy expressible in terms of Fibonacci numbers resulting as a prediction of optimization problem in which Fibonacci numbers are however put in by hand. $p(A)=p(G)=p(C)=p(T)=1/4$ results as a limiting case. The poly-A tail of mRNA (not coded by DNA) could reflect to the compensation of this asymmetry for translated mRNA.

The physical interpretation would be as a breaking of isospin symmetry in the sense that isospin up and down states for quarks (A and G *resp.* T and C) do not appear with identical probabilities. This need not have any effect on protein distributions if the asymmetry corresponds to asymmetry for the third nucleotide of the codon having $A \leftrightarrow G$ and $T \leftrightarrow C$ symmetries as almost exact symmetries. This of course if protein distribution is invariant under this symmetry for the first two codons.

The challenge would be to understand the probabilities $p_3(X)$ for the third codon from a physical model for the breaking of isospin symmetry for the third codon in the sense that u and $\overline{u}$ at DNA space-time sheet are more favored than d and $\overline{d}$ or vice versa. There is an obvious analogy with spontaneous breaking of vacuum symmetry.

Are genes and other genetic sub-structures singlets with respect to QCD color?

Genes are defined usually as transcribed portions of DNA. Genes are however accompanied by promoter regions and other regions affecting the transcription so that the definition of what one really means with gene is far from clear. In the recent case gene would be naturally TQC program module and gene in standard sense would only correspond to its sub-module responsible for the translated mRNA output of TQC.

Whatever the definition of gene is, genes as TQC program modules could be dynamical units with respect to color interaction and thus QCD color singlets (QCD color should not be confused with braid color) or equivalently - possess integer valued anomalous em charge.

One can consider two alternative working hypothesis - in a well-defined sense diametrical opposites of each other.

1. The division of the gene into structural sub-units correlates with the separation into color singlets. Thus various structural sub-units of gene (say transcribed part, translated part, intronic portions, etc...) would be color singlets.

2. Also different genetic codes that I have discussed in [K19] could distinguish between different structural sub-units. For this option only gene - understood as TQC unit with un-transcribed regions included - would be color singlet.

Color singletness condition is unavoidable for mRNA and leads to a testable prediction about the length of poly-A tail added to the transcribed mRNA after translation.

1. The condition of integer valued anomalous charge for coding regions

In the case of coding region of gene the condition for integer charge is replaced by the conditions

$$n(A)+n(G) \ \ mod \ \ 3=0 \ \ , \quad n(C)+n(T) \ \ mod \ \ 3=0 \ \ . \tag{9.3.4}$$

These conditions are not independent and it suffices to check whether either of them is satisfied. The conditions are consistent with $A \leftrightarrow G$ and $T \leftrightarrow C$ symmetries of the third nucleotide. Note that the contribution of the stop codon (TAA, TGA or TAG) and initiating codon ATG to the A+G count is one unit.

2. General condition for integer valued anomalous charge

The anomalous charge of gene or even that of an appropriate sub-unit of gene is integer valued implies in the general case

$$n(A)-n(T)+n(G)-n(C) \ \ mod \ \ 3=0 \ \ . \tag{9.3.5}$$

Note that this condition does not assume that gene corresponds to $3n$ nucleotides (as I had accustomed to think). The surprising (to me) finding was that gene and also mRNA coding region of the gene in general fails to satisfy $3n$ rule. This rule is of course by no means requiredonly the regions coding for proteins can be thought of as consisting of DNA triplets.

A possible interpretation is in terms of TGD based model for pre-biotic evolution [K19] according to which genetic code (or 3-code) was formed as a fusion of 2-code and 1-code. 2-code and 1-code could still be present in genome and be associated with non-translated regions of mRNA preceding and following the translated region. The genes of 2-code and coding for RNA would have $2n$ nucleotides and the genes of 1-code could also consist of odd number of nucleotides.

There might be analogy with drawings for a building. These contain both figures providing information about building and text giving meta-level information about how to interpret figures. Figures could correspond to 3-code coding for proteins and text could be written with other codes and give instructions for the transcription and translation processes. Prokaryotic code would contain mostly figures (CDS). In eukaryotic code intronic portions could carry rich amounts of this kind of metalevel information. In the case of mRNA untranslated region preceding $5'$ end could provide similar information.

1. Repeating sequences consisting of n copies of same repeating unit could obey 1-code or 2-code. The simplest building blocks of repeating sequences are AT and CG having vanishing anomalous em charge. TATATA.... and CGCGCG... indeed appear often. Also combinations of CG and AT could repeat: so called mini-satellites are CG rich repeating sequences. Interpretation in terms of 2-code suggests itself.

2. Triplet of the unit ATTCG with integer charge repeats also often: in this case 3-code suggests itself. Telomeres of vertebrates consist of a repeating unit TTAGGG which does not have integer charge: this unit appears also as 8-nucleotide variant which suggests 2-code. Color singletness would require that this unit appears $3n$ times.

3. I have also proposed that intronic regions could obey memetic code [K22] predicting that intronic codon can be represented as a sequence of 21 3-codons (implying 2^{63} 63-codons!). Individual intronic segments need not satisfy this rule, only their union if even that. Direct experimentation with gene bank data show that neither introns nor their union correspond to integer multiples of 63 nor 3 or 2 in general.

3. Color singletness conditions for gene

Gene is usually defined as the sequence of DNA coding for mRNA. mRNA involves also two untranslated regions (UTRs) [I1].

1. The 5′ end of mRNA contains 5′ cap (methylated G) and 5′ untranslated region (UTR). The latter can be several kb long for eukaryotes. Methylated G is not coded by DNA but added so that it does not contribute to A+G-T-C count at DNA level.

2. mRNA continues after the stop codon as 3′ UTR. Translation assigns to UTR also a poly-A tail (up to several hundreds A: s) not coded by DNA and not contributing to A+G-T-C count in the case of DNA. This region contains also AAUAAA which does not contribute to A+G-T-C count of mRNA.

   One could argue that any amino-acid sequence must allow coding and that one function of UTRs is to guarantee integer valued charge for the part of gene beginning from the initiating codon. Of course, also the non-transcribed regions of DNA not included in the standard definition of gene could take care of this.

4. Color singletness conditions for mRNA

Both poly-A tail and G gap are known to relate to the stabilization of mRNA. The mechanism could be addition of an anomalous charge compensating for the anomalous charge of mRNA to guarantee that second Chargaff's rule is satisfied in a good approximation: this hypothesis is testable.

Second function would be to guarantee color-singletness property. Color singletness would mean that transcribed mRNA + cap G + poly-A tail as a separate unit must be QCD color singlet at DNA space-time sheet. mRNA stability requires the condition

$$n(A) - n(T) + n(G) - n(C) + n_{tail}(A) + 1 \ \ mod \ \ 3 = 0 \tag{9.3.6}$$

to be satisfied. The knowledge of gene would thus predict $n_{tail}(A)$ mod 3. This hypothesis is testable.

5.Chargaff's rule for mRNA

If Chargaff's rule applies also to mRNA strands one obtains one of the following predictions

$$
\begin{aligned}
&2\,[n(A)+n_{tail}(A)-n(T)]-[n(G)+1-n(C)]\simeq 0\ ,\\
&-[n(A)+n_{tail}(A)-n(T)]+2\,[n(G)+1-n(C)]\simeq 0\ ,\\
&-2\,[n(A)+n_{tail}(A)-n(T)]+[n(G)+1-n(C)]\simeq 0\ ,\\
&[n(A)+n_{tail}(A)-n(T)]-2\,[n(G)+1-n(C)]\simeq 0\ .
\end{aligned}
\tag{9.3.7}
$$

Here $n_{tail}(A)$ includes also AAUAA contributing 3 units to it plus possible other structures appearing in the tail added to the translated mRNA. The presence of poly-A tail which could also compensate for the ordinary negative charge of translated part of mRNA would suggest that A corresponds to u or $\overline{d}$ corresponding to options 1 and 4.

6. Moving genes and repeating elements

Transposons [I49], [J9] are moving or self-copying genes. Moving genes cut from initial position and past to another position of double strand. Copying genes copy themselves first to RNA and them to a full DNA sequence which is then glued to the double strand by cut and paste procedure. They were earlier regarded as mere parasites but now it is known that their transcription is activated under stress situations so that they help DNA to evolve. In TQC picture their function would be to modify TQC hardware. For copying transposons the cutting of DNA strand occurs usually at different points for DNA and cDNA so that "sticky ends" result ("overhang" and its complement) [I43]. Often the overhang has four nucleotides. The copied transposon have ends which are reversed conjugates of each other so that transposons are palindromes as are also DNA hairpins. This is suggestive of the origin of transposons.

In order to avoid boring repetitions let us denote by "satisfy P" for having having integer valued (or even vanishing) Q_a. The predictions are following:

1) The double strand parts associated with the segments of DNA produced by cutting should satisfy P.

2) The cutting of DNA should take place only at positions separated by segments satisfying P.

3) The overhangs should satisfy P.

4) Transposons should satisfy P: their reverse ends certainly satisfy P.

In the example mentioned in [I41] the overhang is $CTAG$ and has vanishing Q_a. The cut site $CCTAGG$ has also vanishing Q_a. It is known [J9] that transposons - repeating regions themselves - tend to attach to the repeating regions of DNA [I15].

1. There are several kinds of repeating regions. 6-10 base pair long sequences can be repeated in untranslated regions up to 10^5 times and whole genes can repeat themselves $50-10^4$ times.

2. Repeats are classified into tandems (say TTAGGG associated with telomeres), interspersed repetitive DNA (nuclear elements), and transposable repeat elements. Interspersed nuclear elements (INEs) are classified LINEs (long), SINEs (short), TLTRs (Transposable elements with Long Terminal Repeats), and DNA transposons themselves.

3. LINEs contain AT rich regions. SINEs known as alus (about 280 bps) contain GC rich regions whereas mariner elements (about 80 bps) are flanked by TA pairs. LTRs have length 300-1000 bps. DNA transposons are flanked with two short inverted repeat sequences flanking the reading frame: "inverted" refers to the palindrome property already mentioned.

AT and CG have vanishing Q_a so that their presence in LINEs and SINEs would make the cutting and pasting easy allowing to understand why transposons favor these regions. Viruses are known to contain long repeating terminal sequences (LTR). One could also check whether DNA decomposes to regions satisfying P and surrounded by repeating sequences which satisfy P separately or as whole as in the case DNA transposons.

7. Tests

Some checks of the color singletness hypothesis were made for human genome [I19].

1. For the coding sequences (CDSs) the strong prediction in general fails as expected (condition would pose restrictions on possible amino-acid contents).

2. Color singletness condition fails for genes defined in terms of translated part of mRNA (with gap and poly-A tail excluded). The un-transcribed regions of DNA involved with the gene expression (promoter region, etc...) could guarantee the color singletness. They could also stabilize DNA by bringing in compensating anomalous charge to guarantee second Chargaff's rule. Different genetic codes could distinguish between the subunits of gene.

3. To test color singletness conditions for mRNA one should know the length of poly-A tail. Unfortunately, I do not have access to this information.

4. The computation of total anomalous charges for a handful of genes, introns, and repeat units for some gene bank examples in the case of human genome indicates that both of them tend to carry net em charge which is largest for $(a, g) \leftrightarrow (\overline{d}, \overline{u})$ correspondence. The charge is in the range 5-10 per cent from the charge associated with the phosphates (-2 units per nucleotide). For second option giving negative charge (permute u and d) the anomalous charge is few per cent smaller.

   By Chargaff's law the regions outside genes responsible for the control of gene expression must contain a compensating charge of opposite sign. Kind of spontaneous symmetry breaking of charge conjugation symmetry $A \leftrightarrow T, G \leftrightarrow C$ and analogous to matter antimatter symmetry seems to take place. That control regions and translated regions have opposite densities of anomalous charge might also help in the control gene expression.

5. The poly-A tail of mRNA would carry compensating positive anomalous charge: the RNA-quark assignment could be conjugate to the DNA-quark assignment as suggested by what takes place in transcription. For instance, for the option $A \to \overline{d}$, the prediction for the length of polytail for $A \to \overline{d}$ option would be about $n_{tail}/n_{mRNA} \simeq 3p_a(mRNA)$ where $N(mRNa)$ is the number of nucleotides in transcribed mRNA and $p_a(mRNA)$ is the per cent of anomalous charge which is typically 5-10 per cent. For $p_a(mRNA) = 10$ per cent this gives as much as 30 per cent. For $A \to \overline{u}$ option one has $n_{tail}/n_{mRNA} \simeq 3p_a(mRNA)/2$. In this case also p_a is considerably smaller, typically by a factor of of order 2-3 per cent and even below per cent in some cases. Hence the relative length of tail would around 3-5 per cent. This option is perhaps more since it minimizes anomalous charge and maximizes the effectiveness of charge compensation by poly-A tail.

6. The predictions for transposons and their cut and past process should be easily testable.

Summary of possible symmetries of DNA

The following gives a list of possible symmetries of DNA inspired by the identification of braid color.

1. Color confinement in strong form

The states of quarks and anti-quarks associated with DNA both wormhole wormhole throats of braided (living) DNA strand can be color singlets and have thus integer valued anomalous em charge. The resulting prediction depends on the assignment of quarks and antiquarks to A, T, C, G which in principle should be determined by the minimization of em interaction energy between quark and nucleotide. For instance $2(A-T)-(G-C) \ \ mod \ \ 3 = 0$ for a piece of living DNA which could make possible color singletness. As a matter fact, color singletness conditions are equivalent for all possible for braid color assignments. This hypothesis might be weakened. For instance, it could hold true only for braided parts of DNA and this braiding are dynamical. It could also hold for entire braid with both ends included only: in this case it does not pose any conditions on DNA.

Questions: Do all living DNA strands satisfy this rule? Are only the double stranded parts of DNA braided and satisfy the rule. What about loops of hairpins?

2. Matter antimatter asymmetry at quark level

$A \leftrightarrow T$ and $G \leftrightarrow C$ corresponds to charge conjugation at the level of quarks (quark $\leftrightarrow$ antiquark). Chargaff's rules states $A \simeq T$ and $C \simeq G$ for long DNA strands and mean matter-antimatter symmetry in the scale of DNA strand. Double strand as a whole is matter anti-matter symmetric.

Matter-antimatter asymmetry is realized functionally at the level of DNA double strand in the sense that only DNA strand is transcribed. The study of some examples shows that genes defined as transcribed parts of DNA do not satisfy Chargaff's rule. This inspires the hypothesis about the breaking of matter antimatter symmetry. Genes have non-vanishing net $A - T$ and $C - G$ and therefore also net Q_a with sign opposite to that in control regions. Just as the Universe is matter-antimatter asymmetric, also genes would be matter-antimatter asymmetric.

3. Isospin symmetry at quark level

$A \leftrightarrow G$ and $T \leftrightarrow A$ correspond change of anomalous em charge by 1 unit and these operations respect color confinement condition. Local modifications of DNA inducing these changes should be preferred. The identification for the symmetries $A \leftrightarrow G$ and $T \leftrightarrow A$ for the third nucleotide of code is as isospin symmetries. For the vertebrate mitochondrial code the symmetry exact and for nuclear code slightly broken.

4. Matter antimatter asymmetry and isospin symmetries for the first two nucleotides

The first two nucleotides of the codon dictate to a high degree which amino-acid is coded. This inspires the idea that 3-code has emerged as fusion of 1- and 2-codes in some sense. There are two kinds of 2-codons. The codons of type A have fractional em charge and net quark number (consisting of either matter or antimatter at quark level) and are not able to form color singlets. The codons of type B have integer em charge and vanishing quark number (consisting of matter and antimatter) and are able to form color singlets. The 2-codons of type A (resp. B) are related by isospin rotations and there should be some property distinguishing between types A and B. There indeed is: if 2-codon is matter-antimatter symmetric, 1-codon is not and vice versa.

1. For almost all type A codons the amino-acid coded by the codon does not depend on the last nucleotide. There are two exceptions in the case of the nuclear code: (leu, leu, phe, phe) and (ile, ile, ile, met). For human mitochondrial code one has (ile, ile, ile, ile) and thus only one exception to the rule. The breaking of matter-antimatter symmetry for the third nucleotide is thus very small.

2. For codons of type B the 4-columns code always for two doublets in the case of vertebrate mitochondrial code so that for codons with vanishing net quark number the breaking of matter-antimatter symmetry for the third nucleotide is always present.

5. Em stability

Anomalous em charge Q_a vanishes for DNA and perhaps also mRNA strand containing also the G cap and poly-A tail which could compensate for the Q_a of the transcribed region so that

$$2(A - T) - (G - C) \simeq 0$$

or some variant of it holds true. Chargaff's rules for long DNA strands imply the smallness of Q_a.

6. Summary of testable working hypothesis

Following gives a summary of testable working hypothesis related to the isospin symmetry and color singletness. The property of having integer valued/vanishing Q_a is referred to as property P.

1. Gene plus control region and also DNA repeats should have property P. Transcribed and control regions of gene have Q_a with opposite signs.

2. Transposons, repeating regions, the overhangs associated with the cut and paste of transposon, and the DNA strands resulting in cutting should have property P. This could explain why transposons can paste themselves to AT and GC ($Q_a = 0$) rich repeating regions of DNA. The points at which DNA can be cut should differ by a DNA section having property

P. This gives precise predictions for the points at which transposons and pieces of viral DNA can join and could have implications for genetic engineering.

3. If also mRNA is braided, it has property P. This can be only true if the poly-A tail compensates for the non-vanishing Q_a associated with the translated region.

4. Living hairpins should have property P. If only double helix parts of hairpins are braided, the prediction is trivially true by the palindrome property. tRNA or at least parts of it could be braided. Braids could end to the nuclear membrane or mRNA or to the amino-acid attachable to tRNA. For stem regions Q_a is integer valued. The fact that the nucleotide of the anticodon corresponding to the third nucleotide of codon can base pair with several nucleotides of mRNA suggests that $I(nositol)$ can have Q_a opposite to that of A, T, C and U opposite to that of A, G. For 2-anticodon the pairing would be unique. This would give a lot of freedom to achieve property P in weak sense for tRNA. Braid structure for tRNA + amino-acid could be different that for tRNA alone and also in the translation the braid structure could change.

5. Telomeres [I45] are of special interests as far as anomalous em charge is considered. Chromosomes are not copied completely in cell replication, and one function of telomeres is to guarantee that the translated part of genome replicates completely for sufficiently many cell divisions. Telomeres consists of 3-20 kilobases long repetitions of TTAGGG, and there is a 100-300 kilobases long repeating sequence between telomere and the rest of the chromosome. Telomeres can form can also 4-stranded structures. Telomere end contains a hair-pin loop as a single stranded part, which prevents the action of DNA repair enzymes on the chromosome end. Telomerase is a reverse transcriptase enzyme involved with the synthesis of telomeres using RNA strand as a template but since its expression is repressed in many types of human cells, telomere length shortens in each cell replication. In the case of germ cells, stem cells and white blood cells telomerase is expressed and telomere length preserved. Telomere shortening is known to relate to ageing related diseases. On the other hand, overactive telomere expression seems to correlate with cancer.

   If telomeres possess braid strands, the compensation of Q_a might provide an additional reason for their presence. If this the case and if telomeres are strict multiples of TTAGGG, the shortening of telomeres generates a non-vanishing Q_a unless something happens for the active part of DNA too. Color singletness condition should however remain true: the disappearance of $3n$ multiples of TTAGGG in each replication is the simplest guess for what might happen. In any case, DNA strands would become unstable in cell replication. Q_a could be reduced by a partial death of DNA in the sense that some portions of braiding disappear. Also this would induce ill functioning of TQC harware perhaps related to ageing related diseases. Perhaps evolution has purposefully developed this ageing mechanism since eternal life would stop evolution.

6. Also amino-acids could be braided. Q_a could vary and correspond to Q_a for one of the codons coding for it. The amino-acid sequences of catalysts attaching to DNA strand should have opposite Q_a for each codon-amino-acid pair so that amino-acid would attach only to the codons coding for it. The TGD based model for nerve pulse [K44] inspires the proposal that magnetic flux tubes connecting microtubules to the axonal membrane allow TQC during nerve pulse propagation when axonal membrane makes transition from gel like phase to liquid crystal phase. Amino-acids of tubulin dimers would be connected by 3-braids, smallest interesting braid, to groups of 3-lipids in axonal membrane and tubulin dimers would define fundamental TQC modules.

Empirical rules about DNA and mRNA supporting the symmetry breaking picture

Somewhat surprisingly, basic facts which can be found from Wikipedia, support the proposed vision about symmetry breaking although, the mechanism of matter antimatter symmetry breaking is more complex than the first guess. I am grateful for Dale Trenary for references which made possible to realize this. Before continuing some comments about the physical picture are in order.

1. The vanishing of the induced Kähler field means that the space-time sheet of DNA is a highly unstable vacuum extremal. The non-vanishing of the induced Kähler electric field is thus a natural correlate for both the stability and the non-vanishing quark number density (matter antimatter asymmetry). The generation of matter antimatter asymmetry induces a net density of anomalous em charge, isospin, and quark number in the portion of DNA considered. This in turn generates not only longitudinal electric field but also a longitudinal Kähler electric field along DNA.

2. Weak electric fields play a key role in living matter. There are electric fields associated with embryos, central nervous system, individual neurons, and microtubules and their direction determines the direction of a process involved (head-to-tail direction, direction of propagation of nerve pulse, ...).

3. Same mechanism is expected to be at work also in the case of DNA and RNA. In the case of gene the direction of transcription could be determined by the direction of the electric field created by gene and telomeres at the ends of chromosomes carrying a net anomalous quark number could be partially responsible for the generation of this field. In the case of mRNA the direction of translation would be determined in the similar manner. The net anomalous em charges of poly-A tail and the transcribed part of mRNA would have opposite signs so that a longitudinal electric field would result.

It will be found that this picture is consistent with empirical findings about properties of DNA.

7. Breaking of matter antimatter symmetry and isospin symmetry for entire genome

Chargaff's rules are not exact and the breaking gives important information about small breakings of isospin and matter-antimatter symmetries at the level of entire genome. The basic parameters are em charge per nucleotide, isospin per nucleotide, the amount of quark number per nucleotide, and the ratio of u and d type matters coded by $(G+C)/(A+T)$ ratio. Recall that there are four options for the map of A, T, C, G to quarks and antiquarks and for option 3) *resp.* 4) the anomalous em charge is opposite to that for 1) *resp.* 2).

Table 9.2 gives A, T, C, G contents (these data are from Wikipedia [I10]) provides interesting data about DNA It will be found that so called Szybalski's rules can be interpreted as saying that for coding regions there is breaking of the approximate matter antimatter asymmetry.

Note that matter antimatter asymmetry in the scale of entire genome has largest positive value for human genome and negative value only for yeast genome: this case the magnitude of the asymmetry is largest.

For option 2) the amount of anomalous charge is about.0057e per nucleotide and thus about $3 \times 10^7 e$ for entire human DNA having length of about 1.8 meters. The inspection of tables of [I45] shows that the anomalous em charge for the repeating sequence defining the telomere is always non-vanishing and has always the same sign. Telomeres for human chromosomes consist of TTAGGG repetitions with anomalous em charge with magnitude $5e/3$ for all options and have a length measured in few kbases. Human genome as has 24 chromosomes so that the total anomalous em charge of telomeres is roughly $24 \times (5/18) \times x10^3 e \sim .8 \times 10^3 xe$, $1 < x < 10$. The anomalous em charge of telomeres is three orders of magnitude smaller than that of entire DNA but if DNA is quantum critical system the change the total anomalous em charge and quark number due to the shortening of telomeres could induce instabilities of DNA (due to the approach to vacuum extremal) contributing to ageing. Note that the small net value of quark number in all the cases considered might be necessary for overall stability of DNA. Telomeres are also known to prevent the ends of chromosomes to stick to each other. This could be partially due to the Coulomb repulsion due to the anomalous em charge.

According to [I10] Chargaff's rules do not apply to viral organellar genomes (mitochondria [I27], plastids) or single stranded viral DNA and RNA genomes. Thus approximate matter antimatter symmetry fails for DNA: s of organelles involved with metabolism. This might relate to the fact that the coding portion of DNA is very high and repeats are absent. Chargaff's rule applies not only to nucleotides but also for oligonucleotides which corresponds to DNA or RNA sequences with not more than 20 bases. This means that for single strand oligonucleotides and their conjugates appear in pairs. Matter antimatter asymmetry would be realized as presence

Table 9.2: The table gives A, T, C, G contents (these data are from Wikipedia [I10]), the amount of quark charge per nucleotide for the options 1) *resp.* 2) given by $dq_1/dn = p[2(A-T)-G-C)]/3$ *resp.* $dq_2/dn = p[A-T-2(G-C)]/3$, the amount $dI_3/dn = p(A-G+C-T]/2$ of isospin per nucleotide, the amount $d(q-\overline{q})/dn = p(A-T+G-C)$ of quark number per nucleotide, and $(A+T)/(C+G)$ ratio for *entire genomes* in some cases.

	Human	*Chicken*	*Grass−hopper*	*Sea Urchin*	*Wheat*	*Yeast*	*E.Coli*
$p(A)$	0.3090	0.2880	0.2930	0.3280	0.2730	0.3130	0.2470
$p(T)$	0.2940	0.2920	0.2930	0.3210	0.2710	0.3290	0.2360
$p(C)$	0.1990	0.2050	0.2050	0.1770	0.2270	0.1870	0.2600
$p(G)$	0.1980	0.2170	0.2070	0.1730	0.2280	0.1710	0.2570
$\frac{dq_1}{dn}$	0.0103	−0.0067	−0.0007	0.0060	0.0010	−0.0053	0.0083
$\frac{dq_2}{dn}$	0.0057	−0.0093	−0.0013	0.0050	−0.0000	0.0053	0.0057
$\frac{dI_3}{dn}$	0.0080	−0.0080	−0.0010	0.0055	0.0005	0.0000	0.0070
$\frac{d(q-\overline{q})}{dn}$	0.0140	0.0080	0.0020	0.0030	0.0030	−0.0320	0.0080
$\frac{p(A+T)}{p(G+C)}$	1.5189	1.3744	1.4223	1.8543	1.1956	1.7933	0.9342

(9.3.8)

of matter blobs and their conjugates. This might relate to the mechanism how the sequences of oligonucleotides are generated from DNA and its conjugate.

8. Breaking of matter antimatter symmetry for coding regions

As noticed, one can consider three type of symmetry breaking parameters for DNA in DNA as TQC model. There are indeed three empirical parameters of this kind. Chargaff rules have been already discussed and correspond to approximate matter antimatter symmetry. The second asymmetry parameter would measure the asymmetry between $u\overline{u}$ and $d\overline{d}$ type matter. $p(G+C)$ corresponds to the fraction of $d\overline{d}$ type quark matter for option 1) and $u\overline{u}$ matter for option 2). It is known that G+C fraction $p(G+C)$ characterizes genes [I117] and the value of $p(G+C)$ is proportional to the length of the coding sequence [I23, I117].

Besides Chargaff rules holding true for entire genome also Szybalski's rules [I10] hold true but only for coding coding regions. The biological basis of neither rules is not understood. The interpretation of Chargaff's rules would be in terms of approximate matter antimatter symmetry and the vanishing of net isospin at the level of quarks whereas Szybalski's rule would state the breaking of these symmetries non-coding regions. Hence all the three basic empirical rules would have a nice interpretation in DNA as TQC picture.

Consider now Szybalski's rules in more detail.

1. In most bacterial genomes (which are generally 80-90 % coding) genes are arranged in such a fashion that approximately 50 % of the coding sequence lies on either strand. Note that either strand can act as a template (this came as a surprise for me). Szybalski, in the 1960s, showed that in bacteriophage coding sequences purines (A and G) exceed pyrimidines (C and T). This rule has since been confirmed in other organisms and known as Szybalski's rule [I10, I118]. While Szybalski's rule generally holds, exceptions are known to exist.

   Interpretation. A breaking of matter antimatter symmetry occurs in coding regions such that the net breakings are opposite for regions using different templates and thus different directions of transcription (promoter to the right/left of coding region).

2. One can actually characterize Szybalski's rules more precisely. By Chargaff's rules one has $p(A+T) \simeq 1-p(G+C)$). In coding regions with low value of $p(G+C)$ $p(A)$ is known to be higher than on the average whereas for high value of $p(G+C)$ $p(G)$ tends to higher than on the average.

Interpretation. These data do not fix completely the pattern of breaking of the approximate matter antimatter symmetry.

i) It could take place for both kinds of quark matter ($u\overline{u}$ and $d\overline{d}$): both $p(A)$ and $p(G)$ would increase from its value for entire genome but the dominance of A over G or vice versa would explain the observation.

ii) The breaking could also occur only for the dominating type of quark matter ($u\overline{u}$ or $d\overline{d}$) in which case only $p(A)$ or $p(G)$ would increase from the value for entire genome.

Also a net isospin is generated which is of opposite sign for short and long coding sequences so that there must be some critical length of the coding sequences for which isospin per nucleotide vanishes. This length should have biological meaning.

3. For mRNA $A+G$ content is always high. This is possible only because the template part of the DNA which need not be always the same strand varies so that if it is strand it has higher $A+G$ content and if it is conjugate strand it has higher $T+C$ content.

Interpretation. mRNA breaks always matter antimatter symmetry and the sign of matter antimatter asymmetry is always the same. Thus mRNA is analogous to matter in observed universe. The poly-A tail added to the end of mRNA after transcription to stabilize it would reduce the too large values of isospin and anomalous em charge per nucleon due to the fact that mRNA does not contain regions satisfying Chargaff's rules. It would also generate the needed longitudinal electric field determining the direction of translation. In the case of DNA the breaking of matter antimatter symmetry is realized at the functional level by a varying direction of transcription and variation of template strand so that matter antimatter symmetry for the entire DNA is only slightly broken. Direction of transcription would be determined by the direction of the electric field. The stability of long DNA sequences might require approximate matter antimatter symmetry for single DNA strand if it is long. In the case of simple genomes (mitochondrial, plastid, and viral) the small size of the genome, the high fraction of coding regions, and the absence of repeating sequences might make approximate matter antimatter symmetry un-necessary. An interesting working hypothesis is that the direction of transcription is always the same for these genomes.

One can try to use this information to fix the most probable option for nucleotide quark correspondence.

1. In nuclear physics the neutron to proton ratio of nucleus increases as nucleus becomes heavier so that the nuclear isospin becomes negative: $I_3 < 0$. The increase of the nuclear mass corresponds to the increase for the length of the coding region. Since G/A fraction increases with the length of coding region, G should correspond to either d quark ($(Q_a < 0, I_3 = -1/2)$) or its charge conjugate d_c ($Q_a < 0$). Hence option 1) or its charge conjugate would be favored.

2. If one takes very seriously the analogy with cosmic matter antimatter asymmetry then matter should dominate and only $(A, G, T, C) \to (u, d, \overline{u}, \overline{d})$ option would remain.

Szybalski's findings leave open the question whether non-coding regions obey the Chargaff rules in good approximation or whether also they appear as pairs with opposite matter antimatter asymmetry. Introns are belong to coding regions in the sense that they are transcribed to mRNA. Splicing however cuts them off from mRNA. It is not clear whether introns break the approximate matter antimatter symmetry or not. If breaking takes place it might mean that introns code for something but not chemically. On the other hand, the absence of asymmetry might serve at least partially as a signal telling that introns must be cut off before translation. Many interesting questions represent itself. For instance, how the symmetry breaking parameters, in particular matter antimatter asymmetry parameter, depend on genes. The correlation with gene length is the most plausible guess.

Genetic codes and TQC

TGD suggests the existence of several genetic codes besides 3-codon code [K23, K19]. The experience from ordinary computers and the fact that genes in general do not correspond to $3n$ nucleotides encourages to take this idea more seriously. The use of different codes would allow to tell what kind of information a given piece of DNA strand represents. DNA strand would be

like a drawing of building containing figures (3-code) and various kinds of text (other codes). A simple drawing for the building would become a complex manual containing mostly text as the evolution proceeds: for humans 96 per cent of code would corresponds to introns perhaps obeying some other code.

The hierarchy of genetic codes is obtained by starting from n basic statements and going to the meta level by forming all possible statements about them (higher order logics) and throwing away one which is not physically realizable (it would correspond to empty set in the set theoretic realization). This allows $2^n - 1$ statements and one can select 2^{n-1} statements consistent with a given atomic statement (1 bit fixed) (half of the full set of statements) and say that these are true and give kind of axiomatics about world. The remaining statements are false. DNA would realize only these statements.

The hierarchy of Mersenne primes $M_n = 2^n - 1$ with $M_{n(next)} = M_{M_n}$ starting from $n = 2$ with $M_2 = 3$ gives rise to 1-code with 4 codons, 3-code with 64 codons, and $3 \times 21 = 63$-code with 2^{126} codons [K23] realized as sequences of 63 nucleotides (the length of 63-codon is about $2L(151)$, roughly twice the cell membrane thickness. It is not known whether this Combinatorial Hierarchy continues ad infinitum. Hilbert conjectured that this is the case.

In the model of pre-biotic evolution also 2-codons appear and 3-code is formed as the fusion of 1- and 2-codes. The problem is that 2-code is not predicted by the basic Combinatorial Hierarchy associated with $n = 2$.

There are however also other Mersenne hierarchies and the next hierarchy allows the realization of the 2-code. This Combinatorial Hierarchy begins from Fermat prime $n = 2^k + 1 = 5$ with $M_5 = 2^5 - 1 = 31$ gives rise to a code with 16 codons realized as 2-codons (2 nucleotides). Second level corresponds to Mersenne prime $M_{31} = 2^{31} - 1$ and a code with $2^{30=15\times 2}$ codons realized by sequences of 15 3-codons containing 45 nucleotides. This corresponds to DNA length of 15 nm, or length scale $3L(149)$, where $L(149) = 5$ nm defines the thickness of the lipid layer of cell membrane. $L(151) = 10$ nm corresponds to 3 full 2π twists for DNA double strand. The model for 3-code as fusion of 1- and 2-codes suggests that also this hierarchy - which probably does not continue further - is realized.

There are also further short Combinatorial hierarchies corresponding to Mersenne primes [A5].

1. $n = 13$ defines Mersenne prime M_{13}. The code would have $2^{12=6\times 2}$ codons representable as sequences of 6 nucleotides or 2 3-codons. This code might be associated with microtubuli.

2. The Fermat prime $17 = 2^4 + 1$ defines Mersenne prime M_{17} and the code would have $2^{16=8\times 2}$ codons representable as sequences of 8 nucleotides.

3. $n = 19$ defines Mersenne prime M_{19} and code would have $2^{18=9\times 2}$ codons representable as sequences of 9 nucleotides or three DNA codons.

4. The next Mersennes are M_{31} belonging to $n = 5$ hierarchy, M_{61} with $2^{60=30\times 2}$ codons represented by 30-codons. This corresponds to DNA length $L(151) = 10$ nm (cell membrane thickness). M_{89} (44-codons), M_{107} (53-codons) and M_{127} (belonging to the basic hierarchy) are the next Mersennes. Next Mersenne corresponds to M_{521} (260-codon) and to completely super-astrophysical p-adic length scale and might not be present in the hierarchy.

   This hierarchy is realized at the level of elementary particle physics and might appear also at the level of DNA. The 1-, 2-, 3-, 6-, 8-, and 9-codons would define lowest Combinatorial Hierarchies.

9.4 Constraints On The Fermionic Realization Of Genetic Code From The Model For Color Qualia

The original model for DNA as topological quantum computer assigns to DNA nucleotides quarks at ends of flux tubes or quark pairs at the ends of wormhole flux tubes. This is only the realization that came first to my mind in TGD Universe where dark variants of quarks can define QCD like physics even in cellular length scales. One can actually imagine several realizations of the genetic code and the first realization is far from being the simplest one. It is enough to have four different

particles or many-particle quantum states to build at least formally a map from A, T, C, G to four states. It is obvious that the number of possible formal realizations is limited only by the imagination of the theoretician. Additional conditions are required to fix the model.

9.4.1 Fermionic Representation

Consider first the fermionic representations in the general case without specifying what fermions are.

1. The original proposal was that DNA nucleotides correspond to flux tubes with quark q and antiquark $\overline{q}$ at the ends of the parallel flux sheets extremely near to each other. Second options relies on wormhole magnetic flux tubes in which case quark pair $q\overline{q}$ is at both ends. Quarks u, d and their antiquarks would code for A, T, C, G. The spin of quarks is not taken into account at all in this coding: why not restrict the consideration to single quark. The total quark charge at given end of flux tube pair vanishes and flux tube ends carry opposite quark charges.

   The nice feature of this option is that one could understand the generation of color qualia in the model of sensory receptor in simple manner to be discussed below. Even if one accepts the arguments supporting the view that dark quarks in cell scale are natural outcome of the hierarchy of Planck constants, one could argue that the presence of both quarks and antiquarks does not conform with matter antimatter asymmetry (not that one can however identify the analog of matter antimatter asymmetry at DNA level).

2. Spin states for fermion pairs assigned with two parallel magnetic flux tubes with the magnetic field generated by spin provide much simpler representation for nucleotides. Similar fermion pair would reside at the second end of flux tube pair.

   (a) It is is essential that rotational symmetry is broken and reduces to rotational symmetry around the direction of flux tubes so that spin singlet and spin 0 state of triplet mix to form states for which each fermion is in spin eigenstate. The states must be antisymmetric under exchange of the protons and spin 1/0 states are antisymmetric/symmetric in spatial degrees of freedom (wave functions located to the ends of flux tubes). The states with definite spin for given flux tube are mixtures of s=1 states with vanishing spin projection and s=0 state.

   (b) It is not quite clear whether one should treat fermion pairs as identical bosons with 3+1 spin states since in TGD framework one considers disjoint partonic 2-surfaces and the situation is not that of QFT in M^4. This interpretation would require totally symmetry of the states under permutations of bosonic states defined by the 3+1 spin states. Coding by spin requires that each nucleotide corresponds to a state with a well defined spin. In field theory language the state would be obtained by applying bosonic oscillator operators generating states of given spin localized to a given nucleotide position.

   (c) The classical correlate for the permutations of coordinates of fermions has interpretation as braiding for the flux tubes of the flux tube pair. In the similar manner the permutation of the flux tube pairs associated with nucleotides has interpretation as braiding of the 3-braids formed form from flux tube pairs. Braiding therefore gives a representation of spin analogous to the well-known orientation entanglement relation invented by Dirac and providing geometric representation of spin 1/2 property.

9.4.2 Various Options For The Fermionic Representation Of A, T, C, G

Fermionic representations allows several options since fermion can be electron, u or d quark, or proton. Wormhole magnetic fields would not be needed in this case.

1. The problem of electron and proton options is that it does not allow realization of color qualia. There is also the well-known problem related to the stability of DNA caused by the phosphate charge of -2 units per nucleotide. Somehow this charge should be screened. In any case, the charge -2 should correspond to the electron pair at the DNA end of the flux tube

for electron option. For proton option the charge would be screened completely. One could of course consider also the large $\hbar$ color excitations of ordinary protons instead of quark at its nucleotide ends. This option would however require the modification of quark wave functions inside proton and this option will not be discussed here.

2. Quark option would give rise to both color and allow also to reduce the electronic charge of -2 units by 4/3 units to -2/3 units in the case of u quark pair. This would help to stabilize DNA. In the case of d quarks the charge would increase to -10/3 units and is not favored by stability argument. Flux tube pairs assigned to single nucleotide define diquarks with spin 1 or spin 0.

   (a) Diquarks behave ass identical bosons with 3+1 spin states and 3×3 color states. They form formally super-multiplet of $\mathcal{N} = 2$ SUSY. The states with well defined symmetry properties in spin degrees of freedom have such properties in spatial degrees of freedom. This means that one obtains a superposition of flux tube pairs with are either braided or unbraided. Triplet/singlet state is symmetric/antisymmetric and total asymmetry could be guaranteed by assuming symmetry/antisymmetry in spatial degrees of freedom and antisymmetry/symmetry in color degrees of freedom. This would give anti-triplet/6-plet in color degrees of freedom. Spatial symmetry would favor antitriplet and diquark would behave like antiquark with respect to color. Let us assume antitriplet state for definiteness.

   (b) DNA codon corresponds to three-di-quark state. This state must be totally symmetric under the exchange of bosons. One can have total symmetry in both spatial and color degrees of freedom or total antisymmetry/symmetry in spatial and total antisymmetry/symmetry in color degrees of freedom.The first option gives 10-dimensional color multiplet and the second one color singlet. Braiding is maximal and symmetric/antisymmetric in these case. One can consider also mixed symmetries. In this case one has color octet which is antisymmetric with respect to the first nucleotide pair and symmetric with respect to first nucleotide pair and third nucleotide. The braiding of the first two nucleotides must be antisymmetric and the braiding of this pair with third nucleotide. The conclusion would be that color multiplets correspond to well defined braidings and one would therefore have directed connection with topological quantum computation. Color octet is especially interesting concerning the representation of color qualia.

The challenge of all these options (note that the representability of color selects quark option) is to find a good justification for why the assignment of A, T, C, G to quark states or spin states is unique dynamically. Stability argument is expected to help here.

9.4.3 Realization Of Color Qualia For Quark Option

Consider now how one could understand the generation of qualia for quark option.

1. The generation of qualia involves interaction with external world giving rise to a sensory percept. In the case of visual colors it should correspond to a measurement of quark color and should give rise to eigenstages of color at the ends of flux tubes at DNA nucleotides for a nucleus or cell of photoreceptor. A modification of capacitor model is needed. Color polarization is still essential but now polarization in nucleus or cell scale is transformed in the generation of color quale to a polarization in longer length scale by the reconnection of flux tubes so that their ends attach to "external world". The nucleus/cell becomes color and state function reduction selects well defined quantum numbers. It is natural to assume that the entanglement in other degrees of freedom after color measurement is negentropic.

2. Does the "external world" corresponds to another cell or to the inner lipid layers of the cell membrane containing the nucleus. In the first case flux tubes would end to another cell. If the nuclei of receptor cells are integrate to a larger structure by magnetic flux sheets traversing through them one can also consider the possibility that the polarization in the scale of cell

nucleus (recall that the nucleus has also double lipid layer) is transformed to a polarization in cell scale so that similar process in cell scale gives rise to qualia.

The entire receptor unit must have net color charge before the state function reduction. This requires that there are flux tubes connecting the receptor unit to a unit representing "external world" and having vanishing color charge. If second cell is the "external world" these flux tubes must go through the pair of lipid layers of both cell membrane and end up to the nucleus of cell in the environment. If external world correspond to the complement of nucleus inside cell the inner layers of cell membrane represents external world. Cell membrane indeed serves as sensory receptor in cell length scale. One can of course have sensory qualia in various length scales so that both options are probably correct and a kind of fractal hierarchy is very natural giving rise also to our qualia at some higher level. Living matter as conscious hologram metaphor suggests a fractal hierarchy of qualia.

After state function reduction reducing the entanglement the flux tubes split and the receptor becomes un-entangled with external world and has vanishing color charges. At the level of conscious experience this means that there can be only memory about the quale experience. The sensation of quale lasts with respect to subjective time as long as the negentropic entanglement prevails. There is an obvious analogy with Orch-OR (see `http://tinyurl.com/ylfv6pp`) proposal of Hameroff and Penrose in which also conscious experience ends with state function reduction.

3. Consider now how the color qualia are generated.

   (a) There must be two flux tube states. In the first state there are two flux tube beginning from cell nucleus A and ending to the inner lipid layer a_1 and flux tube beginning from the outer lipid layer a_2 and ending cell nucleus B. Both flux tubes have vanishing net color so that cells have vanishing net colors. This could be regarded as the resting state of the receptor. The lipids in layers a_1 and a_2 are connected by another short flux tube. Same for b_1 and b_2.

   (b) The second flux tube state corresponds to long flux tubes connecting the nuclei of cells A and B. The ends carry opposite color charges. In this case the net color of both A and B is non-vanishing. This state would be an outcome of a reconnection process in which the flux tubes from A to a_1 and B to a_2 re-connect with the short flux tube connecting lipid layers a_1 and a_2.

   (c) When these flux tubes carry opposite colors numbers at their ends, the cell possess net color charge and can represent color quale. Or rather, creation of this kind of flux tube connections would give rise to the color charging of the receptor cell with external world carrying opposite color charge.

One can argue that this mechanism is not quite in spirit with color capacitor model. Polarization is still essential but now polarization in receptor scale is transformed to polarization in longer length scale by the reconnection of flux tubes. The analog of di-electric breakdown however still applies in the sense that its analog induces large polarization. Several mechanisms generating larger polarization are of course possible. One can ask how essential the electromagnetic polarization of cell membrane is for the generation of qualia at cell level. Note also that biomolecules are quite generally polar molecules.

The unexpected prediction of the model is that braiding would correlate directly with qualia. This would mean also a connection between quantum computation and qualia. This condition emerges from Fermi/Bose-Einstein statistics correlating braiding with symmetric properties of color states and spin states. Quite generally, the correlation of braiding with the symmetries of wave functions as functions of points of braid end points would allow to have direct geometric correlate between induced entanglement and braiding as naive intuitive expectations have suggested.

This model is not consistent with the naive expectation that the quale is generated after state function reduction. Rather, the beginning of sensation of quale means beginning of negentropic entanglement and fusion with external world and state function usually associated with the quantum measurement would mean the end of the sensation and separation from the external world! Maybe one can say that state function reduction means that experience is replaced with a memory "I had the sensation of quale" ! Krishnamurti would certainly agree!

9.5 Realization Of Genetic Code In Terms Of Dark Baryons

Either dark baryon code or code based on u, d and their anti-quarks could be involved with various pairings. For dark baryon code DNA would not decompose into codons. For latter code this would be the case. One could also consider the possibility that the regions genes realized the dark baryon code and the regions between them are realized in terms of ududbardbar code. The latter code could be also involved with TQC.

9.5.1 Dark Nuclear Strings As Analogs Of DNA-, RNA- and Amino-Acid Sequences and Baryonic Realization Of Genetic Code?

Water memory is one of the ugly words in the vocabulary of a main stream scientist. The work of pioneers is however now carrying fruit. The group led by Jean-Luc Montagnier, who received Nobel prize for discovering HIV virus, has found strong evidence for water memory and detailed information about the mechanism involved [L2, K24, **?**], [L2] , [I94]. The work leading to the discovery was motivated by the following mysterious finding. When the water solution containing human cells infected by bacteria was filtered in purpose of sterilizing it, it indeed satisfied the criteria for the absence of infected cells immediately after the procedure. When one however adds human cells to the filtrate, infected cells appear within few weeks. If this is really the case and if the filter does what it is believed to do, this raises the question whether there might be a representation of genetic code based on nano-structures able to leak through the filter with pores size below 200 nm.

The question is whether dark nuclear strings might provide a representation of the genetic code. In fact, I posed this question year before the results of the experiment came with motivation coming from attempts to understand water memory. The outcome was a totally unexpected finding: the states of dark nucleons formed from three quarks can be naturally grouped to multiplets in one-one correspondence with 64 DNAs, 64 RNAS, and 20 amino-acids and there is natural mapping of DNA and RNA type states to amino-acid type states such that the numbers of DNAs/RNAs mapped to given amino-acid are same as for the vertebrate genetic code.

The basic idea is simple. Since baryons consist of 3 quarks just as DNA codons consist of three nucleotides, one might ask whether codons could correspond to baryons obtained as open strings with quarks connected by two color flux tubes. This representation would be based on entanglement rather than letter sequences. The question is therefore whether the dark baryons constructed as string of 3 quarks using color flux tubes could realize 64 codons and whether 20 amino-acids could be identified as equivalence classes of some equivalence relation between 64 fundamental codons in a natural manner.

The following model indeed reproduces the genetic code directly from a model of dark neutral baryons as strings of 3 quarks connected by color flux tubes.

1. Dark nuclear baryons are considered as a fundamental realization of DNA codons and constructed as open strings of 3 dark quarks connected by two colored flux tubes, which can be also charged. The baryonic strings cannot combine to form a strictly linear structure since strict rotational invariance would not allow the quark strings to have angular momentum with respect to the quantization axis defined by the nuclear string. The independent rotation of quark strings and breaking of rotational symmetry from SO(3) to SO(2) induced by the direction of the nuclear string is essential for the model.

   Baryonic strings could form a helical nuclear string (stability might require this) locally parallel to DNA, RNA, or amino-acid) helix with rotations acting either along the axis of the DNA or along the local axis of DNA along helix. The rotation of a flux tube portion around an axis parallel to the local axis along DNA helix requires that magnetic flux tube has a kink in this portion. An interesting question is whether this kink has correlate at the level of DNA too. Notice that color bonds appear in two scales corresponding to these two strings. The model of DNA as topological quantum computer [K17] allows a modification in which dark nuclear string of this kind is parallel to DNA and each codon has a flux tube connection to the lipid of cell membrane or possibly to some other bio-molecule.

2. The new element as compared to the standard quark model is that between both dark quarks and dark baryons can be charged carrying charge $0, \pm 1$. This is assumed also in nuclear string

model and there is empirical support for the existence of exotic nuclei containing charged color bonds between nuclei.

3. The net charge of the dark baryons in question is assumed to vanish to minimize Coulomb repulsion:

$$\sum_q Q_{em}(q) = -\sum_{flux\ tubes} Q_{em}(flux\ tube) \ . \tag{9.5.1}$$

This kind of selection is natural taking into account the breaking of isospin symmetry. In the recent case the breaking cannot however be as large as for ordinary baryons (implying large mass difference between Δ and nucleon states).

4. One can classify the states of the open 3-quark string by the total charges and spins associated with 3 quarks and to the two color bonds. Total em charges of quarks vary in the range $Z_B \in \{2,1,0,-1\}$ and total color bond charges in the range $Z_b \in \{2,1,0,-1,-2\}$. Only neutral states are allowed. Total quark spin projection varies in the range $J_B = 3/2, 1/2, -1/2, -3/2$ and the total flux tube spin projection in the range $J_b = 2,1,-1,-2$. If one takes for a given total charge assumed to be vanishing one representative from each class (J_B, J_b), one obtains $4 \times 5 = 20$ states which is the number of amino-acids. Thus genetic code might be realized at the level of baryons by mapping the neutral states with a given spin projection to single representative state with the same spin projection. The problem is to find whether one can identify the analogs of DNA, RNA and amino-acids as baryon like states.

States in the quark degrees of freedom

One must construct many-particle states both in quark and flux tube degrees of freedom. These states can be constructed as representations of rotation group SU(2) and strong isospin group SU(2) by using the standard tensor product rule $j_1 \times j_2 = j_1 + j_2 \oplus j_1 + j_2 - 1 \oplus ... \oplus |j_1 - j_2|$ for the representation of SU(2) and Fermi statistics and Bose-Einstein statistics are used to deduce correlations between total spin and total isospin (for instance, $J = I$ rule holds true in quark degrees of freedom). Charge neutrality is assumed and the breaking of rotational symmetry in the direction of nuclear string is assumed.

Consider first the states of dark baryons in quark degrees of freedom.

1. The tensor product $2 \otimes 2 \otimes 2$ is involved in both cases. Without any additional constraints this tensor product decomposes as $(3 \oplus 1) \otimes 2 = 4 \oplus 2 \oplus 2$: 8 states altogether. This is what one should have for DNA and RNA candidates. If one has only identical quarks *uuu* or *ddd*, Pauli exclusion rule allows only the 4-D spin 3/2 representation corresponding to completely symmetric representation -just as in standard quark model. These 4 states correspond to a candidate for amino-acids. Thus RNA and DNA should correspond to states of type uud and ddu and amino-acids to states of type *uuu* or ddd. What this means physically will be considered later.

2. Due to spin-statistics constraint only the representations with $(J, I) = (3/2, 3/2)$ (Δ resonance) and the second $(J, I) = (1/2, 1/2)$ (proton and neutron) are realized as free baryons. Now of course a dark -possibly p-adically scaled up - variant of QCD is considered so that more general baryonic states are possible. By the way, the spin statistics problem which forced to introduce quark color strongly suggests that the construction of the codons as sequences of 3 nucleons - which one might also consider - is not a good idea.

3. Second nucleon like spin doublet - call it 2_{odd} - has wrong parity in the sense that it would require $L = 1$ ground state for two identical quarks (*uu* or *dd* pair). Dropping 2_{odd} and using only $4 \oplus 2$ for the rotation group would give degeneracies $(1,2,2,1)$ and 6 states only. All the representations in $4 \oplus 2 \oplus 2_{odd}$ are needed to get 8 states with a given quark charge and one should transform the wrong parity doublet to positive parity doublet somehow. Since open string geometry breaks rotational symmetry to a subgroup SO(2) of rotations acting

along the direction of the string and since the boundary conditions on baryonic strings force their ends to rotate with light velocity, the attractive possibility is to add a baryonic stringy excitation with angular momentum projection $L_z = -1$ to the wrong parity doublet so that the parity comes out correctly. $L_z = -1$ orbital angular momentum for the relative motion of *uu* or *dd* quark pair in the open 3-quark string would be in question. The degeneracies for spin projection value $J_z = 3/2, ..., -3/2$ are $(1, 2, 3, 2)$. Genetic code means spin projection mapping the states in $4 \oplus 2 \oplus 2_{odd}$ to 4.

States in the flux tube degrees of freedom

Consider next the states in flux tube degrees of freedom.

1. The situation is analogous to a construction of mesons from quarks and anti-quarks and one obtains the analogs of π meson (pion) with spin 0 and ρ meson with spin 1 since spin statistics forces $J = I$ condition also now. States of a given charge for a flux tube correspond to the tensor product $2 \otimes 2 = 3 \oplus 1$ for the rotation group.

2. Without any further constraints the tensor product $3 \otimes 3 = 5 \oplus 3 \oplus 1$ for the flux tubes states gives 8+1 states. By dropping the scalar state this gives 8 states required by DNA and RNA analogs. The degeneracies of the states for DNA/RNA type realization with a given spin projection for $5 \oplus 3$ are $(1, 2, 2, 2, 1)$. $8\times$ 8 states result altogether for both *uud* and *udd* for which color bonds have different charges. Also for *ddd* state with quark charge -1 one obtains $5 \oplus 3$ states giving 40 states altogether.

3. If the charges of the color bonds are identical as the are for *uuu* type states serving as candidates for the counterparts of amino-acids bosonic statistics allows only 5 states ($J = 2$ state). Hence 20 counterparts of amino-acids are obtained for *uuu*. Genetic code means the projection of the states of $5 \oplus 3$ to those of 5 with the same spin projection and same total charge.

Analogs of DNA, RNA, amino-acids, and of translation and transcription mechanisms

Consider next the identification of analogs of DNA, RNA and amino-acids and the baryonic realization of the genetic code, translation and transcription.

1. The analogs of DNA and RNA can be identified dark baryons with quark content *uud*, *ddu* with color bonds having different charges. There are 3 color bond pairs corresponding to charge pairs $(q_1, q_2) = (-1, 0), (-1, 1), (0, 1)$ (the order of charges does not matter). The condition that the total charge of dark baryon vanishes allows for *uud* only the bond pair $(-1, 0)$ and for *udd* only the pair $(-1, 1)$. These thus only single neutral dark baryon of type *uud resp. udd*: these would be the analogous of DNA and RNA codons. Amino-acids would correspond to *uuu* states with identical color bonds with charges $(-1, -1)$, $(0, 0)$, or $(1, 1)$. *uuu* with color bond charges (-1, -1) is the only neutral state. Hence only the analogs of DNA, RNA, and amino-acids are obtained, which is rather remarkable result.

2. The basic transcription and translation machinery could be realized as processes in which the analog of DNA can replicate, and can be transcribed to the analog of mRNA in turn translated to the analogs of amino-acids. In terms of flux tube connections the realization of genetic code, transcription, and translation, would mean that only dark baryons with same total quark spin and same total color bond spin can be connected by flux tubes. Charges are of course identical since they vanish.

3. Genetic code maps of $(4\oplus2\oplus2)\otimes(5\oplus3)$ to the states of 4×5. The most natural map takes the states with a given spin to a state with the same spin so that the code is unique. This would give the degeneracies $D(k)$ as products of numbers $D_B \in \{1, 2, 3, 2\}$ and $D_b \in \{1, 2, 2, 2, 1\}$: $D = D_B \times D_b$. Only the observed degeneracies $D = 1, 2, 3, 4, 6$ are predicted. The numbers $N(k)$ of amino-acids coded by D codons would be

$$[N(1), N(2), N(3), N(4), N(6)] = [2, 7, 2, 6, 3] \quad .$$

The correct numbers for vertebrate nuclear code are $(N(1), N(2), N(3), N(4), N(6)) = (2, 9, 1, 5, 3)$. Some kind of symmetry breaking must take place and should relate to the emergence of stopping codons. If one codon in second 3-plet becomes stopping codon, the 3-plet becomes doublet. If 2 codons in 4-plet become stopping codons it also becomes doublet and one obtains the correct result $(2, 9, 1, 5, 3)$!

4. Stopping codons would most naturally correspond to the codons, which involve the $L_z = -1$ relative rotational excitation of uu or dd type quark pair. For the 3-plet the two candidates for the stopping codon state are $|1/2, -1/2\rangle \otimes \{|2, k\rangle\}$, $k = 2, -2$. The total spins are $J_z = 3/2$ and $J_z = -7/2$. The three candidates for the 4-plet from which two states are thrown out are $|1/2, -3/2\rangle \otimes \{|2, k\rangle, |1, k\rangle\}$, $k = 1, 0, -1$. The total spins are now $J_z = -1/2, -3/2, -5/2$. One guess is that the states with smallest value of J_z are dropped which would mean that $J_z = -7/2$ states in 3-plet and $J_z = -5/2$ states 4-plet become stopping codons.

5. One can ask why just vertebrate code? Why not vertebrate mitochondrial code, which has unbroken $A - G$ and $T - C$ symmetries with respect to the third nucleotide. And is it possible to understand the rarely occurring variants of the genetic code in this framework? One explanation is that the baryonic realization is the fundamental one and biochemical realization has gradually evolved from non-faithful realization to a faithful one as kind of emulation of dark nuclear physics. Also the role of tRNA in the realization of the code is crucial and could explain the fact that the code can be context sensitive for some codons.

If the pairing is based on the assumption that total quark spins and total flux tube spins are identical, the pairing of dark variants of DNA and its conjugate and DNA and mRNA are are not unique at the level of dark matter but respect the genetic code. Divisor code to be discussed later and equivalent with dark baryon code in realization based on magnetic flux tubes predicts similar non-uniqueness.

Is the genetic code a composite of $64 \to 40$ and $40 \to 20$ codes?

As found, dark baryon counterpart of tRNA could correspond to the multiplet of states containing 40 states. According to [I54] most organisms have fewer the 45 species of tRNA. Typical value of anticodons is around 30 and in some organisms the number is as low as 22. This means that the number of different anticodons in tRNA is not larger than 45 and could be at most 40. Unfortunately I do not know what the real situation is. The realization of mRNA-tRNA pairing is known to be based on wobble base pairing [I54]. This means that the pairing is not unique for the third nucleotide of the anticodon so that all mRNA codons can pair with tRNA in a manner consistent with the genetic code.

This finding suggests that tRNA could correspond to a 40-plet of anticodons at the level of dark matter then for tRNA-amino-acid genetic code the numbers of codons $N(k)$ with given degeneracy k would be $(N(1), N(2), N(3)) = \{5, 10, 5\}$. The interpretation would be as $DNA \to tRNA$ dark baryon genetic code projection of states of $4 \oplus 2 \oplus 2$ to states of 4 with the same spin in color bond degrees of freedom to a state with same spin in $J = 2$ multiplet with 5 states. Numbers of dark aminocids with given degeneracy k would $(N(1), N(2)) = \{16, 24\}$. Ordinary genetic code would result as a composite of the projections associated with these codes. If the identification in terms of 40-plet makes sense one might consider the possibility that the evolution for tRNA-dtRNA correspondence has not yet achieved the ideal situation in which tRNA anti-codons would be in 1-1 correspondence with their dark counterparts.

Objections

Consider next some particle physicist's objections against this picture.

1. The realization of the code requires the dark scaled variants of spin 3/2 baryons known as Δ resonance and the analogs (and only the analogs) of spin 1 mesons known as ρ mesons. The lifetime of these states is very short in ordinary hadron physics. Now one has a scaled up variant of hadron physics: possibly in both dark and p-adic senses with latter allowing arbitrarily small overall mass scales. Hence the lifetimes of states can be scaled up.

2. Both the absolute and relative mass differences between Δ and N *resp.* ρ and π are large in ordinary hadron physics and this makes the decays of Δ and ρ possible kinematically. This is due to color magnetic spin-spin splitting proportional to the color coupling strength $\alpha_s \sim .1$, which is large. In the recent case α_s could be considerably smaller - say of the same order of magnitude as fine structure constant 1/137 - so that the mass splittings could be so small as to make decays impossible.

3. Dark hadrons could have lower mass scale than the ordinary ones if scaled up variants of quarks in p-adic sense are in question. Note that the model for cold fusion that inspired the idea about genetic code requires that dark nuclear strings have the same mass scale as ordinary baryons. In any case, the most general option inspired by the vision about hierarchy of conscious entities extended to a hierarchy of life forms is that several dark and p-adic scaled up variants of baryons realizing genetic code are possible.

4. A heavy objection relates to the addition of $L_z = -1$ excitation to $S_z = |1/2, \pm 1/2\rangle_{odd}$ states which transforms the degeneracies of the quark spin states from $(1, 3, 3, 1)$ to $(1, 2, 3, 2)$. The most plausible answer is that the breaking of the full rotation symmetry induced by nuclear string reduces $SO(3)$ to $SO(2)$. Also the fact that the states of massless particles are labeled by the representation of $SO(2)$ might be of some relevance.

The conclusion is that genetic code can be understood as a map of stringy baryonic states induced by the projection of all states with same spin projection to a representative state with the same spin projection. Genetic code would be realized at the level of dark nuclear physics and biochemical representation would be only one particular higher level representation of the code. A hierarchy of dark baryon realizations corresponding to p-adic and dark matter hierarchies can be considered. Translation and transcription machinery would be realized by flux tubes connecting only states with same quark spin and flux tube spin. Charge neutrality is essential for having only the analogs of DNA, RNA and amino-acids and would guarantee the em stability of the states.

9.5.2 DNA As Topological Quantum Computer Hypothesis And Dark Genetic Code

The coding of DNA codons by assigning to A, G *resp.* T, C of u and d quarks *resp.* their anti-quarks works nicely in the model of DNA as topological quantum computer. One can however consider also the option for which dark baryons code for entire DNA codons.

1. DNA as TQC using dark baryons to represent DNA codons would require that DNA strand is accompanied by a nuclear string parallel to it. If the pairing of baryons at the ends of string requires only opposite total quark spins and total flux tube spins the map would obey genetic code rather than being 1-1. The situation changes if dark baryon states are in 1-1 correspondence with the integers (n_a, n_b) labeling the page of book at which magnetic body of the codon resides.

2. The condition that the other end of flux tube beginning from the DNA codon contains nuclear string made from anti-baryons is natural but matter antimatter asymmetry if present also for dark matter does not favor this while mesonic strings with quarks at their ends are natural.

3. Rotating kinks assignable to 16 codons might be problematic from the point of TQC unless they represent codons with some special significance and play some special role - perhaps representing control commands in TQC program.

4. The flux tubes assignable to codons -instead of nucleotides as for earlier realization - would be basic units connected to lipids. The entanglement between dark baryon states of dark nuclear string would replaced the entanglement between quarks and anti-quarks at the ends of the flux tubes.

5. Only the portions of DNA having interpretation as gene have a natural decomposition to codons. Hence the dark baryon representation of codons is not attractive idea in intronic portions of the genome forming the most plausible candidates for quantum computing part of

DNA since the portion of introns has been increasing during evolution and highest variation of this portion is encountered in human brain [I56]. Hence one might think that TQC as relatively late outcome of the evolution and that only this part of genome is responsible for TQC so that the mpa of nucleotides to quarks would realize genetic code. Furthermore, braiding matters in TQC much more than the colors of braid strands determined by nucleotides so that intronic portions could quite well be repeating sequences without any obvious as information carriers in standard sense and therefore interpreted as junk DNA. There would be also an analogy between emergence of written language meaning that words as holistic entities were replaced with sequences of letters having as such no meaning.

9.6 Could One Find A Geometric Realization For Genetic And Memetic Codes?

Many-sheeted space-time makes possible large deviations from gravitation predicted by GRT, which in TGD framework can be seen as a description of gravitation at the long length scale limit. A fundamental distinction between GRT and TGD is that in TGD framework gravitational constant and cosmological constant - actually space-time dependent cosmological "constants" emerge as predictions of the theory rather than as fundamental constants of Nature.

For almost two decades ago I deduced by purely dimensional considerations a formula for gravitational constant G in terms of p-adic length scale and exponent of Kähler action for CP_2 type vacuum extremal defining the line of generalized Feynman diagram representing graviton [K34]. The prediction was that G should have an entire spectrum of values and approach p-adic length scale squared $L_p^2 = pR_{CP_2}^2$ when the action of the deformed CP_2 type vacuum extremal becomes small: this happens at short length scale limit. In particular, hadronic strings would correspond to strong gravitation limit, and TGD predicts fractally scaled up variants of ordinary hadron physics so that a rich spectrum of strong gravities follows as a prediction. This means that in TGD Universe the the gravitational effects on space-time geometry can be rather dramatic even in condensed matter length scales whereas in GRT the effects are extremely small.

The cosmic honeycomb having voids with size of order 10^8 ly as basic building bricks is one possible quasi-lattice like structure suggested by these considerations. In condensed matter length scales strong gravitation could allow similar quasi-lattice like structures and icosahedral water clusters having tetrahedrons as building bricks could be examples of structures of this kind.

Cosmic honeycombs and their possible counterparts for water clusters modeled as consisting of icosahedral pieces of S^3 bring in mind foams (see `http://tinyurl.com/3a29pz`). Soap film foam is perhaps the most familiar example about foam. Plateau's laws (see `http://tinyurl.com/y7rrstej`) govern the structure of many foams. Mean curvature is constant for each film and physically derives from area minimization assuming constant pressure difference over the film. 3 films meet at angle of 120 degrees along a line known as Plateau border and 4 Plateau borders meet at each vertex at tetrahedral angle of $arcos(-1/3) \simeq 109.47$ degrees (tetrahedral angle is defined as the angle between radii drawn from the center of tetrahedron to its vertices). This suggests spherical tetrahedron as a basic building brick in a model as a honeycomb built from pieces of S^3. Plateau's laws can be derived mathematically for foams, for which films are minimal surfaces (pressure difference vanishes).

The idea that that icosahedral structures assignable to water clusters could define a geometric representation of some kind of code is very intriguing. Genetic code is of course the code that comes first in mind. The observation that the number of faces of tetrahedron (icosahedron) is 4 (20) raises the question whether genetic code might have a geometric representation and the following piece of text is inspired by this question. In TGD framework also a second code emerges: I have christened it memetic code [K23]. Also memetic code could have a geometric realization. Another purely TGD-based notion is that of dark DNA allowing to assign the states of dark protons with DNA, RNA, tRNA and amino-acids and to predict correctly the numbers of DNA codons coding for a given amino-acid in vertebrate genetic code [L2].

In the following some observations suggesting that this kind of geometric representation might exist are first discussed. After that a proposal for how genetic and memetic codes could be realized geometrically is considered.

9.6.1 The Notions Of Memetic Code And Dark Genetic Code

Before going to the topic two TGD inspired concepts must be introduced, namely the notions of memetic code and dark genetic code. From the perspective of standard biology the talk about codes in plural might sound highly speculative. If one takes serious the analogy of living matter with a computing system, it becomes easier to imagine that genetic code could have generalizations and that these codes could have several representations just as computers use an almost unlimited number of different languages. Living matter would in this picture consist of sub-systems emulating each other just as ordinary computers do.

The notion of memetic code

The notion of memetic code introduced for more than 20 years ago allows to interpret the sequences of 21 DNA codons as memetic codons [K23]. The starting point is so called Combinatorial Hierarchy [A23]. Mersenne integers are defined as numbers $M_n = 2^n - 1$. For some values of n, which belong to a subset of primes, one obtains Mersenne primes. In particular the lowest members in the hierarchy defined by the recursive formula $M(n+1) = M_{M(n)}$ with $M(1) = 1$, one obtains the sequence $M(1) = 1$, $M(2) = 3$, $M(3) = 7$, $M(4) = 127$, $M(5) = 2^{127} - 1$, ... All the explicitly listed Mersenne integers $M(n)$, $n > 1$, are Mersenne primes. An unproven conjecture by Hilbert is that all numbers $M(n)$, $n > 1$ in the sequence are Mersenne primes.

What makes this sequence so interesting is that the $M(n) + 1$ as a power of 2 defines the number of elements for a Boolean algebra. One can say that in a structure with $M(n)$ elements one has thrown single element out from the Boolean algebra. This procedure is natural if Boolean algebra is represented as subsets of a set: the subset which is empty is not realizable physically and must be thrown out. One can say that Combinatorial Hierarchy corresponds to an abstraction hierarchy with levels consisting of statements, statements about statements, statements about.... The geometric analog of this hierarchy would be a fractal structure consisting of geometric objects consisting of points, geometric objects consisting of points replaced with geometric objects, ... Something like this one might expect in living systems.

Furthermore, in Boolean algebra each element has negation and only half of the elements can represent statements, which are simultaneously true. Therefore for a Boolean algebra with 2^n elements only 2^{n-1} elements can represent mutually consistent truths, "axioms". For the Combinatorial Hierarchy the numbers of "axioms" would be $1, 2, 4, 64, 2^{126}, ...$ At the third level one obtains the number 4 of DNA nucleotides, at the next level the number 64 of DNA codons, and at the next level one obtains the number $(2^6)^{21} = 2^{126}$ of DNA sequences obtained from 21 DNA codons. This led to the proposal that there might exist a hierarchy of analogs of the genetic code and that the highest physically realized code in the sequence could be "memetic code" assignable to M_{127}.

The notions of dark nucleus and dark genetic code

The notions of dark nucleus and dark genetic code belong to the most speculative ideas of TGD inspired quantum biology. The original motivation for the notion of dark proton came from the observations suggesting that in atto-second time scale 1/4: th of protons of water molecules are dark in the sense that are not visible in electron scattering and neutron diffraction [D9, D7, D12].

The proposed TGD-based interpretation is that the protons are dark in the sense of having large value of effective Planck constant assignable to their magnetic body [L2]. The varying fraction of dark protons could explain the rich spectrum of anomalous temperature and pressure dependences of many observables related to water.

A model for dark nucleons as consisting of 3 dark quarks leads to a completely unexpected connection with genetic code. One can group the states of the dark nucleon (proton) to groups such that these groups correspond to DNA, mRNA, tRNA, and amino-acids and there is a natural map realizing vertebrate genetic code in the sense that the numbers of dark DNA codons mapped to a given dark amino-acid is the same as for vertebrate genetic code.

The recent work of Persinger's group [J14, J15, J16] combined with the observation of Hu and Wu [J20] that the magnetic interaction energy between protons assigned to the opposite sides of cell membrane corresponds to frequency in EEG range led to the conjecture that the pair of cell membrane lipid layers is accompanied by a pair of dark proton strings analogous to DNA double

strand and indeed representing double DNA strand. There is also a close connection with the model of DNA as topological quantum computer [K17]: in this model magnetic flux tubes connecting nucleotide with lipids are responsible for braiding defining the quantum computer programs.

9.6.2 Could The Faces Of Tetrahedron Correspond To The Four DNA Nucleotides?

Consider first the intriguing observations suggesting that tetrahedral and icosahedral geometries relate to genetic code and its generalization to memetic code [K23]

1. The opening solid angle for each of the 20 tetrahedrons in S^3 icosahedron is $\Psi = 4\pi/20$. On the other hand, in DNA strand this angle corresponds in a good approximation to the twist angle for a single nucleotide from the fact that 30 DNA nucleotides (10 codons corresponds to twist angle of 6π (and to a length of 10 nm for DNA strand). For twist angle of 2π the number of nucleotides is not divisible by 3 (integer number of codons). This could be seen as a hint that S^3 icosahedral water clusters are biologically important.

2. Tetrahedron has 4 faces. Could they somehow correspond to the 4 DNA nucleotide? In order to distinguish between codons one must be able to distinguish between the faces of the tetrahedra - mark them - , to assign to given face a unique DNA, and to select one of the faces of tetrahedron - to "activate" it. In the case of DNA double strand this could mean that two of the faces of a given tetrahedron are glued to the predecessor and successor of the nucleotide in the DNA strand. The third face would be paired with conjugate strand by hydrogen bonds so that one open face would remain and would represent DNA nucleotide.

   The marking of the faces of the S^3 tetrahedron would require a breaking of $SO(3)$ symmetry. Symmetry breaking could take place when one looks the tetrahedron in E^3 geometry. One could say that $SO(4)$ symmetry of S^3 geometry breaks the $SO(3) \times T^3$ symmetry of E^3 (emergence of high space-time symmetry is not consistent with high imbedding space symmetry). For instance, the faces of the tetrahedron could have different areas in E^3 metric. The breaking of symmetries could be due to the shift of the S^3 tetrahedron from North Pole of S^3 to some other point, and due to the breaking of translational invariance of E^3 for S^3 tetrahedron. The external face of an icosahedral tetrahedron can be distinguished from the other three faces which are internal even without the breaking of $SO(3)$ symmetry (only breaking of $SO(4)$ symmetry of S^3).

9.6.3 Could The 20 Outer Faces/Tetrahedrons Of The Icosahedron Correspond To Amino-Acids?

S^3 icosahedron has 20 faces. Could they somehow correspond to 20 different amino-acids? To achieve this two conditions must be satisfied.

1. One must be able to distinguish between the outer faces of the icosahedron so that one can associate to a given face only single amino-acid. As already explained, symmetry breaking allowing to distinguish between the faces is possible in E^3 geometry if the S^3 icosahedron is moved from the origin of S^3 to some other point.

   For instance, the areas of the faces could be different and if the amino-acid is glued only to the face which it "fits" (recall the analogy with lock and key mechanism) one would have the desired 1-1 correspondence with amino-acids and icosahedrons. The outcome could be that only single amino-acid can be glued to a given face. Note that magnetic flux tubes could realize the correspondence between amino-acids and icosahedral outer faces in very concrete manner: this mechanism is proposed as a general mechanism of bio-catalysis making it possible for two reacting molecules to find each other in the thick molecular soup [K17, K14].

2. One must also be able to "activate" a given face, perhaps by gluing something to it. This "something" could be amino-acid but also something else, say additional tetrahedron representing a genetic codon.

Dark DNA codon corresponds to dark proton identified as 3-quark state. Could this 3-quark state have a geometric representation? The decomposition of icosahedral surface to triangles suggests that triangle is a natural geometric object for DNA, and in the sequel a geometric model for dark DNA codons based on a repeated division of equilateral triangle to equilateral triangles is considered. One must however keep in mind that this kind of representation might not be necessary. It is enough to assume single dark proton per each tetrahedral building brick of icosahedron. Dark protons would in turn be connected to nuclear string.

9.6.4 Icosahedral Realization Of The Memetic Code?

In the presence of symmetry breaking allowing to distinguish between the 20 icosahedral tetrahedrons the external faces of the icosahedron can be in 1-1 correspondence with amino-acids. One can consider even more ambitious option. The icosahedron + tetrahedron structures with 20 icosahedral tetrahedrons plus 1 tetrahedron glued to some icosahedral face could be perhaps interpreted as memetic codons if each tetrahedron represents a genetic codon. A crucially important constraint is that the icosahedral tetrahedrons have a unique linear ordering.

These memetic codons could be also associated with real amino-acids if a given amino-acid can attach only to single face of the icosahedron and there is a mechanism which selects which face is "active". This particular amino-acid would be naturally coded by the 21^{st} DNA codon at the surface of the icosahedron so that one would kill to flies with single blow obtaining both the a representation of memetic codons and assign to the 21^{st} DNA codon corresponding amino-acid. If so, water clusters could represent immense amount of dark biological information.

How could one realize dark memetic codons as dark nuclei? The obvious possibility is as strings of 21 dark protons: in this case the linear ordering of protons would be essential for the realization of the code. A realization inspired by the conventional nuclear physics framework leads naturally to the icosahedral structure.

1. A nucleus carrying 20 protons or neutrons is a magic nucleus (exceptionally stable). For instance, the biologically important ion Ca^{++} corresponds to double magic nucleus has 20 protons and 20 neutrons. Also neutrons are present in ordinary nuclei, and I have proposed that protons and neutrons could correspond to different space-time sheets: perhaps these space-time sheets could correspond to Northern and Southern hemispheres of S^3.

2. The information about the ordering of dark nucleons is not lost if icosahedral nucleus + single proton is obtained by a convolution of a dark proton nuclear string. The icosahedral core of S^3 icosahedral dark nucleus consisting of 20 dark protonic tetrahedra would be magic and analogous to a closed shell of an atom.

   From the net representation (see `http://tinyurl.com/yatsguy5`) of icosahedron obtained by cutting the icosahedron open, it is clear that there are at least two paths of this kind but differing only by orientation. Each of them can be regarded as a union of 5 4-triangle paths of the net combining to form a connected triangle path at the surface of icosahedron when appropriate identifications of the edges are made. The step between neighboring triangles corresponds to reflecting with respect to the common edge. Each 4-triangle path corresponds to a path containing vertices of "big" tetrahedron (not one of the twenty tetrahedrons with one vertex at the center of icosahedron) shared also by icosahedron. This sequence corresponds to the orbit of the icosahedral isometry group, which is the alternating group A_5 (60 even permutations of 5 letters) acting transitively so that the orbit visits all triangles at the isosahedral surface. A good guess is that these two oppositely oriented orbits and their images under A_5 define the only manners to fill the icosahedral surface by single path. The number of images is 12 since each of the 12 vertices of icosahedron defines one tetrahedron. Note that this identification for the folded DNA sequence allows also to think that it traverses the surface of the icosahedron rather than filling the entire icosahedron.

3. In chemistry valence electrons dictate the chemistry and in complete analogy with this the 21^{st} dark proton at the surface of the icosahedron would code for the amino-acid attached to it. This icosahedral folding of the nuclear string would be analogous to the folding of protein to a globular shape in its resting state. This folding could indeed characterize the resting

state of dark DNA and when dark DNA becomes active - say during a transcription like process - unfolding would occur. Similar unfolding takes place also for the ordinary DNA.

If each icosahedral tetrahedron corresponds to one particular amino-acid, one can argue that a given tetrahedron can be associated only to those DNA codons which code the amino-acid associated with the tetrahedron. As following arguments show, this correspondence leads to problems.

1. If the genetic code dictates the correspondence between tetrahedra and DNA codons, then the three stopping sign codons cannot be contained by the memetic codons so that memetic code would not be fully realised.

2. The allowed memetic codons would code for sequence of 20 different amino-acids and there would be strong correlations between neighboring amino-acids in the sequence since the DNA sequence would define a non-self-intersection path visiting every triangle at the surface of the icosahedron only once, and a given amino-adic would have as edge neighbors only three amino-acids. If only single sequence is possible as proposed above, then only single amino-adic sequence containing all amino-acids would be allowed and the number of memetic codons coding for it would be product of numbers of codons coding for the 20 amino-acids.

9.6.5 Geometric Representation Of Dark DNA Codons

Could one have a concrete geometric representation for DNA codons and nucleotides in the proposed model? The fact that dark DNA codon consisting of 3 quarks corresponds to triangle (or corresponding icosahedral tetrahedron) is highly suggestive.

1. Icosahedral surface triangle would naturally correspond to a triplet defining DNA codon and the vertices of the triangle to the letters A, T, C, G. This could be achieved geometrically by dividing a given icosahedral surface triangle, call it T, to 4 equilateral triangles T_i, $i = 1, 2, 3, 4$ and assigning the three letters of the codon to the resulting three triangles T_i, $i = 1, 2, 3$, sharing a vertex with T. The inner triangle T_4 would remain unpopulated.

2. How to represent codon geometrically for T and perhaps also the letter A, T, C, G for T_i? One manner to achieve the latter goal is to divide T_i to further equilateral triangles T_{ij}, $j = 1, 2, 3, 4$ and assign A, T, C, G to T_i by some kind of symmetry breaking distinguishing between them geometrically. The dark codon consisting of 3 quarks could select somehow this triangle. The simplest possibility is that the spatial wave function of i^{th} quark of proton is located inside one T_{ij}, $i = 1, 2, 3$, $j = 1, 2, 3, 4$. The connection with quark model of nucleon would be that the quarks are at the vertices of triangle T_i and are connected to the centre of T_i by color flux tubes. Inside T_i the location of quark is inside T_{ij}. An alternative option is that quarks are connected by color flux tubes directly to each other.

A couple of remarks are in order.

1. The model for dark DNA does *not* allow to represent the counterparts of DNA codons as unentangled products of 3-quark states: the states are quantum superpositions of 3-quark states and the decomposition of codon to letters is not possible. This means that DNA codons are "irreducible". One can however deduce correspondence between codons and amino-acids and it corresponds to the vertebrate genetic code. The geometric representation for the codons as mapping of DNA codons to geometric objects however still make sense if the positions of quarks obey the above rule for a given entangled quark triplet.

2. The model for dark DNA [L2] assumes that dark DNA strand is linear so that symmetry breaking of rotational symmetry to SO(2) consisting of rotations around the strand takes place. In the recent situation similar breaking of symmetry must take place and the natural axis is no the axes defined by the normal of the triangle defining dark DNA codon.

3. One can also wonder what might be the geometric counterparts of dark mRNA, tRNA, and amino-acids.

9.6.6 Could Water Clusters Represent Memetic Code?

Could the dark protons realizing dark genetic codons as nuclear strings be associated with water molecules or clusters of them? One can imagine two alternative realizations of the icosahedral memetic codons.

1. It is known that water molecules themselves have tetrahedral structure with 2 lone electron pairs and H_+ nuclei are at the vertices of the tetrahedron (maybe regular S^3 tetrahedron). There is chemical symmetry breaking since the faces come in two types: 2 faces of type $H_+H_+(2e)$ and 2 faces of type $H_+(2e)(2e)$. If the second proton is of the water molecule is dark, a further symmetry breaking takes place and one has faces of 3 types. The symmetry of $H_+H_+(2e)$ faces could be broken if they correspond the two lone electron pairs are located the center of icosahedron and it surface. The chemical symmetry breaking and perhaps also magnetic flux tubes would help to assign to unique amino-acid to one of the tetrahedrons.

   Icosahedron would consists of a folded linear sequence of tetrahedral water molecules - formed perhaps perhaps by hydrogen bonding. The representation of memetic codon as a single icosahedral cluster of 21 water molecules would predict single dark proton per water molecule. Recall that the average in atto-second time scale would be 1/4 dark protons per water molecule. I do not know whether icosahedral clusters of this kind exist.

2. It is however known that known (see `http://tinyurl.com/yb9waklg`) that 14 water molecules indeed combine to form tetrahedral structures (see `http://tinyurl.com/ybl9eqt9` [D9], and that these in turn combine to form icosahedral structures. The size scale of the 14 molecule cluster is nearer to the size scale of single DNA nucleotide so that perhaps this option is more realistic. If these structures provide a representation of memetic codons with tetrahedral structure of 14 water molecules representing single DNA codon or amino-acid, there are 14 water molecules per single dark proton representing dark DNA codon.

9.7 Pythagoras, Music, Sacred Geometry, And Genetic Code

The conscious experiences generated by music demonstrate a fascinating connection between algebra and emotions. How can major and minor scale using different frequency ratios generate so different emotional experiences. This strongly suggests the we experience music as entire time interval, 4-D patterns - rather than time=constant snapshots. Also the ability remember the key and the tension lasting as long as the return to the basic key has not taken place, is example of this. One of the key questions is why octaves - that is powers of 2 of the basic note of the scale - are experienced as equivalent? One can also wonder what is behind consonance and dissonance.

I have already earlier tried to understand music experience and considered some ideas inspired by p-adic numbers fields - such as the idea that Pythagorean scale coming as powers of 3 for the basic note modulo octave equivalence might relate to 3-adicity. Reading of a book titled "Interference: A Grand Scientific Musical Theory" by Richard Merrick [J24] freely available in web (`http://tinyurl.com/8d2hfka`) re-stimulated my interest. In particular, I found the idea about a connection between music scale and harmonies with Platonic solids (3-D "sacred geometry") as highly inspiring. The basic question was whether the 12-tone scale could be mapped to a curve going once through each point of icosahedron having 12 vertices and whether the 20 faces of icosahedron, which are triangles could define the basic chords in 12-tone scale. These curves are known as Hamiltonian cycles and in the case of icosahedron there are 2^{10} of them: those obtained from each other by rotation leaving icosahedron invariant are however equivalent.

A given triangle of icosahedron can contain 0, 1 or 2 edges of the cycle and the numbers of the triangles corresponding to these triangle types classify partially the notion of harmony characterized by the cycle. Quint cycle suggests the identification for the single edge of curve as quint interval so that triangles would represent basic 3-chords of the harmony with 0, 1, or 2 quints.

One can make same questions also for other Platonic solids- tetrahedron (4 vertices), octahedron and cube which are duals of each other and have (6 and 8 vertices respectively, and dodecahedron which is dual of icosahedron having 20 vertices and 12 faces. Arabic music uses half intervals and scales with 19 and 24 notes are used. Could 20-note scale with harmony defined by 5-chords assigned to the pentagons of dodecahedron have some aesthetic appeal? Nowadays it is

possible to develop electronically music based on this kind of scale and this kind of experimentation might be a fascinating intellectual and artistic adventure for a young composer.

I have also played with the idea that the 20 amino-acids could somehow correspond to the 20 triangles of icosahedron. The combination of this idea with the idea of mapping 12-tone scale to a Hamiltonian cycle at icosahedron leads to the question whether amino-acids could be assigned with the equivalence class of Hamiltonian cycles under icosahedral group and whether the geometric shape of cycle could correspond to physical properties of amino-acids [I46]. The identification of 3 basic polar amino-acids with triangles containing no edges of the scale path, 7 polar and acidic polar amino-acids with those containing 2 edges of the scale path, and 10 non-polar amino-acids with triangles containing 1 edge on the scale path is what comes first in mind.

The number of DNAs coding for a given amino-acid [I16] could be also seen as such a physical property. The model for dark nucleons leads to the vertebrate genetic code with correct numbers of DNAs coding for amino-acids. It is not however clear how to interpret DNA codons geometrically.

It however turns out that one can understand only the role of 60 codons in the icosahedral framework. The treatment of the remaining 4 codons and of the well-known 21st and 22nd amino-acids requires the fusion of icosahedral code with tetrahedral code represented geometrically as fusion of icosahedron and tetrahedron along common face which has empty interior and is interpreted as punct coded by stopping codons. In this manner one can satisfy the constraints on the Hamiltonian cycles, and construct explicitly the icosahedral Hamiltonian cycle as (4, 8, 8) cycle whose unique modification gives (4, 11, 7) icosa-tetrahedral cycle. Remarkably, two months after writing the first version of the article I learned that the data needed to calculate the Hamiltonian cycles can be found from web and that (4, 8, 8) cycle allows at least two realizations whereas the original candidate (3, 10, 7) allows no realization with symmetries but could do so with no symmetries.

9.7.1 Could Pythagoras Have Something To Give For The Modern Musicology?

The ideas of Pythagorean school about music were strongly based on the number theory of that time. So called modern approaches tend to seem music scales as cultural phenomena. There are however many reasons to suspect that Pythagorean school might have been much nearer to truth.

Pythagoras and transition from rational numbers to algebraic numbers

Pythagoras was one the greatest ancient mathematicians. The prevailing belief at that was that the world can be described solely in terms rational numbers. During the times of Pythagoras the ancient mathematical consciousness had entered at the verge of a profound revolution: the time had become ripe for the discovery of algebraic numbers expanding rational numbers to an infinite series of algebraic extensions of rationals containing also rational multiples for finite number of algebraic numbers emerging as roots of polynomials with rational coefficients. Euclid introduces square root geometrically as length of the diagonal of square. In ancient India it was discover 800-500 BC, possibly much earlier. Unfortunately, the emergence of Christianity stopped the evolution of mathematics and new progress began at times of Newton when also reformation took place.

The well-known but story (good story but probably not true) tells that a pupil of Pythagoras demonstrated that the diagonal of unit square ($\sqrt{2}$) cannot be rational number and had to pay with his life for the discovery. Pythagoras himself encountered $\sqrt{2}$ through music theory. He asked what is the note exactly in the middle of the of the scale. Modern mathematician would answer half of octave corresponding to the frequency ratio $2^{1/2}$. Algebraic numbers did not however belong to the world of order of Pythagoras and he obtained to a non-satisfactory rational approximation of this number. This was very natural since only rational approximations of algebrais are possible in the experimental approach using only strings with rational number valued lengths. $\sqrt{2}$ represents the interval $C - F_{\#}$ known as tritone and this this interval was associated with devil and its use was denied also by church. Only after reformation $\sqrt{2}$ was accepted and this interval appears repeatedly in the compositions of Bach.

The amazing connections between evolution of mathematics and evolution of the religious beliefs inspires the question whether the evolution of consciousness could at basic level correspond to th evolution of the complexity of the number field behind the dynamics underlying consciousness.

For instance, in TGD framework the vision about physics as generalized number theory allows one can to ask whether the mathematical evolution could have meant quite concretely the emergence of increasingly algebraic extensions of rationals for the coefficients of polynomials describing space-time surfaces serving as space-time correlates of consciousness.

Pythagoras and music

Pythagoras was both mathematician and experimentalist studying the world of musical experience experimentally. String instruments were his tool. The notion of frequency was not know at the time and length of vibrating part of string was the notion used. The experienced equivalence of notes differing by octave was known at that time and octave equivalence was understood as a fundamental symmetry of music manifesting itself as a scaling-by-2 symmetry for the length of a vibrating string.

Pythagoras developed 8 note scale CDEFGAHC (as a matter fact, 7 notes by octave equivalence) as we know as a combination of two scales EFGA and HCDE using octave equivalence and it was established as the official music scale. Pythagorean scale is expressed solely in terms of rational number valued ratios of the string length to that for the basic note of the scale (ratio of frequency to the fundamental).

Pythagorean scale (`http://tinyurl.com/28cu6j`, `http://tinyurl.com/7mc4ut`) is expressed solely in terms of powers of the ratio 3/2 for lengths of vibrating strings correspond to an interval known and complete fifth (C-G). The series of complete fifths (C-G-D-A...) known as progression by fifths gives very nearly 7 octaves but not quite: $(3/2)^{12} \simeq 128+1.75 = 2^7+1.745$. It would have been very natural to build 12-note scale as powers of rational (3/2) or by octave equivalence as powers of 3. The failure to close is very small but people with absolute ear experience the transponation of a melody to different key as dissonant since the frequency ratios do not remain quite same. At the time of Bach (Well tempered Klavier) the equal tempered scale obtained by diving the logarithmic scale to 12 equally long parts emerged and replacing powers of 3/2 with the 12 powers of algebraic number $2^{1/12}$ inside same octave even without octave equivalence emerged.

By octave equivalence Pythagorean scale means that all notes of the scale come in powers of 3 which strongly brings in mind 3-adicity. If one does not use octave equivalence when generalization of p-adicity to q-adicity with $q = 3/2$ is highly suggestive. q-adic numbers do not in general form number field, only an algebra.

Later more complex rational number based representations of scale using octave equivalence have been developed. The expression of the frequency ratios of the notes of the scale in terms of harmonic of fundamental modulo octave equivalence and involving only integers consisting of primes 2, 3, 5 is known as just intonation (`http://tinyurl.com/7mc4ut`).

1. Music and Platonic solids

Pythagoras was also aware of a possible connection between music scales and Platonic solids. Pythagoras is claimed to have discovered tetrahedron, hexahedron (cube) and dodecahedron while octahedron and icosahedron would have been documented by greek mathematician Thaletus two hundred years later. The tetrachord and was assigned with tetrahedron and one and imagined that Pythagorean scale could have been assigned with pair of tetrahedra somehow - cube or octahedron which comes in mind. Note that this would require that basic note and its octave should be regarded as different notes.

These attempts inspire the question whether the mapping music scales to the vertices of Platonic solids could provide insights about music experience. One can also ask whether there might be a mapping of music understood as melodies and chords in some scale to the geometries defined by Platonic solids.

1. Since 12-note scale is used in practically all classical western music and even in atonal music based on 12-note scale, the natural question is whether 12-note scale could be mapped to a connected, closed, non-self-intersecting path on icosahedron going through all 12 vertices and consisting of edges only. Closedness would mean that base note and its octave are identified by octave equivalence.

2. This mathematical problem is well-known and curves of this kind are known as Hamilton cycles and can be defined for any combinatorial structure defined by vertices and faces.

Hamilton proved that Hamiltonian cycles (possibly identifiable as 20-note scale) at dodecahedron is unique module rotations and reflection leaving dodecahedron invariant. Also in the case of tetrahedron and cube the Hamiltonian cycle is unique.

3. For octahedron and icosahedron this is not the case [A14] and there are both cycles containing only faces with at least 1 edge of the path and also cycles containing no faces containing no edges of the path. Numerical experimentation is rather straightforward manner to determine Hamiltonian cycles and $H = 2^{10} = 1024$ cycles can be found. The number of topologically non-equivalent cycles (not transformable to each other by the isometries of icosahedron) is factor of this number. The group of orientation preserving isometries of icosahedron is the alternating group A_5 of 60 even permutations of five letters. The full group of isometries is $G = A_5 \times Z_2$ containing $N = 120$ elements.

4. Some subgroup of G leaves given path invariant and its order must be factor M of N so that topological equivalence class of cycles contains $R = N/M$ elements. The number of topologically non-equivalent cycles in given class with $H(top)$ elements is $N_{tot} = H(top)/R$ so that Rmust be a factor of $H(top)$.

Before continuing it is good so summarize the geometry of icosahedron shortly. There are 20 faces which are triangles, 12 vertices, and 30 edges. From each vertex 5 edges. Therefore the construction of Hamiltonian cycles means that at each vertex on path one must select between four options edges since one cannot return back. This gives $4^{12} = 2^{24} \sim 1.6 \times 10^7$ alternatives to be considered. Therefore the numerical search should be relatively easy. Keeping account of the points already traversed and not allowing self intersections, the actual number of choices is reduced. The construction requires labeling of the vertices of the icosahedron by integers 1, ..., 12 in some manner and defining 12×12 matrix $A(i, j)$ whose element equals to 1 if vertices are neighbours and 0 if not. Only the edges for with $A(i, j) = 1$ holds true are allowed on the path. A concrete representation of icosahedron as a collection of triangles in plane with suitable identifications of certain edges is needed. This helps also to visualize the classification of triangles to three types discussed below. This can be found in the Wikipedia article (see `http://tinyurl.com/ns9aa`).

2. Numbers of different triangles as characterizers of harmony

A possible interpretation for topologically non-equivalent paths is as different notions of harmony.

1. Proceeding in Pythagorean spirit, the neighboring points would naturally correspond to progression by fifths - that is scalings by powers of 3/2 or in equal temperated scale by powers of $2^{7/12}$. This would mean that two subsequent vertices would correspond to quint.

2. The twenty triangles of the icosahedron would naturally correspond to 3-chords. Triangles can contain either 0, 1, or 1 edges of the 12-edge scale path. The triangle containing 3 edges is not possible since it would reside on a self-intersecting path. A triangle containing one edge of path the chord would contain quint which suggest a chord containing basic note, quint and minor or major third. The triangle containing two edges would contain subsequent quints - CDG is one possible example by octave equivalence. If the triangle contains no edges of the path one can say that the chord contains no quints.

   The numbers of triangles classified according to the number of path edges contained by them serves as the first classification criterion for a given harmony characterized by the Hamiltonian cycle (note that one cannot exclude the possibly of non-closed paths since Pythagorean construction of the scale by quints does not yield quite precisely octave as outcome).

Fig 1. There are 3 different types of triangles characterized by the number of edges contained by them. This predicts chords with 0, 1 or 2 quints.
`http://tgdtheory.fi/appfigures/kolmiot.jpg`

Consider now the situation in more detail.

1. The topologically equivalent cycles must have same numbers of faces containing 0, 1, or 2 edges of the Hamiltonian path since isometries do not change these numbers. Let us denotes these numbers by n_0, n_1 and n_2. The total number of faces is 20 so that one has

$$n_0 + n_1 + n_2 = 20 \ .$$

Furthermore, each of the 12 edges on the path is contained by two faces so that by summing over the numbers of edges associated with the faces one obtains twice the number of edges:

$$0 \times n_0 + 1 \times n_1 + 2 \times n_2 = 2 \times 12 = 24 \ .$$

From these constraints one can solve n_0 and n_1 as function of n_2:

$$\begin{aligned} n_0 &= n_2 - 4 \ , \quad n_2 \geq 4 \ , \\ n_1 &= 24 - 2n_2 \ , \quad n_2 \leq 12 \ . \end{aligned}$$

If these integers characterize the topological equivalence completely and if the allowed combinations are realized, one would have 12-4=8 topologically nonequivalent paths. The actual number is $N_{tot} = 2^k$, $k \geq 7$, so that the integers cannot characterize the topology of the path completely.

2. The number of Hamiltonian cycles on icosahedron is known to be 2560 [A3]. Numerical calculations [A9] (`http://tinyurl.com/pmghcwd`) shows that the number of Hamiltonian cyclesw with one edge fixed is $2^{10} = 1024$. Here one regards cycles with different internal orientation as different. This would mean that the sum over the numbers $N(n_2)$ if cycles associated with differ values of n_2 satisfies

$$\sum_{n_2=4}^{12} \sum_i N(n_2, i)) = 2^{10} \ .$$

$N(n_2, i)$ is the number of paths of given topology with fixed n_2. The numbers $N(n_2, i)$ are integers which are factors of $N = 120$ of the order of the isometry group of the icosahedron. The average of $N(n_2, i)$ is $2^7 = 128$.

3. Additional topological invariants characterizing the notion of harmony

The interpretation of amino-acids in terms of 20 triangles of icosahedron interpreted as allowed chords for a given notion of harmony leads to a unique identification of the integers n_i as $(n_0, n_1, n_2) = (3, 10, 7)$. The attempt to interpret this "biological harmony" leads to the identification of additional topological invariants characterizing the notion of harmony. It will be assumed that edges correspond to quints. If they would correspond to half-step the chords would contains 0, 1, or 2 subsequent half-intervals which does not conform with the usual views about harmony. In Pythagorean scale quint corresponds to 3/2 and in equal tempered scale quint corresponds to the algebraic number number $2^{7/12}$.

Above the attention was paid to the properties of the triangles in relation to the Hamiltonian cycle. One can consider also the properties of the edges of the cycle in relation to the two neighboring triangles containing it. Restrict first the attention to the biological harmony characterized by $(n_0, n_1, n_2) = (3, 10, 7)$.

Fig. 2. The edge of the cycle belongs to 2 triangles, which as chords can correspond to 1 resp.2, 1 resp. 1 and 2 resp. 2 quints.
`http://tgdtheory.fi/appfigures/sivut.jpg`

1. Everyone of the 12 quints $C-G$, $C_\# - G_\#$, ... would be contained to neighboring triangles tht is 3-chords containing at least one quint. Denote by p_{12}, p_{11} resp. p_{22} denote the number of edges shared by 1-quint triangle and 2-quint triangle, by 2 1-quint triangles, resp. 2 2-quint triangles. Besides $p_{ij} \geq 0$ one has

$$\sum p_{ij} = 12 \ .$$

since the cycle contains 12 edges. There are $p_{12} + 2p_{11} = n_1$ 1-quint triangles and $(p_{12} + 2p_{22})/2 = n_2$ 2-quint triangles (note double counting responsible for division by two). Altogether this gives

$$\begin{aligned} p_{22} &= 12 - p_{11} - p_{22} \ , \\ p_{22} &= p_{11} + n_2 - \tfrac{n_1}{2} \ , \\ p_{22} &= n_2 - \tfrac{p_{12}}{2} \ . \end{aligned}$$

2. These three Diophantine equations are for integers and would allow for real numbers only single solution and for integers it in the generic case there are no solutions at all. Situation changes if the equations are not independent which can happen if the integers n_i satisfy additional conditions. By subtracting first and second and second and third equation from each other one obtains the consistency condition

$$n_1 = 24 - 2n_2 \ .$$

This condition is however second of the conditions derived earlier so that only two equations, say the first two ones, are independent.

$$\begin{aligned} p_{22} &= p_{11} + n_2 - \tfrac{n_1}{2} \ , \\ p_{22} &= n_2 - \tfrac{p_{12}}{2} \ . \end{aligned}$$

giving

$$\begin{aligned} p_{11} &= (n_1 - p_{12})/2 \ , \\ p_{22} &= p_{11} + n_2 - \tfrac{n_1}{2} = n_2 - \tfrac{p_{12}}{2} \ . \end{aligned} \quad .$$

One must have $0 \leq p_{ij} \leq 12$ and $p_{12} \leq n_1$ from $p_{11} = (n_1 - p_{12})/2$. Here one has $p_{12} \in \{0, 2, ...Min\{12, 2n_2, n_1\}$ so that $Min\{7, n_2 + 1, [n_1/2] + 1\}$ solutions are possible. The condition that the cycle has no self-intersections can forbid some of the solutions.

3. The first guess for the "biological harmony" possibly associated with amino-acids would be $(n_0, n_1, n_2) = (3, 10, 7)$: this if one neglects the presence of 21st and 22th amino-acid also appearing in proteins. It turns out that a more feasible solution fuses tetrahedral code and icosahedral codes with $(n_0, n_1, n_2) = (4, 8, 8)$ giving $(n_0, n_1, n_2) = (4, 11, 7)$ for icosatetrahedral code.

   For instance, $(n_0, n_1, n_2) = (3, 10, 7)$ would give $p_{12} \in \{0, 2, 4, 6, 8, 10\}$, $p_{11} \in \{5, 4, 3, 2, 1, 0\}$, $p_{22} \in \{7, 6, 5, 4, 3, 2\}$ so that one has 6 alternative solutions to these conditions labelled by p_{12}. The number of neighboring triangles containing single quint is even number in the range $[0, 10]$: this brings in mind the possibility that the neighboring single quint triangles correspond to major-minor pairs. Clearly, the integer p_{12} is second topological invariant characterizing harmony.

4. Distribution of different types of edges

Also the distribution of the 12 edges to these 3-types is an invariant characterizing the shape of the curve and thus harmony as isometric invariant.

Fig. 3. There are different distributions of edge types characterized by the neighboring triangles of the edge.
`http://tgdtheory.fi/appfigures/jakauma.jpg`

1. p_{12} 1-1 edges can be chosen in

$$N(1-1, p_{12}) = \begin{pmatrix} 12 \\ p_{12} \end{pmatrix}$$

manners and 1-2 edges in

$$N(1-2,p_{12}) = \begin{pmatrix} 12-p_{12} \\ p_{12} \end{pmatrix}$$

manners. The remaining 2-2 edges can be chosen only in one manner. This gives altogether

$$N(p_{12}) = N(1-1,p_{12}) \times N(1-2,p_{12})$$

manners for given value of p_{12}.

To summarize, one obtains large number of notions of harmony are possible although one cannot expect that the absence of self-intersections does not allow all topologies for the cycle.

Would you come with me to icosadisco?

This map would allow one-to-one map of the notes of any music piece using icosahedral geometry. If octave equivalence is assumed, a given note would be mapped to a fixed vertex of icosahedron at which lamp is turned on and also to the wavelength of the light in question since visible light spans an octave. Chords would correspond to the turning on of lights for a group of icosahedral points. Icosahedrons with size scaled up by two could correspond to octave hierarchy: for practical purposes logarithmic scale implying that icosahedrons have same distance would be natural as in the case of music experience since piano spans 7 octaves and human ear can hear 10 octaves. Church would nowadays allow icosadiscos to use also half octaves to amplify further the audiovisual inferno effect so characteristic for discos. One could also try to realize special effects like glissandos, vibratos and tremolos.

9.7.2 Connection Between Music Molecular Biology?

Music affects directly emotions, and consciousness is one aspect of being living. This raises the question whether the Platonic geometries might have something to do with basic building bricks of life and with genetic code.

Could amino-acids correspond to 3-chords of icosahedral harmony?

The number of amino-acids is 20 and same as the number of triangular faces of icosahedron and the vertices of dodecahedron. I have considered the possibility that the faces of icosahedron could correspond to amino-acids [K17]. Combined with the idea about connection between music scale and icosahedron this inspires the following consideration.

1. For a proper choice of the mapping of the 12-note scale to the surface of icosahedron the 20 triangles could correspond to 20 amino-acids analogous to 3-chords and that the 3 types of 3-chords could correspond to 3 different classes of amino-acids. One can of course consider also the mapping of amino-acids to a unique sequence of 20 vertices of dodecahedron representing 20-note scale or 20-chord scale and replacement of the 3-chords defining the harmony with 12 5-chords.

2. Amino-acids are characterized by the non-constant side chain and these can be classified to three categories: basic polar, non-polar, and polar (`http://tinyurl.com/ycvm6yjs`). The numbers of amino-acids in these classes are $a_0 = 3$, $a_1 = 10$, $a_2 = 7$. Could these classes correspond to the numbers n_i characterizing partially some topological equivalence classes of Hamiltonian paths in icosahedron? There is indeed a candidate: $a_0 = n_0 = 3$, $a_1 = n_1 = 10$, $a_2 = n_2 = 7$ satisfies the conditions discussed above. 3 basic polar amino-acids would correspond to the triangles with no edges on the Hamiltonian cycle, 10 non-polar amino-acids to triangles containing one edge, and 7 acidic polar and polar amino-acids to those containing two edges. One can criticize the combination of polar and acidic polar amino-acids in the same class. One can also classify amino-acids to positively charged (3), negatively charged (2) and neutral (15) ones. In this case the condition is however not satisfied. Thus the proposal survives the first test - assuming of a course that these Hamiltonian cycles exist! This has not been proven and would require numerical calculations.

Table 9.3: The number of amino acids N associated with a given degeneracy d telling the number of DNA triplets mapped to the amino acid in the genetic code. The degeneracies are always smaller than 7 as predicted by the proposed explanation of the Genetic Code.

d	6	4	3	2	1
N	3	5	2	9	2

3. As found Hamiltonian paths have also other topological characteristics and they could correspond to physical characteristics and it would be interesting to see what theyh are. To proceed further one should find the total number of the Hamiltonian paths with $n_2 = 7$ and identify the isometries of different topological equivalence class having $n_2 = 7$.

Amino-acid sequences would correspond to sequences of 3-chords. The translation of mRNA of gene to amino-acid sequence would be analogous to the playing of a record. The ribosome complex would be the record player, the amino-acid sequence would be the music, and mRNA would be the record. Hence genes would define a collection of records characterizing the organism.

Can one understand genetic code?

What remains open is the interpretation of genetic code [I16]. DNA triplets would correspond naturally to triangles but why their number is 64 instead of 20. They would be obviously the analogs of written notes: why several notes would correspond to the same chord?

1. Could different DNA triplets coding for the same amino-acid correspond to various octaves of the chord? The most natural expectation would be that the number of octaves so that one would have 3 DNAs would code single amino-acid and stopping codon would correspond to 4 DNAs. It is difficult to understand why some 3-chords could correspond to 6 octaves and one of them only one.

2. Could the degeneracy correspond to the ordering of the notes of the 3-chord? For the 3-chords there are 6 general orderings and 3 cyclic orderings modulo octave equivalence and characterizing by the choice of the lowest note. The simplest assumption would be that the allowed orderings - degeneracies - are characterized by a subgroup of the cyclic group S_3 yielding the allowed permutations of the notes of the chord. The subgroup orders for S_3 are 1, 2, 3, and 6. The allowed degeneracies are 6, 4, 3, 2, and 1 so that this identification fails for $D = 4$.

3. Could the different correspondences between DNA codons and amino-acids correspond to the different topological equivalence classes of $n_2 = 7$ Hamiltonian cycles. This does not seem to be the case. The number of different DNA-amino-acid correspondences obtained by choosing one representative from the set of DNAs coding for a given amino-acid (and not stopping sign) is the product of the numbers $D(a_i)$ coding amino-acid a_i. From **Table 9.3** this number is given by $6^3 \times 4^5 \times 3^1 \times 2^9 \times 1^2 = 3^4 \times 2^{21}$ and clearly much larger than $N = 2^{10}$.

4. Could the different codons coding for codon code for some additional information so that amino-acids would in some aspect differ from each other although they are chemically identical? Here the magnetic body of amino-acid is a natural candidate. This would suggest that the folding pattern of the protein depends on what DNA sequence codes it. This information might be analogous to the information contained by notes besides the frequencies. Durations of notes corresponds is the most important information of this kind: the only candidate for this kind of information is the value of $h_{eff} = n \times h$ associated with the amino-acid magnetic body determining its size scale. Magnetic fields strength could be also code by DNA codon besides amino-acid.

Second question concerns genetic code itself. Could the DNA degeneracies $D(a_i)$ (number of DNAs coding for amino-acid a_i) be understood group theoretically in terms of icosahedral geometry? The triangles of the icosahedron are mapped the triangles under the isometries.

1. One can start by looking the **Table 9.3** for the genetic code telling the number $N(d)$ of amino-acids coded by d DNA codons. One finds that one can divide DNAs to three groups containing $n = 20$, $n = 20$, resp. $n = 21$ codons.

   (a) There are 3 amino-acids codes by 6 codons and 2 amino-acids coded by 1 DNA: $3 \times 6 + 2 \times 1 = 20$ codons altogether.
   Note: One could also consider 1 amino-acid coded by 2 codons instead of 2 coded by 1 codon $3 \times 6 + 1 \times 2 = 20$.

   (b) There are 5 amino-acids coded by 4 codons making $5 \times 4 = 20$ codons altogether.

   (c) There are 9 amino-acids coded by 2 codons and 1 by 3 codons making $9 \times 2 + 1 \times 3 = 21$ codons.
   Note: One could also consider the decomposition $8 \times 2 + 2 \times 1 + 1 \times 3 = 21$ codons implied if 1 amino-acid is coded by 2 codons in the first group.

This makes 61 codons. There are however 64 codons and 3 codons code for stopping of the translation counted as punct in the table.

1. This would suggest the division to 60 + 4 codons. The identification of additional 4 codons and corresponding amino-acids is not so straightforward as one might first think. 3 of the 4 additional codons could code for punct (Ile) and 1 of them to Ile (empty amino-acid).

2. What suggests itself strongly is a decomposition of codons in 3 different manners. 3 groups of 6 codons plus 2 groups of 1 codon (1 group of 2 codons), 5 groups of 4 codons, and 10 groups of 2 codons (9 groups of 2 codons plus plus 2 groups of 1 codon).

This kind of decompositions are induced by the action on the triangles of icosahedron by three subgroups of the isometry group $A_5 \times Z_2$ of the icosahedron having $120 = 2 \times 2 \times 2 \times 2 \times 3 \times 5$ elements and subgroups for which number of elements can be any divisor of the order. The orbit associated with a subgroup with n elements has at most n triangles at its orbit. This allows immediately to deduce the values of n possibly explaining the genetic code in the proposed manner.

1. The 3 amino-acids coded by 6 codons must correspond to $n = 6$. This subgroup must have also two 1-element orbits (1 2-element orbit): in other words, 2 triangles must be its fixed points (form its orbit).

   (a) The non-abelian group S_3 permuting the vertices of is the first candidate for the subgroup in question. The triangles at the opposite sides of the icosahedron remain invariant under these permutations. S_3 however has two orbit consisting of 3 triangles which are "wall neighbours" of the triangles which remains fixed.

   (b) Second candidate is the abelian group $\tilde{Z}_2 \times Z_3$. Here Z_3 permutes the vertices of triangle and $\tilde{Z}_2$ is generated by a reflection of the triangle to opposite side of icosahedron followed by a rotation by π. This group has 3 orbits consisting of 6 triangles and 1 orbit consisting of 2 triangles (the triangles at opposite side of icosahedron). This group seems to be the only working candidate for the subgroup in question.

2. The 5 amino-acids coded by 4 codons must correspond to $n = 4$ and therefore to $\tilde{Z}_2 \times Z_2$. This is indeed subgroup of icosahedral group which permutes triangles at the vertices of inscribed tetrahedron. Now all orbits contain 4 triangles and one must have 5 orbits, which are obtained by acting on the 5 triangles emanating from a given vertex. Note that also Z_5 is subgroup of icosahedral group: this would give a variant of code with 4 amino-acids coded by 5 codons if it were possible to satisfy additional consistency conditions.

3. Consider next the group consisting of 9 amino-acids coded by 2 codons and Ile ("empty" amino-acid) coded by 3 codons. Since only the $\tilde{Z}_2 \times Z_3$ option works, this leaves 9 amino-acids coded by 2 codons and 2 amino-acids coded by 1 codon. The subgroup must correspond to $n = 2$ and thus Z_2 acting on fixed triangle and leaving it and its $\tilde{Z}_2$ image invariant. One has 9 2-triangle orbits and two single triangle orbits corresponding to the triangles at opposite sides of the icosahedron. The 9 amino-acids coded by 2 codons are all real or 8 of them are real and 1 corresponds to "empty amino-acid" coded by two codons.

3-element orbits are lacking and this forces to consider a fusion of of icosahedral code with tetrahedral code having common "empty-acid" - common triangle of icosahedron and tetrahedron) coded by 2 icosahedral codons and 1 tetrahedral codon. Ile would be coded by 3 codons assignable to the orbit of Z_3 subgroup of tetrahedral symmetry group S_3 and would be associated with the tetrahedron. This would predict 2 additional amino-acids which could be understood by taking into account 21st and 22nd amino-acid (Sec and Pyl [I46]).

The Hamiltonian cycle is not explicitly involved with the proposed argument. Some property of the cycle respected by the allowed isometries might bring in this dependence. In Pythagorean spirit one might ask whether the allowed isometries could leave the Hamiltonian cycle invariant but move the vertices along it and induce a mapping of faces to each other.

The amino-acid triangle at given orbit cannot be chosen freely. The choices of amino-acid triangles associated with the three groups of 20 DNAs must be different and this gives geometric conditions for the choices of the three subgroups and one can hope that the assignment of amino-acid toa given triangle is fixed about from rotational symmetries.

Does the understanding of stopping codons and 21st and 22nd amino-acids require fusion of tetrahedral and icosahedral codes?

Several questions remain. Could one also understand the additional 4 DNA codons? Could one understand also how one of them codes amino-acid (Ile) instead of stopping codon? Can one related additional codons to music?

1. Attachment of tetrahedron to icosahedron as extension if icosahedral code

The attachment of tetrahedron to icosahedron allows to understand both stopping codons and punct as well as the 21st and 22nd amino-acids geometrically.

1. Something is clearly added to the geometric structure, when at least 4 additional DNA codons and 2 amino-acids are brought in. The new codons could represent orbits of faces of Platonic solid with 4 faces representing punct and 3 real amino-acids: say Ile, Pyl, and Sec. The 4 faces should be triangles and actually must be so since tetrahedron is the only Platonic solid having 4 faces and its faces are indeed triangles. Tetrahedron has symmetry group S_3 containing Z_3 and Z_2as subgroups. Z_3 leaves one of the tetrahedral triangles invariant so that one has two orbits consisting of 1 and 3 triangles respectively.

2. One amino-acid is coded by 3 rather than only 2 codons. One can indeed understand this symmetry breaking geometrically. Suppose that the tetrahedron is attached on icosahedron along one of its triangular faces and that this icosahedral face corresponds either Ile or punct coded by 2 icosahedral codons. This face remains also fixed by the action of Z_3 and S_3 subgroups of tetrahedron so that 1 tetrahedral codon codes also for the amino-acid in question.

3. The three other faces of tetrahedron r should bring in three additional amino-acids. punct could correspond to either one of them or to the common base triangle which is indeed geometrically in unique position. One could even demand that this triangle is "empty" so that tetra-icosahedron would be non-singular continuous manifold. The 3-triangle orbit outside the icosahedron would correspond to Ile and base triangle to empty amino-acid. Base triangle would be coded by 1 tetrahedral codon plus 2 icosahedral codons.

4. One of the outsider triangles would thus corresponds to Ile but two other triangles to two new exotic amino-acids. In some species there indeed are 21st and 22nd amino-acids (selenocysteine (Sec) and pyrrolysine (Pyl), `http://tinyurl.com/2byr2b`) with sulphur replaced with selene. This modification does not change the polarity properties of cys and lys: cys and thus Sec is non-polar and lys and thus Pyl is basic polar implying $(n_0, n_1, n_2) = (3, 10, 7) \to (4, 11, 7)$.

5. The two other outsider tetrahedral triangles could correspond to the orbits of Z_2 subgroup of S_3 acting as reflection with respect to median of the base triangle. Outside faces form orbits consisting of 1 triangle and 2-triangles. Could these orbits correspond to 21st and 22nd amino-acids coded by 1 and 2 exotic codons?

Since Ile and Sec are non-polar, they can correspond to 1-quint triangles at tetrahedron. 2-quint triangle cannot however correspond to Pyl which should correspond 0-quint triangle. Hence the 0-quint triangle must be at the isosahedron and the 2-quint triangle must correspond to basic polar amino-acid coded by single codon: Tyr is the only possible option). Hence the tetrahedral amino-acids are fixed to be Ile, Sec, and Tyr and Pyl must correspond to some icosahedral amino-acid.

The second implication is that the icosahedral Hamiltonian cycle from which the icosatetrahedral cycle is obtained as deformation must correspond to (4, 8, 8) since one cannot deform (3, 7, 10) in such a manner that one would obtain one additional 0-quint triangle.

It should be noticed that the 2 exotic amino-acids are coded by codons which are usually interpreted as stopping codons. Something must however distinguish between standard and exotic codings. Is it "context" giving different meaning for codons and perhaps characterized by different magnetic bodies of codons [K62] ?

Fig. 4. tetra-icosahedron is obtained by attaching tetrahedron along one of its faces to icosahedron. The resulting structure is topological manifold if the common face is replaced with empty set and it is natural to identify it as punct.
`http://tgdtheory.fi/appfigures/tetra-icosahedron.jpg`

2. How the icosahedral Hamiltonian cycle is modified?

The properties of exotic amino-acids give constraints on how the modification of the Hamiltonian cycle should be carried out. The naive expectation that the outer triangles of added tetrahedron correspond to punct and 2 exotic amino-acids is not correct. A more appropriate interpretation is as a fusion of icosahedral and tetrahedral codes having common "empty amino-acid" coded 2 icosahedral and 1 tetrahedral 1 stopping codons respectively and obtained by gluing these Platonic solids together along the triangle representing the "empty" amino-acid. That the common triangle corresponds to punct means geometrically that its interior is not included so that the resulting structure is continuous manifold having topology of sphere.

Consider now the detailed construction.

1. One should be able to modify the icosahedral Hamiltonian cycle so that the numbers (n_0, n_1, n_2) charactering icosahedral cycle change so that they conform with the properties of the two exotic amino-acids. Selenocystein (Sec) is nonpolar like cys and pyrrolysine (Pyl) basic polar like Lys so that $(4, 11, 7)$ seems to be the correct characterization for the extended system. One must have $(n_0, n_1, n_2) \to (4, 11, 7)$.

2. One must visit the additional vertex, which means the replacement of one edge from the base triangle with wedge visiting the additional vertex. There are several cases to be considered depending on whether the base triangle is 1-quint triangle or 2-quint triangle, and what is the type of the edge replaced with wedge. One can even consider the possibility that the modified cycle does not remain closed.

   If the icosahedral cycle has $(n_0, n_1, n_2) = (3, 10, 7)$, the value of n_2 is not changed in the construction. For a closed cycle edge is replaced with wedge and the only manner to preserve the value of n_2 is that the process producing 1 tetrahedral 2-quint triangle transforms 1 icosahedral 2-quint triangle identified as base triangle to 1-quint triangle. If the replaced edge of base triangle is of type 2-1, one has $n_1 \to n_1 + 1$ since one icosahedral 1-quint triangle disappears and 2 tetrahedral ones appear. Icosahedral n_0 increases by 1 units. Hence the condition $(3, 10, 7) \to (4, 11, 7)$ would be met. It however seems that $(4, 8, 8)$ is more promising starting cycle as the argument below shows.

3. The number options is at most the number n_2 of 2-quint triangles serving as candidates for punct. An additional condition comes from the requirement that replaced edge is of type 2-1.

Fig. 4. tetra-icosahedron is obtained by attaching tetrahedron along one of its faces to icosahedron. The resulting structure is topological manifold if the common face is replaced with

empty set and it is natural to identify it as punct.

Fig. 5. The modification of $(4,4,8)$ icosahedral Hamiltonian cycle consistent with the constraints that icosatetrahedral cycle corresponds to $(4,11,7)$ consistent the classification of amino-acids in three classes.
http://tgdtheory.fi/appfigures/tetraikosahedroni.jpg

3. Direct construction of Hamiltonian cycle corresponding to bio-harmony

Consider bio-harmony as an example about Hamiltonian cycle taking seriously the extension of the genetic code. I have made very many unsuccessful triangles starting from the assumption that icosahedral cycle satisfies $(n_0, n_1, n_2) = (3, 10, 7)$, and the following proposal starts from different icosahedral cycle. The following is just a trial, which should be checked by a direct calculation.

1. The most obvious guess for the cycle to be modified to cycle at tetra-icosahedron having $(n_0, n_1, n_2) = (4, 11, 7)$ (the triangle corresponding to "empty" amino-acid (to be called punct) is not counted) is $(n_1, n_2, n_3) = (3, 10, 7)$. I have not found cycle with these characteristics.

2. It seems however possible to find cycle with $(n_1, n_2, n_3) = (4, 8, 8)$. From this can obtain the desired kind of extended cycle if the "empty" triangle is 2-quint triangle and the edge replaced with the wedge is of type 2-2. The replacement of icosahedral edge eliminates two icosahedral 2-quint triangles and generates 1 tetrahedral 2-quint triangle giving $n_2 \to n_2 - 2 + 1 = n_2 - 1 = 7$. The disappearance of the icosahedral edge generates two icosahedral 1-quint triangles of which second one corresponds to empty amino-acid and is not counted and 2 tetrahedral 1-quint triangles giving $n_1 \to n_1 + 3 = 11$.

The figure below represents the construction of cycle $(4, 8, 8,)$. The icosahedron is constructed from regions $P(I)$ glued to the triangle t along one edge each. The arrows indicate that the one pair of edges of type 1 and 2, 1 and 3 and 3 and 2 are identified. Also the long edges I of T are identified with pairs of subsequent edges of $P(I)$ as the arrows indicate.

Fig. 6. A proposal for a Hamilton cycle realizing bio-harmony $(n_1, n_2, n_3) = (4, 8, 8)$ allowing extension to cycle $(3, 11, 7)$ on tetra-icosahedron. Circled "0", "1" and "2" indicates whether a given small triangle is 0-, 1-, or 2-quint triangle. It is relatively easy to verify that the condition $(n_1, n_2, n_3) = (4, 8, 8)$ for bio-harmony is satisfied.
http://tgdtheory.fi/appfigures/aikosahedroni.jpg

4. Stopping codons and music

What could be the interpretation of the attached tetrahedron in terms of music harmony?

The attachment of tetrahedron means addition of an additional note to the 12-note scale. The scale constructed in Pythagorean spirit identifying quint as scaling by 3/2 contains the 12th note as scaling by $(3/2)^{12}$ of the basic frequency modulo octave equivalence. This is slightly more than scaling by 2^7 so that exact octave is not obtained. The attempt to solve this problem has lead to scales in which one allows a pair of notes with a very small interval between them - say $G_{\#}$ and A_b being regarded as different notes.

This suggests that the outsider vertex of the attached tetrahedron corresponds to a note very near to some note of the 12-note scale. Which note is in question depends on which of the 10 1-quint triangles is chosen as the base triangle. This is expected to imply additional refinements to the notion of bio-harmony. 2 or three additional 3-chords emerge depending on whether empty amino-acid is interpreted as a real chord.

5. Geometric description of DNA-amino-acid correspondence

The mathematical structure which suggests itself is already familiar from some earlier attempts to understand genetic code [K23]. For icosahedral part of code one would have a discrete bundle structure with 20 amino-acids defining the base space and codons coding the amino-acid forming the fiber. The number of points in the fiber above based point depends on base point and

is the number of codons coding the corresponding amino-acid. A discrete variant of singular fiber bundle structure would be in question.

Forgetting for a moment the 4 troublesome codons, the bundle would be the union of the orbits associated with groups S_3, Z_4 and Z_2 of icosahedral group, and the base would consist of 20 amino-acids, one for each orbit. The point of orbit must be selected so that the selections for orbits of two different groups are different.

The addition of the additional codons, punct and two exotic amino-acids would mean gluing of tetrahedron along one of its faces to icosahedron. This would induce extension of the singular bundle like structure. To each of the new faces one would attach the orbit of triangles representing the codons coding for the corresponding amino-acid.

To sum up, in its strongest form the model makes several purely mathematical predictions, which could easily kill it.

1. The identification of the 3-chords assignable to the triangles of the icosahedron.

2. The existence of $n_2 = 7$ Hamiltonian cycle requiring however the lumping of acidic polar and polar amino-acids in the same class.

How could one construct the Hamiltonian cycles on icosahedron with a minimal computational work?

Although the construction of Hamiltonian cycles is known to be an NP hard problem for a general graph, one can hope that in case of Platonic solids having high symmetries, a direct construction instead of straightforward numerical search might work. The followingis a proposal for how one might proceeed. It relies on paper model for icosahedron.

1. The basic observation about one can get convinced by using paper model is following. One can decompose the surface of icosahedron to three regions $P(I)$, $I = 1, 2, 3$, with pentagonal boundary and containing 5 triangles emanating from center vertex plus one big triangle T containing 4 pentagonal triangles and one lonely small triangle t opposite to it. These 5 regions span the surface of icosahedron. There is clearly a symmetry breaking and there is great temptation to assume that t corresponds to the triangle along which the tetrahedron is glued to the icosahedron in the model of genetic code realizing the modification of $(3, 7, 10)$ bio-harmony.

2. The Hamiltonian cycle must visit at the centers of each $P(I)$: one enters pentagonal region $P(I)$, $I = 1, 2, 3$ along one of the five interior edges beginning at pentagonal vertex $a_{I,i}$, $i = 1, .., 5$ and leaves it along second edge ending at vertex $b_{I,j}$, $j \neq 5$. One can call these edges interior edges. The edges at boundaries of $P(I)$ can be called boundary edges. Interior edge can correspond to $|i - j| = 0, 1$ or $i - j > 1$. For $|i - j| = 1$ the interior edge gives rise to 2-quint triangle. For $i - j = 0$ there is no boundary edge after $b_(I, j)$.

3. Pentagonal boundary edges come in three types. 2 of them are shared with T, 1 with t opposite to it, and 2 with another pentagonal region $P(I)$. One can label $P(i)$ in such a manner that the $P(I)$ shares two boundary edges with $P(I + 1)$.

   The boundary edges of small and big triangle are boundary edges of the 3 pentagonal regions so that they are not counted separately.

4. One can assume that the cycles begins from a vertex of T. Since the cycle is closed it returns back to this vertex. The last edge is either at the boundary of T or goes through one or two edges of the small interior triangle of T so that this triangle is either 0-, 1- or 2-quint triangle.

   t can be 0-, 1-, or 2-quint triangle.

5. The total number of the interior edges inside the 3 pentagonal regions is $3 \times 2 = 6$ so that 6 remaining edges must be boundary edges associated with $P(I)$ and interior edges of T: otherwise one would visit some pentagonal center twice and self-intersection would occur. The boundary edges associated with t and T are boundary edges of $P(I)$, $I = 1, 2, 3$

6. At the vertex $b_(I,j)$ of pentagonal region one must turn right or left and move along the boundary edge. One can move at most $n_I = 4 - j$ boundary edges along the pentagonal boundary in clockwise direction and $n_I = j-2$ edges in counterclockwise direction (clockwise is the direction in which the index labelling 5 vertices grows). The maximum number of boundary edges is 3 and obtained for $j - i \pm 1$.

7. The condition $\sum n_I + n(T) = 6$, where $n(T) = 1, 2$ is the number of interior edges of T, holds true so that one has $\sum n(I) \equiv n_{tot} \in \{4, 5\}$. The numbers and types (shared with pentagon, T, or t) of the boundary edges of $P(I)$, the differences $\Delta(I) = j_I - i_I$, the number of edges in t and the number of interior edges of T characterize the Hamiltonian cycle besides the condition that it is closed. The closedness condition seems possible to satisfy. One must enter big triangle through one of the vertices of T and this vertex is uniqely determined once the third pentagon is fixed. One can therefore hope that the construction gives directly all the Hamiltonian cycles with relatively small amount of failed attempts, certainly dramatically smaller than $n = 2^{24} \sim 10^7$ of blind and mostly un-succesful trials.

8. Each $P(I)$ containing boundary edges gives rise to least 2 2-quint triangles associated with $b_I(I)$ and a_{I+1}.

   If all 3 $P(I)$ have $|i-j| > 1$, one has $n_2 = 3\times 2 = 6$. The contribution of regions $P(I)$ is larger if some pentagon interiors have $|\Delta(I)| = |j(I) - i(I)| = 1$. $|j(I) - i(I)| = 1$ gives $\Delta n_2(I) = 1$ and $\Delta n_1(I) = 0$ since 2 1-quint triangles are replaced with single 2-quint triangle.

   The interior of the T can give 1 2-quint triangle.

9. The number n_1 of 1-quint triangles can be estimated as follows.

   (a) Each pentagonal interior edge pair leading from $a(I,j)$ to $b(I,j)$ contributes 2 1-quint triangles for $\Delta(I) \neq \pm 1$, otherwise one obtains only 1 2-quint triangle. This would give maximum number of 6 1-quint triangles associated with the interior edges of 3 pentagons.

   (b) $P(I)$ pentagonal boundary edges contribute $2 \times (P(I) - 1)$ additional 1-quint triangles.

   (c) T contributes at most 4 1-quint triangles.

   (d) t can correspond 1-quint triangle and would do so if the interpretation of extended code is correct.

10. The construction also breaks the rotational symmetry since the decomposition of icosahedron to regions is like gauge fixing so that one can hope of obtaining only single representative in each equivalence class of cycles and therefore less than 2^{10}. By the previous argument related to icosatetrahedral code, t and the triangle opposite to it cannot however correspond to amino-acids coded by 1 codon as one might guess first. Rather, t corresponds to punct and to 1-quint triangle belonging to Z_2 orbit.

The number of cycles should be 2^{10}. One can try to estimate this number from the construction. Each $b_{I,j}$ can be chosen in 4 manners at the first step but at later steps some vertices of the neighboring pentagon might have been already visited and this reduces the available vertices by $n + 1$ if n subsequent edges are visited. At each vertex $b_{I,j}$ one has 4 options for the choice of the boundary edges unless some boundary edges of pentagon (shared with other pentagons) have been already visited. It is also possible that the number of boundary edges vanishes. One can start from any vertex of triangle. This gives the upper bound of 2^4 choices giving $N < 2^{12}$ paths going through 4 pentagon-like regions. The condition that the path is closed, poses constraints on the edge path assignable to T but the number of choices is roughly 24. The condition that path goes through all vertices and that no edge is traversed twice must reduce this number to 2^{10}.

The numerical construction of Hamiltonian cycles should keep account about the number of vertices visited and this would reduce the number of candidates for $b(I,j)$ and for the choices of $P(I)$ for $I > 1$ as well as the number of edge paths associated with T.

Icosahedral Hamiltonian cycles numerically

A couple of months after writing the article I decided to look at the numerical problem of calculating the Hamiltonian cycles for icosahedron. Recall that the earlier source [A9] (`http://tinyurl.com/pmghcwd`) telling that there are 2^{10} different Hamiltonian cycles when orientation is taken into account and one edge is fixed: if orientation does not matter there re 2^9 cycles. If one does not fix one cycle one obtains 2560 cycles - not Hamiltonian paths as I had erratically concluded. The cycles were actually listed (`http://tinyurl.com/yacgzm9x`) and classified to five different basic classes according to their symmetries. Even better, examples of cycles with symmetries were illustrated.

Cycles can be divided to isomorphy classes within which cycles have same shape.

1. It is possible to perform a shift of the edges along the cycle. The shape of the cycle is not affected but cycle changes. Using music terms the key changes. There are 12 different keys.

2. Also the mirror image mapping i^{th} edge to $(13-i)^{th}$ edge is a symmetry which in the generic case produces a new cycle. This symmetry should be distinguished from the change of the internal orientation which does not affect the cycle.

3. Also the isometries of icosahedron leaving the fixed edge as such act as symmetries. Fixed edge belongs to a triangle and the reflection mapping the two other edges of the triangle to each other is this kind of symmetry. Therefore there are two reflection symmetries and the number of cycles of same shape in the generic case is expected to be $4 \times 12 = 48$. If some of the symmetries acts trivially or if some isometries of icosahedron act as its symmetries, the number of isomorphic cycles is reduced.

It is even possible to find illustrations of the symmetric cycles (`http://tinyurl.com/y8ek7ak8`) obtained using Brendan McKay's NAUTY software (`http://tinyurl.com/dkftsr`)! From these illustrations (see **Figs. 9.6**, **9.12** and **9.9**) one can by visual inspection deduce the numbers (n_0, n_1, n_2) charactering the cycle for classes involving symmetries. Also the basic chords can be deduced. If one trusts the condition $n_1 + 2 \times n_2 = 24$, it is enough to count the number n_2 triangles containing to path edges. I have also directly checked that n_1 comes out correctly.

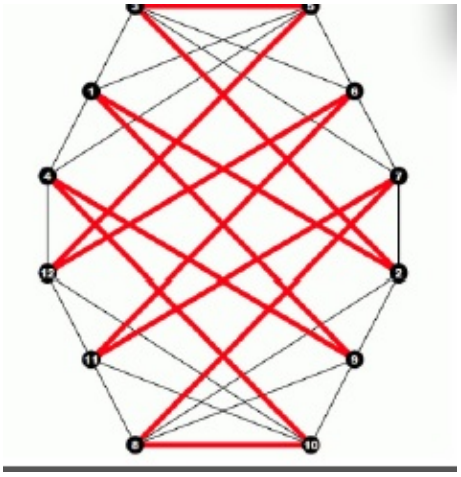

Figure 9.1: $((n_0, n_1, n_2) = (4, 8, 8)$ Hamiltonian cycle with 2 reflection symmetries acting in vertical and horizontal directions.

There are following isomorphic collections.

1. 6 asymmetric collections containing the maximal number of 48 cycles each. In this case images are not given.

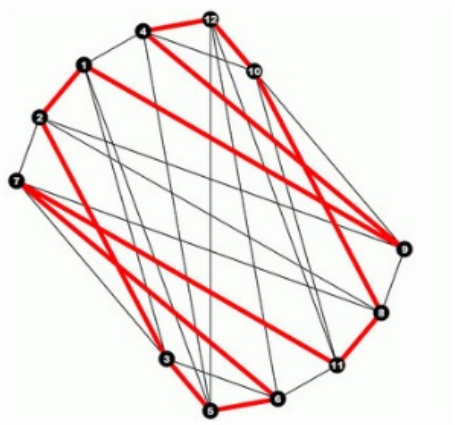

Figure 9.2: $((n_0, n_1, n_2) = (4, 8, 8)$ Hamiltonian cycle with 2-fold rotational symmetry acting as 6-quint rotation.

2. 3 collections with 2-fold rotation symmetry containing 48/2=24 cycles each. One has $(n_0, n_1, n_2) \in \{(0, 16, 4), (0, 16, 4), (4, 8, 8)\}$.

3. 5 collections with reflectional symmetry containing 48/2=24 cycles each. One has $(n_0, n_1, n_2) \in \{(2, 12, 6), (2, 12, 6), (4, 8, 8), (2, 12, 6), (2, 12, 6)\}$.

4. 2 collections with 2 reflectional symmetries containing 48/4=12 cycles each. One has $(n_0, n_1, n_2) \in \{(0, 16, 4), (4, 8, 8)\}$.

5. 1 collection with 6-fold rotational symmetry containing 48/6= 8 cycles. One has $(n_0, n_1, n_2) = (2, 12, 6)$.

There are therefore 5 different notions of harmony and they correspond to $n = \{6, 3, 5, 2, 1\}$ sub-harmonies. This gives altogether 6+3+5+2+1= 17 different notions of harmony.

What is remarkable that the original candidate $(3, 10, 7)$ for bio-harmony is not realized as a cycle possessing symmetries (it might be realized as one of the asymmetric cycles) but that there are at least three realizations for $(4, 8, 8)$, which is forced by the condition that bio-harmony corresponds to the extended genetic code! The three $(4, 8, 8)$ cycles are illustrated in **Figs. 9.6**, **9.9** and **9.12**.

9.7.3 Other Ideas

The book of Merrick discusses also other ideas. The attempts to understand music in TGD framework relate to these ideas.

p-Adic length scale hypothesis and music

One of the key ideas is the reduction of the octave phenomenon to the p-adic length scale hypothesis predicting that octaves and half-octaves correspond to p-adic scalings allowed by the hypothesis $p \simeq 2^k$ for the preferred values of the p-adic primes, and yielding scaled variants of physical systems. This idea will not be discussed in the following: suffice it to say that Pythagorean scale coming as powers of $p = 3$ strongly suggests approximate 3-adicity.

EEG and music

First of the key ideas relates to the idea that genetic code relates to the music scale.

1. Music metaphor is key element of TGD inspired view about biology and neuroscience. In particular, TGD based view about dark matter leads to the proposal that bio-photons are

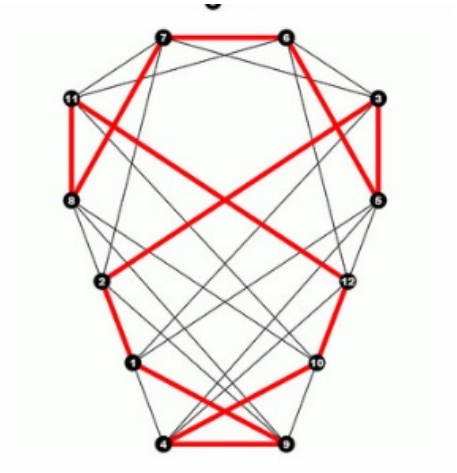

Figure 9.3: $((n_0, n_1, n_2) = (4, 8, 8)$ Hamiltonian cycle with 2-fold refection symmetry acting as horizontal reflection.

ordinary photons resulting as transformations of dark photons with large Planck constant $h_{eff} = nh$ to ordinary photons. The further hypothesis is that the energy spectrum of bio-photons is universal and contains visible photons and UV photons, which defined transition energies of biomolecules. This hypothesis follows if the value of h_{eff} assignable to a magnetic flux tube characterizes ion and is proportional to its mass number. The notion of gravitational Planck constant identified as $\hbar_{gr} = GMm/v_0$, where v_0 is a velocity parameter assignable to the two-particle system can be identified in the case of elementary particles and ions with h_{eff} and predicts also the universality of bio-photon spectrum.

2. In this framework bio-photons would represent music as light inducing molecular transitions. Notes that is different energies of bio-photons would correspond to different magnetic field strengths at magnetic flux tubes as was proposed much earlier in the quantum model of hearing [K43]. Could the biochemical and physiological aspects involved with the generation of music experience be realized in terms of bio-photon emission induced by the listening of music?

Standing waves and music

Merrick consider the idea that standing waves are essential for music experience. Preferred extremals of Kähler action representing standing waves does not seem to be feasible. The known preferred extremals (with "massless extremals" (MEs) included) would represent superpositions of Fourier components with four-wave-vectors which are proportional to each other. Essentially pulse propagating in fixed direction. For more general extremals this direction can depend on position.

Although standing waves are not feasible, effects which would be explained in Maxwell's theory in terms of standing waves are possible in many-sheeted space-time. A particle in a region of Minkowski space containing several space-time sheets touches all space-time sheets having non-vanishing Minkowski space projection to this region and the forced experience by it is sum of the forces caused by them. This leads to an operational defines of gravitational and gauge fields of Einstein-Maxwell limit of TGD as sum of the deviations of the induced metric from Minkowski metric and sum of the components of the induced spinor connection defining classical gauge potentials in TGD framework.

Test particles can clearly experience the presence of standing waves. It is enough to take two massless extremals with opposite directions of three momentum but same energy with non-empty projections to same M^4 region. Particle with experience standing wave oscillating with the frequency involved. The arrangements in which photons are taken to rest effectively could correspond to this kind of situations since if it is the motion of test particles which serves as a

signature. Note however that there are also vacuum extremals for which the light velocity at the space-time surface corresponds to arbitrarily low velocity at the level of imbedding space.

Emotions and 4-D character of music experience

Music experience involves in an essential manner time unlike visual experience which is essentially 3-dimensional. Music experience affects also emotions very directly. For instance, we somehow know the key of the piece and expect that it ends to the basic note and chord. We somehow know also the scale used (say major or minor) by the emotional response stimulated by it. All this requires information about entire time evolution of the music piece. The recent neuroscience based models of memory do not help much in attempts to understand how this is possible. The reason is that in the ordinary materialistic view in which the state of the brain at fixed time should determine the contents of consciousness.

The general vision in Zero Energy Ontology and Quantum Classical Correspondence is that space-time surface provide classical physics correlates for quantum states and also quantum jumps: the failure of the strict determinism is essential for the latter. The space-time surfaces are restricted inside causal diamond (CD) and have space-like 3-surface as their ends: the interpretation is as counterparts for the initial and final states of physical events.

The replacement of states with events makes it possible to understand mysterious looking facts about living matter such as standardized temporal patterns - say those appearing during morphogenesis. The maxima of the vacuum function defined by the exponent of Kähler function in term identified as Kähler action for Euclidian space-time regions representing analogs for the lines of Feynman graph correspond to the most probably temporal patterns.

The basic aspect of emotions is positive/negative dichotomy. An attractive identification for the physical correlated of this aspect is whether the quantum jump generating the emotion increases or decreases the negentropy of the subsystem involved. For instance, pain would correspond to a reduction of the negentropy for the body part involved. In music experience negentropy could flow between different parts of the system involved and create also sensation with local negative coloring but with overall positive coloring (by NMP [K32]). The ability of temporal patterns of music to generate negentropy flows inside the system involved could explain its effectiveness in generating emotions.

Dissonances were used by composes like Bach to generate melancholic emotions which suggests that the dissonance represent local reduction of negentropy. Also vibrato has emotional content. Physically dissonance and vibrato are assignable to the interference of frequencies which are near to each other (`http://tinyurl.com/5r34ch`). The basic formula is

$$cos(x) + cos(y) = cos((x+y)/2) \times cos((x-y)/2) \ .$$

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9.8 Geometric Theory Of Harmony

For some time ago I introduced the notion of Hamiltonian cycle as a mathematical model for musical harmony and also proposed a connection with biology: motivations came from two observations [L16], [K43, K53]. The number of icosahedral vertices is 12 and corresponds to the number of notes in 12-note system and the number of triangular faces of icosahedron is 20, the number of amino-acids and the number of basic chords for the proposed notion of harmony. This led to a group theoretical model of genetic code and replacement of icosahedron with tetra-icosahedron to explain also the 21st and 22nd amino-acid and solve the problem of simplest model due to the fact that the required Hamilton's cycle does not exist.

This article was meant to be a continuation to the mentioned article providing a proposal for a theory of harmony and detailed calculations. It however turned out that the proposed notion of bio-harmony was too restricted: all isosahedral Hamilton cycles with symmetries turned out to be possible rather than only the 3 cycles forced by the assumption that the polarity characteristics of the amino-acids correlate with the properties of the Hamiltonian cycle. This working hypothesis

had to be given up. The fuel of the minirevolution was the observation the symmetries of the Hamiltonian cycles (Z_6, Z_4, Z_2) are nothing but the icosahedral symmetries needed to predict the basic numbers of the genetic code and its extension to include also 12st and 22nd amino-acids. Thus icosahedral Hamiltonian cycles predict genetic code without further assumptions.

One also ends up with a proposal for what harmony is leading to non-trivial predictions both at DNA and amino-acid level.

1. 3-adicity and also 2-adicity are essential concepts allowing to understand the basic facts about harmony. The notion of harmony at the level of chords is suggested to reduce to the notion of closeness in the 3-adic metric using as distance the distance between notes measures as the minimal number of quints allowing to connect them along the Hamilton's cycle. In ideal case, harmonic progressions correspond to paths connecting vertex or edge neighbors of the triangular faces of icosahedron.

2. An extension of icosahedral harmony to tetra-icosahedral harmony was proposed as an extension of harmony allowing to solve some issues of icosahedral harmony relying on quint identified as rational frequency scaling by factor 3/2.

   This extension is kept also now. One must however give up the idea about correlation between polarity characteristics of proteins and properties of Hamilton cycles. One must allow *all* 11 icosahedral harmonies with symmetries as bio-harmonies: their symmetry groups Z_6, Z_4, Z_2 can be identified as the symmetry groups defined the decomposition of 60 DNA codons to 20+20+20 codons in the model of the genetic code. The 4 remaining DNAs and amino-acids can be assigned to both tetra-icosahedron and tetrahedron and icosahedron regarded as defining separate genetic codes. This explains why stopping codons can code for the 21st and 22nd amino-acid under some circumstances.

   Tetrahedral code is second member in the hierarchy of genetic codes [K23] inspired by the notion of Combinatorial Hierarchy $M(n+1) = M_{M(n)} = 2^{M(n)} - 1$ giving the numbers $2, 4, 7, 64, 2^{126}, ...$ as numbers of DNA codons. The fourth member would correspond to what I called "memetic code" allowing representation of codons as sequences of 21 DNAs. It is not known whether the Combinatorial Hierarchy of Mersenne primes continues as Hilbert conjectured.

3. The notion of bio-harmony is partially characterized by the triplet $n = (n_0, n_1, n_2)$, characterizing the numbers of 0-, 1-, and 2-quint chords which in turn correspond to DNA codons in consistency with the observation that codons indeed correspond to triplets of nucleotides. n-quint chord corresponds to a triangle (face of icosahedron) containing n edges of the Hamiltonian. Particular bio-harmony requires a selection of a specific Hamiltonian cycle from each class of cycles (1 Z_6 symmetric cycle having $n = (2, 12, 6)$, 2 Z_4 symmetric cycles $n \in \{(0, 16, 4), (4, 8, 8)\}$, 3 $Z_2 = Z_2^{rot}$ with $n \in \{(0, 16, 4), 1(2, 12, 6), (4, 8, 8))\}$ and 5 $Z_2 = Z_2^{refl}$ symmetric cycles with $(n \in \{(2, 12, 6), (4, 8, 8)\}$. Note that the are only three different triplets n.

4. The original idea was that the rules of bio-harmony could be applied to amino-acid sequences interpreted as sequences of basic 3-chords. DNA would have represented the notes of the music. For *given choice of harmony* as Hamiltonian cycle meaning selection of of 4, 5 or 10 amino-acids coded by the 20 DNAs in question, the hypothesis had to be modified by replacing amino-acid sequences with DNA sequences.

   These DNA sequences however define also amino-acid sequences identifiable as specific triangle at the orbit of Z_n defining the DNA codons assigned to that amino-acid (there is a singular fiber space structure). Together the three 20-plets of DNAs define an amino-acid harmony with (4+5+10 =19 chords with tetrahedral extension defining a harmony with 22 chords/amino-acids). Hence both DNA sequences and amino-acid sequences define "bio-music".

5. The assumption that harmonic transitions between chords (DNA codons) minimize the distance between chords defined by quint-metric leads to highly non-trivial and testable predictions about both DNA sequences and amino-acid sequences. Negentropy Maximization Principle (NMP) [K32] suggests that evolution favors the generation of harmony which

should thus increase in the proposed sense for DNA sequences defining particular genes or other functional units of DNA during evolution. Large quint-distances between subsequent codons/chords would tend to polished out under evolutionary pressures.

6. Could icosahedron, tetrahedron, and tetra-icosahedron have direct physical counterparts in living matter? For instance, water molecules form icosahedral clusters and the chlathrates associated with synaptic contacts have icosahedral symmetries. Tetra-icosahedron has 13 vertices with the added vertex representing one note- say E- in C-key as note with slightly different frequency to resolve the basic problem of rational number based 12-note scale (12 quints give slightly more that 7 octaves). Intriguingly, microtubules consist of basic structures consisting of 13 tubulins with 2 states defining bit: could these bit sequences define representation for the 3-chords and thus representation of sequence of DNA codons and realization of genetic code.

7. Music is language of emotions and peptides are molecules of emotion as Candace Pert [J7] expressed it. Could bio-harmonies serve as direct correlates for emotions? What is bio-music? A natural TGD inspired guess is that sounds can be replaced with $h_{eff} = n \times h$ dark photons with low frequencies and having energies in the range of bio-photons (visible and UV range maximally effective biologically) as proposed on basis of some physical facts and theoretical ideas [K43]. The frequency spectrum of dark cyclotron photons along magnetic flux tubes would define bio-music as "music of dark light" and bio-harmonies would correlate with emotions and moods.

If one can find various icosahedral Hamilton's cycles one can immediately deduce corresponding harmonies. This would require computer program and a considerable amount of analysis. My luck was that the all this has been done. One can find material about icosahedral Hamilton's cycles (see `http://tinyurl.com/pmghcwd`) in web, in particular the list of all 1024 Hamilton's cycles with one edge fixed [A3, A9] (this has no relevance since only shape matters). If one identifies cycles with opposite internal orientations, there are only 512 cycles. If the cycle is identified as a representation of quint cycle giving representation of 12 note scale, one cannot make this identification since quint is mapped to fourth when orientation is reversed. The earlier article about icosahedral Hamiltonian cycles as representations of different notions of harmony is helpful [L16].

The tables listing the 20 3-chords of associated with a given Hamilton's cycle make it possible for anyone with needed computer facilities and music generator to test whether the proposed rules produce aesthetically appealing harmonies for the icosahedral Hamiltonian cycles. Biologist with access to DNA sequences could experiment with DNA codons to see whether their are harmonious in the sense that the distance between subsequent chords assignable to DNA codons tend to be small in quint metric. Note that DNA decomposes to pieces corresponding to different Hamiltonian cycles (harmonies) so that the comparison is not quite straightforward.

9.8.1 What Could Be The Basic Principles Of Harmony?

It indeed seems that the idea about definition of notion of harmony in terms of Hamiltonian cycles makes sense.

Icosahedral harmonies

1. Chords (major and minor) are labeled by their basic tones and comes either as major or minor. Harmony in classical sense requires that the transitions from key to another take place by a small number of quints and that the piece does not wander too far from the major key, say C.

   If quint corresponds to a step along the edge of the cycle in the direction of its orientation, the notion of tonal closeness corresponds to the closeness in the metric of icosahedron. For instance C, F, and G are commonly used keys in same piece and correspond to 3 subsequent points along Hamiltonian cycle. Note that the number of ♯s of the key increases by one unit in standard direction and the number of ♭s by one unit in opposite direction.

2. It turns out that major and minor 3-chords and are mapped to each other in the orientation reversal for icosahedral path so that basic moods "happy" and "sad" in music have this orientation as a geometric correlate. The effect of orientation reversal does not actually depend on the icosahedral representation but is implied by quint cycle representation alone. C and half-octave $F\sharp$ defining the tritonus interval are the fixed points of the orientation reversal. Orientation reversal induces pairings ($C \leftrightarrow C$, $F\sharp \leftrightarrow F\sharp$, $G \leftrightarrow F$, $D \leftrightarrow B\flat$, $A \leftrightarrow D\sharp$, $E \leftrightarrow G\sharp$, $H \leftrightarrow C\sharp$. Quints of cycle correspond to the fourths of oppositely oriented cycle so that majors and minors are mapped to each other and one can say that the moods "happy" and "sad" have geometric correlates in the sense that majors and minors are transformed to each other in the reversal of orientation of the cycle.

The notion of harmony can be characterized in terms of numbers of basic 3-chords identified as faces of the icosahedron and their neighborhood relationship telling when corresponding chords are near to each other or vertex or face neighbours. The wall neighbours assignable to given edge are expected to be in very special relationship harmonically since they possess a common quint.

The basic classification is according to the number $n = 0, 1, 2$ of edges of cycle contained by them and the triplet $n = (n_0, n_1, n_2)$ for the numbers of faces of various kinds gives the first rough classification. 2-quint chords have common edge and thus two common notes with two 1-quint chords and are therefore natural intermediates in transitions between them. 0-quint chords are tonal loners having no edge neighbours turns out that they involve dissonances since they consists of three notes spanning length of 1 or 3/2 steps (say EFG, $EF\sharp G$ or $D\sharp EF$). Maximally symmetric harmony is an exception: 0-quint chords correspond to augmented chords of type $CEG\sharp$ with two major thirds.

The numbers of three different kinds of face neighbor pairs for the 12 edges of the path serve as an additional classification criterion in terms of the $p = (p_{1,1}, p_{1,2}, p_{2,2})$ for the numbers $p_{i,j}$ of different kind of edges. Note that the neighbor faces of an edge correspond to 3-chords, which possess two common notes and are in this sense close to each other. These numbers characterize the most natural transitions between the chords of the harmony. A further criterion is the distribution of these neighbor pairs along the cycle.

Why quints are near to each other harmonically?

The naive expectation would be that frequencies near to each other (using half-note as unit) are close to each other. This is not true. Their simultaneous presence is experienced as dissonance. This probably has a neurophysiological correlate: in ear the hair cell groups detecting notes which are near to each other in frequency space are overlapping. This explanation does not however tell why the conscious experience is dissonance.

The distance measure for notes could be formulated in terms of distance defined as the number of quints connecting them. For quint the distance would be minimal. This measure applies also to chords and allows to understand the basic rule of classical harmony stating that harmonic transitions take place the chords related by quint shift of the basic note (adding either one $\sharp$ or one $\flat$ to the scale). Also the key changes can be understood using the same rule: consider the changes C$\rightarrow$ G and C$\rightarrow$F as examples. Note that in this case the chords have common note.

One could of course question the assumption that it is possible to choose the shortest route. The notes obtained by quint scaling are not quite same in the two directions and means that $\sharp$ is the inverse of $\flat$ in well tempered scale only. Could it be that people with absolute ear are able to distinguish between the two slightly differing scales and experience notes of quint C-G as harmonically close when 1 quint connects them but as harmonically distant 11 quints in opposite direction connects them?

If cognition is p-adic, one can ask whether the notion of harmony can be formulated in terms of p-adic distance concept.

1. By octave equivalence the scaling by power of two means nothing so that the scalings by 3/2 are equivalent with scalings by 3 and the distance defined by 3-adic norm having values 3^k, where k is the number of quints makes sense. The distance defined as quints could be identified the absolute value of k along the quint cycle in the direction in which the distance is shorter. If so, the maximal distance is 6 units.

2. 3-adic measure of distance seems to be rather realistic. Quint corresponds to 1 unit distance. Half step corresponds to a distance of 5 units and 6 units defines the largest distance and corresponds to the tritonus interval which was forbidden by catholic church. Fourth (C-F) corresponds to 1- step in opposite direction and 11 steps in standard direction.

3. There is also a problem. Second (C-D) corresponds to 3 quints but third (C-E) corresponds to 4 quints and small third to 3 quints in opposite direction. Major third would thus correspond to a longer harmonic distance than second. This is a genuine problem, whose solution might be provided by the extension of icosahedral scale to icosatetrahedral one bringing in one additional note which is very near to one of the icosahedral notes and is major or minor third of icosahedral note.

4. Could one use the number of icosahedral edges as distance between notes but not as a minimal distance along the Hamiltonian cycle but along a minimal edge path along icosahedron? The icosahedral measure of distance would be analogous to a distance between points of object along shortest route in space that it inhabits and depends on harmony characterized by the shape of icosahedral cycle. C and E (and also C and $F\sharp$!) could be close to each other in some harmony and distant from each other in some other harmony. Icosahedral geometry would become an active determinant of the harmony.

To sum up, music seems to have both 2-adic (octave equivalence) and 3-adic (12-note scale by quint scalings) characters. The principle of tonal unity for classical music stating that modulations of key should not lead too many quints away from the basic chord would have 3-adic interpretation.

What could be the rules for building a harmony?

What guarantees good harmony when one has fixed the key/harmony/representation of particular Hamilton cycle?

1. One should pose conditions on the allowed transitions between chords. Are there principles would imply harmonic smoothness in geometric sense? Could the transitions occur only between chords with a common note? Or can one require a common pair of notes? Or can one require even a common quint. If so, 0-quint chords would become tonal hermits and could not be used at all. In practice their dissonant character has eliminated them in popular music and much of classical music too.

   The standard quint and fourth transitions (say C to G and C to F) are basic examples in which there is only one common note between chords, and it seems that one cannot require more than this in the general case. Playing with the chords of bio-harmony however suggests that smooth bossa nova/jazz emotionally ambivalent mood is created if common pair of notes or even quint connects the neighboring chords. The rule is that only transitions between chords with same basic note are allowed. Obviously this is too stringent a condition.

2. Could 2-quint chords act as bridges between two 1-quint chords? For instance, for the maximally symmetric harmony consisting of disjoint groups of chords related by half-octave scaling the augmented chords ($F^{aug} = FAC\sharp$ and G^{aug} mapped to each other both by half-octave scaling and reversal of orientation could serve as mediating bridges.

3. Could harmonic transitions take place only between neighboring faces of icosahedron (see `http://tinyurl.com/ns9aa`) or should it only tend to minimize the quint distance between subsequent chords (this distance vanishes if they have a common note)? For the 0-quint distance harmony, the harmonic movement could be seen as a path in dodecahedron which is dual of icosahedron. In the most general case the transition can take place to both wall and vertex neighbors, whose total number is 3+3=6. In this geometric picture harmony and melody could be seen as duals of each other.

   Dodecahedron is dual of icosahedron and one can ask whether the harmonic motion could correspond to a path at dodecahedron. The vertex of dodecaehdron is pentagon and has 3 neighbours (see `http://tinyurl.com/mp5d8`). The above argument gives $3 + 3 > 3$ neighbors for the triangle of icosahedron. Are the wall neighbors of icosahedral triangle

mapped to nearest neighbor vertices? If so then transitions between vertex neighbor triangles should correspond to longer steps at dodecahedron. By the duality triangles of icosahedron correspond to three pentagons associated with the vertex of dodecahedron. The rule that comes in mind is that steps can occur between vertices for which the 3-pentagons have one or 2 common pentagons.

Note that if the dodecahedral path is Hamiltonian cycle, it is unique apart from isometries of dodecahedron and would define a unique chord progression. One can - and of course must - allow self-intersecting harmonic paths. The condition that there exists a basic chord from which everything begins and to which everything ends implies that closed but in general self-intersecting path is in question.

4. An interesting test for the idea would a computerized generation of random chord sequences satisfying at least one common vertex rule and finding whether they are aesthetically appealing. Incidence matrix (see Appendix) for the icosahedral (and tetra-icosahedral) triangles wholes element tells how many common vertices two chords have have allows computational construction of the allowed chord sequences as random sequences.

5. For most harmonies 0-quint chords involve dissonances induced by three nearby notes (such as $CC\sharp D$) and spanning large number of quints (maximally symmetric harmony has 2 0-quint chords, which do not have dissonances and second harmony with 2 reflection symmetries has no 0-quint chords). Also maj7_-, $sus4_+$, and 6_- 1-quint chords have half-note dissonances. Dissonances as such are however not un-sesthetical. For instance, Bach used them to create a deeply melacholic feeling.

More general notion of harmony

The notion of harmony discussed in previous section is rather conservative and certainly too stringent.

1. 0-quint rule is too restrictive already in chord based music. For instance, the downwards progression Am, G, F, E appearing in Spanish music and music forms like Passacaglia would have chords with 1-quint distance. Hence one must consider also a weaker notion of harmonic chord progression according to which this distance is minimized and below some maximum value k_{max}. One quint would define the smallest non-vanishing maximal distance. One can define incidence matrices for chords with n-quint distance. The incidence matrices with different values of k_{max} have disjoint sets of non-vanishing elements and the total incidence matrix is their sum.

2. Even this is not enough. The direction of step matters for scales (major-minor difference) and it seems to matter also for chord harmonies. The inverse E, F, G, Am of the above mentioned progression does not sound harmonic in the same Am key. The impression of achieving the goal/ending down to something dictated by fate is lost.

   Instead of $EFGA$ one often has $EF\sharp G\sharp A$ as a melodic progression and with $E, B7, E7, Am$ as a chord progression having only 0-quint steps. The rule seems to be that 1-quint steps are possible only downwards in minor harmony, whereas upwards steps are 0-quint steps. Climbing slowly upwards by 0-quint steps and falling down by 1-quint steps! Could this "gravitational analogy" serve as a metaphor?

   Also the number of n-quint steps between chords matters. The larger this number, the closer the chords are. Two 0-quint steps means that chords have two common notes, 1 0-quint stet that they have single common note. The two 1-quint steps for downwards step $Am - G$ are between 3rd and 1st ($C \to G$) and 5th and 3rd ($E \to H$). For upwards 0-quint steps $E - H7$ 1-quint steps are between 5th and 5th ($H \to F\sharp$) and 1st and 1st ($E \to H$). For $H7 \to E$ the reversals of these steps occur. For $E7 \to Am$ one has 3 1-quint steps: (the reversals 1-quint steps $E \to A$ and $H \to E$ steps and 1 quint step $D \to A$. The laste step seems to be the smallest one in a well-defined sense.

   For G-F step the number of 1-quint steps is one ($C \to C$): same is true for F-E step (A and E).

Using geometry language, for chords connected by 1-quint step(s) the mutual orientation of corresponding triangles with shape defined by the intervals involved matters since the number of 1-quint steps depends on the orientation.

The notion of chord harmony does not apply as such to polyphonic music with several simultaneous melodies unless on can say that it involves definite chord sequence. One could try to apply the concept of harmony for melody also in this case. The challenge is to guess what harmony for melodies could mean.

1. A conjecture inspired by the genetic code is that the codons defining the allowed melody notes associated with a given chord are in one-one correspondence with the triangles at the orbit of the triangle associated with the chord under the group Z_6, Z_4, or Z_2 characterizing the chord as a counterpart of amino-acid. In table **??** the Z_6 orbits are represented as groups of 6 similar chords (2 for 1-quint chords and 1 for 2-quint chords). In table **??** for Z_4 chords the groups consist of 4 similar chords and in the tables **??** and**??** for Z_2 harmony the chord groups consist of 2 similar chords.

2. The first guess is that the union of the notes of these chords could define the chords, whose notes are compatible with chord in the time scale shorter than the duration of the chord. Note that same triangle can appear at orbits of several chords since the orbits of each group span entire icosahedron.

   If the note lasts for a duration of several chords, the notes must be consistent with all the chords involved. The rule would explain why fast chromatic sequences (in the scale of chord duration) sound harmonic but slow chromatic sequences do not.

   For melodies in Am key $EFGA$ is rare and does sound harmonic being often replaced with $E, F\sharp, G\sharp, A$. As far as intervals are considered, this is the inversion $D\sharp, F, G, G\sharp$ of $AGFE$ shifted upwards by 5 quints. Could one regard progressions (say Am, G, F, E) breaking the strongest rule for chord harmony as polyphonic progressions satisfying the rules for polyphonic progressions.

To conclude whether the DNA inspired notion of harmonic is realistic, one should understand how the sub-groups Z_n, $n = 6, 4, 2$ of the isometries of the icosahedron and defining the genetic code act on the Hamiltonian cycles.

1. The simplest guess is that these groups are represented as subgroups of Z_{12} (also a subgroup of icosahedral group) representing quint cycle. Z_n generator would shift the basic note of the chord by $12/n$ - that is $2, 3, 6$ quints.

2. Z_n maps chords of same type to chords of same type only if it is a *rotational* symmetry of the harmony. For instance, the action of Z_6 (see **Fig. 9.4**) on icosahedron allows doublet orbit consisting of $Xaug$ type chords, since Z_3 maps 2 0-quint triangles in the middle of the figure to themselves and reflection group Z_2 permutes them. 6-element orbits consist of either minor or major chords. More generally, the inspection of the cycles shows that the cyclic orbits of triangle under Z_n correspond to the orbits of corresponding subgroups of icosahedral group.

3. Z_2refl maps the shape of the chord to its mirror images and so that the character of the chord can vary along Z_4 orbits. The rules are $(M \leftrightarrow m)$, $(6 \leftrightarrow 7)$). For other chords the character is unaffected.

4. Any subgroup of icosahedral isometry group $A_5 \times Z_2^{refl}$ having 120 elements must map chords to chords (faces to faces). In particular any Z_n) even if it is not a symmetry of a particular harmony. The character of the chord is not preserved and the number of quints can change. Whether these maps have interpretation in terms of music remains unclear.

These considerations forced me to finally realize that the 3 groups Z_6, Z_4, and Z_2 that I had assigned to 20+20+20 DNA codons in the model of the genetic code are nothing but Z_6-, Z_4-, and Z_2-symmetric Hamilton cycles! The numbers of amino-acids associated with various types would be 3+1=4, 5, and 10 (with empty amino-acid included). Tetrahedral extension based on gluing

of tetrahedron at triangle corresponding to $X6$ type chord possessed by all Z_2^{refl} type harmonies would give 3 additional real amino-acids giving altogether real 22 amino-acids as required. This has implications.

1. All 11 Hamilton cycles are realized separately as DNA level harmonies. Amino-acid level harmonies would correspond to selection of three Hamiltonian cycles, one for each Z_n.

2. To get something one must give something away. Now one must give up the idea that $(4, 8, 8)$ is special via the corresponding of n-quint property with polarity properties. This is a pity, since just taking this correspondence seriously led to the extension of the icosahedral cycles to tetra-icosahedral ones. Fortunately, the extension itself makes sense for all Hamiltonian cycles.

To understand the action of symmetries one must look how the groups Z_n act on C major chord.

1. Z_2 would induce half-octave shift and map $C = (C, E, G)$ to $F\sharp m = F\sharp, B\flat, D\sharp)$. The assignment of $F\sharp$ -tritonus - with C note sounds strange in the ears of harmonic conservatives.

2. Z_4 would map $C = (C, E, G)$ to $A = (A, C\sharp, E)$, $F\sharp = (F\sharp, B\flat, C\sharp)$ and $D\sharp = D\sharp = (D\sharp, G, B\flat)$. These would span 8 notes since $E, G, B\flat, C\sharp$, appear twice. Note that C, E, G, A are the notes assignable to the tetrahedron in the extension of the scale and pentatonic scale corresponds to C, D, E, G, A. Z^4 orbit does not contain the notes $DFG\sharp H$ but the orbit of G chord does so. The orbit of C chord plus $G7$ chord alone define the notes of C major key.

3. Z_6 would map C and E to the same "impressionistic" 6-note scale consisting of 6 whole notes. Together with the Z_6 image of G one obtains all 12 notes of the scale.

9.8.2 Harmony And Biology

Could harmonic principles be realized in biology?

The basic idea behind icosahedral harmony is connection with biology suggested by the fact that the number of icosahedral basic chords is 20 which is also the number of amino-acids. Actually there are two additional amino-acids and one ends up to an extension of genetic code by attaching to icosahedron a tetrahedron and thus adding one vertex more. The number of DNA codons increases from 60 for icosahedral code to 64 for the real code. The triangle along which icosahedral and tetrahedral amino-acids are attached together corresponds to punct coded by stopping codons. Also the following amusing observation supports the notion of bioharmony. Simple music pieces tend to begin with the basic chord CM or Am. Interestingly, mRNA starts always with a codon coding met which could correspond to $CM = CEG$ for one of the tetrahedral faces (see `http://tinyurl.com/3b9ymnq`)

Could the application of harmonic principles to biology make sense? The triangles of icosa-tetrahedon correspond to amino-acids or DNA codons for the amino-acids coded by 20 codons in question.

1. The strictest rule stating that there must be common edge of Hamiltonian cycle between the amino-acids/DNAs cannot be satisfied since 0-quint amino-acids/DNA codons would be total loners and effectively eliminated from biology.

2. The weaker "common edge or vertex" rule could however make sense. A given codon in the group of 20 codons/amino-acid could be followed only by 3+3 different nearest neighbor similar codons/amino-acids. If the first amino-acid is fixed there would be only 6^N N-amino-acid sequences instead of 20^N sequences. This kind of symmetry would have been probably observed if exact but one can ask whether harmonic pairs could more probable than completely random pairs.

3. A more plausible formulation is obtained by restricting the rule to the level of DNA sequences and generalizing it so that it applies also to transitions between harmonies with different symmetries so that a transition between corresponding amino-acids is induces.

4. An even weaker formulations states that the transitions occur with highest probabilities between codons/amino-acids having shortest quint distance.

A natural conjecture is that evolution favors the generation of harmony even in the very concrete sense that proteins defined by harmonious chord sequences for bio-harmony are emerge as what Darwinist would call the fittest ones.

1. Icosahedral water clusters made from tetrahedra

The obvious questions concern the concrete realization of the icosahedron - or more generally icosahedral symmetries. One should also understood what the attachment of tetrahedron to icosahedron means (note that tetra-icosahedron is not the same thing as icosi-tetrahedron, which is Archimedean (not Platonic) solid (`http://tinyurl.com/6onvry`)). What comes in mind is attachment of an information molecule to the receptor of cell membrane.

Water molecules form icosahedral structures and - what is amazing to me - Plato regarded icosahedron as a symbol of water (`http://tinyurl.com/y7bo9omm4a3378c13bcad793a52213a325db7db0-30.html`)! The page "Water structure and science" of Martin Chaplin gives illustrations about the rather complex icosahedral structures. Icosahedral structures of size 3 nm can be formed from 20 14-molecule tetrahedral water molecule clusters containing 280 water molecules altogether. They can also consists of cyclic pentamers and tricyclo-decamers and also from bi-cyclo-octomers. The 20 tetrahedrons correspond to the faces of the icosahedron and tetra-icosahedron would be formed as tetrahedron is glued to the icosahedron along one of the faces.

The bioharmonies could manifest themselves already in the structure of water molecules. Second - more plausible - option is that they differ only at the level of the magnetic body of the biomolecule. Bio-harmony suggests that 3 radial magnetic flux tubes or flux tube pairs emerge from each water tetrahedron. Hamilton's cycle could be realized as a flux tube connecting the vertices of the icosahedron and assigning the quint cycle to the cyclotron frequencies (magnetic field strengths).

This scenario raises several questions related to the pairings between ordinary DNA/amino-acids, their icosahedral representations, and their representations as dark proton sequences.

Suppose that one takes seriously the idea that genetic code is represented as dark proton sequences with the states of dark protons formed from 3 quarks representing DNA and RNA codons, amino-acids, and even tRNA.

1. How dark proton sequences are realized? Could one regard them as icosahedral bound states of 20 dark protons? Or with a Hamiltonian cycle consisting of penta-quarks and representing dark nuclear string? Could the icosahedral representation as dark nucleus consisting of 20 dark protons and dodecahedral representation as dark nucleus consisting of 12 dark 5-proton states be dual manners to interpret the state or are they different states related duality. Equivalence of the two pictures would require that dark protons are color excited and in an entangled state.

2. Could dark proton sequences correspond to sequences of icosahedrons connected by flux tubes connecting the dark protons assignable to the dark proton states assignable to the faces of the icosahedrons? These dark nuclei would be definitely different from those possibly associated with the Hamiltonian cycle.

3. What about the tetrahedral part of the genetic code in relation to dark protons sequences? What dark proton states could tetrahedral codons and amino-acids correspond? Are they associated with water tetrahedrons representing the faces of the water icosahedron? Note the amusing numerological co-incidence that the vertices of tetrahedron have 3 quarks associated with them and those of icosahedron 5 and that the quint for icosahedral edge is replaced with third for tetrahedral edge.

4. Could the chords correspond to triplets of cyclotron frequencies for quarks associated with the three flux tubes emanating from the each face of the icosahedron? Could the breaking of the rotational symmetry from SO(3) to SO(2) - now actually $Z_3 \subset SO(2)$ - assumed to occur for dark proton states correspond to the reduction forced by the triangular geometry?

5. How DNA -amino-acid correspondence is represented at the level of dark DNA? The correspondence should be realized in terms of magnetic flux tube triplets connecting dark DNA and dark amino-acid and resonance condition would be essential. When the chords at the orbits of Z_n are of same type, different DNAs correspond to the same chord but with different key. When Z_2^{refl} is involved, the two chords at the orbit are not of same type (note the analogy with left and right-handed biomolecules). The only manner to circumvent the problem is to assume that the chord associated with amino-acids magnetic body is that of DNA. Information is not actually lost in translation, it is only transformed to different kind of information perhaps representing correlates of emotions.

6. Could the non-representability of one of the Z_6 codons as amino-acid have an analog?

The fiber space having icosahedron as a base and 3 copies of icosahedron assigned with 3 regions of icosahedron corresponding to Z_n, $n = 6, 4, 2$, defines a formal geometric representation of genetic code. Could this space represented in terms of water icosahedra?

1. Perhaps one should first try to identify the function of water icosahedrons. The first guess is that they serve as local bridges between dark DNA/amino-acid sequences and ordinary DNA/amino-acid sequences. This would suggest that dark proton of dark DNA forms a flux tube connection with the face of water icosahedron dictated by the state of the dark proton: this would take place by flux tube reconnection and cyclotron resonance. Water icosahedron in turn couples with the DNA/amino-acid like DNA conjugate codon with codon so that kind of double helix is formed.

2. What about the pairing of ordinary DNA/amino-acids and water icosahedrons? Water icosahedron has size of about 3 nm. The size of single DNA codon is about 1 nm. Single codon corresponds to a twist of $3\pi/5$=36 degrees, an angle closely related to Golden Mean. If the radius of the helix consisting of water icosahedrons is above some minimal radius which is easy to estimate from an equation for the helix. There are 10 DNAs per $L(151) = 10$ nm and they correspond to a total twist of $3 \times 2\pi$. Therefore the twist angle is $\Delta\Phi = \pi/5 = 36$ degrees for single codon and corresponds to a distance of $L(151)/10 = 1$ nm). From this one has equation for DNA and icosahedron helices as $z = k\Phi$, $k = h/(6\pi)$, $h = L(151) = 10$ nm (radii are constant). Single codon corresponds to a distance $s = \sqrt{dz^2 + R^2 d\phi^2}\Delta\Phi$ along the water icosahedron helix of radius R accompanying DNA helix. One must have $s \geq L = 3$ nm defining the size of water icosahedron in order to avoid overlap. $\Delta s \geq L = 3$ nm gives the condition $R \geq 10 \times \sqrt{2}/(3\pi)$ nm $\simeq 1.5$ nm.

3. If the representation of genetic code is possible, do the fiber icosahedrons correspond to subsets of faces of the icosahedron itself? Or do they correspond to faces the of icosahedrons in some manner associated with the amino-acid icosahedron. Direct attachment is not possible but association could be achieved by connecting the icosahedrons by flux tubes with the tetrahedron at the ends of flux tubes identified as representation of the same amino-acid. This kind of structure with three icosahedra emanating from a given icosahedron could be iterated and one would obtain a fractal structure representing a binary tree. Could the water icosahedrons organize in this manner to form larger clusters?

What could be the physical correlates of Hamilton cycles representing harmonies?

1. Could Z_6, Z_4 and Z_2 orbits associated with the Hamiltonian cycles be realized even in the structure of water icosahedrons? Could they be realized as structures formed by the water tetrahedra and correspond to three separate regions of these icosahedral structures? Could one assign to each of the three regions of icosahedron icosahedron such that the attached icosahedron decomposes to the orbits associated with that particular region? Could the hierarchy of the icosahedral symmetry breakings have a direct counterpart at the level of the icosahedral structures formed by water molecules? My intuitive feeling is that the answer to these questions is negative.

2. Could Hamiltonian cycles be realized only at the level of dark photons as quint cycles defined by closed flux tube giving rise to dark nucleus, that is in terms of 3-chords formed by

dark photons propagating along flux tubes emanating from the icosahedron? If cyclotron frequencies of dark quarks are in question then the magnetic fields associated with the flux tubes would define the notes.

3. The breaking of Z_2^{refl} symmetry is of special interest since it could serve as a prebiotic analog of chiral selection and could relate to dark variant of weak physics with effectively massless weak bosons in nano-scales. This would require dark magnetic body. Half-octave scaling is second broken symmetry and would have also an analog in Z_2^{refl} variant of icosahedron. Note that 256 variants of the bio-harmony are predicted and could be realized for magnetic body naturally. The presence of electric fields at flux tubes is possible and if the electric and magnetic fields are non-orthogonal, U(1) instanton density is non-vanishing and induces parity breaking. Is this breaking associated with Z_2^{refl} only?

2. Clathrin molecules as icosahedral structures

Clathrin (`http://tinyurl.com/y8ho23zf` is a structure appearing at the ends of microtubules and necessary for the transmission of signals between the presynaptic and post-synaptic neurons. Clathrin consists of triskelions - kind of triangular structures with three spiral like legs and having as symmetries the rotational symmetry group Z_3 of equilateral triangle. Clathrins can form hexagonal planar lattices and pentagonal icosahedral lattices consisting of 12 pentagonal faces - the number of vertices of icosahedron. One can associate 3 triskelions with each pentagonal face: this makes $12 \times 3 = 36$ triskelions altogether. One can regard the centers of the 12 faces as vertices of icosahedron and assign to this structure 20 faces, which are triangles formed by 3 pentagons.

If proteins and other molecules attach to the faces of clathrin, one can ask whether each icosahedral triangle of this kind has an address formed by the three notes associated with it and serving as a password: only those molecules, which "know" this password can attach to the face. The realization would be in terms of three U-shaped magnetic flux tubes emerging from the 3 pentagonal faces representing the three notes as frequencies of dark $h_{eff} = n \times h$ cyclotron photons with ELF frequencies but energies of bio-photons (in visible and UV range). The binding of the molecule to the face triangle would be preceded by reconnection of U-shaped flux tubes of the clathrin and molecule, by a resonant interaction by dark cyclotron photons, and by an h_{eff} reducing phase transition bringing the molecule to the face.

3. Microtubules as music instruments?

It has become clear that microtubules have a central role in biology, neuroscience and perhaps also in consciousness theory and the evidence that they are quantum coherent systems is accumulating. Could music metaphor could help to understand microtubules?

1. Tetra-icosahedron has 13 vertices with the added vertex representing one note- say E- in C-key as note with slightly different frequency to resolve the basic problem of rational number based 12-note scale (12 quints give slightly more that 7 octaves). Intriguingly, microtubules consist of basic structures consisting of 13 tubulins with 2 states defining bit: could these bit sequences define representation for the 3-chords and thus representation of sequence of DNA codons and realization of genetic code.

2. The recent TGD inspired model of microtubules [L14], [K62] was inspired by the findings of the group of Bandyopadhyay (see `http://tinyurl.com/ze366ny`) [J4], [J17] relies on the general vision about bio-communications and control as being based on dark cyclotron photon radiation travelling along magnetic flux tubes.

   These dark photons have a universal energy spectrum in the range of bio-photons (visible and UV) to which they transform as the value of $h_{eff} = n \times h$ reduces to its standard value. Frequencies would span a wide energy range but EEG frequencies would be of special importance since they would also couple to acoustic vibrations. The precise value of the energy scale of cyclotron photons would be determined by the strength of the magnetic field at flux tube.

3. Frequency modulation would be the general manner to code information in living matter: "whale's song" would be a good metaphor for it. This is assumed in the model for cell

membrane as generalized Josephson junction: the modulation would be now induced by the variations of generalized Josephson frequency by variations of the membrane potential. Also microtubules have been proposed to base their communications on frequency modulation.

4. The first possibility coming in mind is that the continually varying microtubule length codes for the frequency [L14]. The change of the frequency by say octave would however require quite fast and large variations of microtubule length. Neither does this realization conform with the idea that the state of single tubulin corresponds to frequency. Microtubule length could also code for the length of the music piece represented by the microtubule serving as a music instrument or musician at the bio-molecular level. It would also the number of microtubular units and thus the size of the orchestra consisting of 13-units.

5. Another possibility inspired by the proposal is that magnetic flux tubes form an analog of 3-D grid ideal for communication purposes using 12-note (or actually 13-note) system as a code equivalent with genetic code. Also microtubules would involve three kinds of flux tubes [L14] defining coordinate grid of cylindrical coordinates: longitudinal, radial and those which rotate along the microtubule. Radial flux tubes would be ideal for communication using 13-note system as a realization of genetic code.

6. 13-note system as cyclotron frequency spectrum for given value of h_{eff} would be determined by the spectrum of the magnetic field strengths going transversally through the microtubule and each tubulin would correspond to one particular note represented as magnetic field strength. The system would be highly analogous to the system formed by hair cells in cochlear. Note would indeed characterize single tubulin molecule rather than entire microtubule as required if one wants to code chords using the two tubulin conformations as a bit. Tubulin conformation would determine whether the tubulin serves as a sending/receiving antenna or not.

7. Melody in 12-note system can be interpreted as a discretized version of frequency modulation with frequency being piece-wise constant in time. Obviously the 13 bit sequences defined by tubulin conformations code for the chords of rational 12-note scale involving a representation of one particular note (the third note of the Pythagorean scale) with two slightly different frequencies in order to avoid problems caused by the rational number ratios of frequencies. 13th bit could also serve as a kind of period. Also chords could be coded up to a chord with 13 notes so that microtubules would have quite a high representative power.

The is an objection against the model.

1. One could argue that a unit consisting of 13 tubulins allows only one octave to be represented. One can of course assume that the magnetic field strengths for subsequent units differ by octave. What makes this interesting is that microtubules allow two variants, called A and B. B type microtubules appear as 13-units since microtubular surface has a gap so that the helical symmetry is broken. For variant A, which is not found in vivo or in vitro, 13-units integrate to form longer helical units. This is assumed in Penrose-Hameroff model and the experimental absence of A type microtubules is one of the basic objections against Penrose-Hameroff hypothesis.

2. The TGD inspired proposal is that A type microtubules corresponds to a critical state having therefore an enhanced symmetry and long range correlations: criticality would explain their experimental absence. The experiments of the group of Bandyopadhyay support that the critical state is induced by a resonant excitation at specific AC frequencies [L14]. Long range correlations would mean enchance helical symmetry - that is fusion of several 13-units to form a longer helical structure. This structure would allow an interpretation as a structure with frequency spectrum of several octaves represented coherently in terms of magnetic field strength: the 10 octave span for hearing would mean the integration of 10 microtubule units meaning length scale of order micrometer assuming that tubulin size is of order 10 nm.

3. If the field strength for subsequent units differ by octave, one can argue that for variant B various octaves play their own music without knowing of each other and thus without

coherence. In state A they would play together forming something analogous to orchestra or choir.

If the octave is same for all 13-units, the phase transition would involve octave scaling of the magnetic field strength at the flux tubes. The flux tube radius should suffer p-adic scaling by an integer number of half-octaves, which makes sense if one accepts p-adic length scale hypothesis. This kind of phase transition have been proposed as candidate for a basic step of energy metabolism since they can store or liberate cyclotron energy as metabolic energy.

4. Microtubules could directly couple with both DNA and clathrin molecules if they represent 12 note system as a resonant system able to receive the radiation with corresponding frequencies. 12-note system and the 3-chord system associated with it could define universal communication code allowing communications between DNA, proteins, and microtubules.

To sum up, 13-note extension of 12-note system could be seen as a realization of the genetic code in terms of frequencies. The existence of kind of realization was obvious from the beginning and I proposed it in the model of microtubules as quantum antennas during the first years of TGD inspired theory of consciousness [K36]. Discovering the precise realization of the proposal has however required time.

Could biology help in the understanding of musical harmony?

One can also ask whether biology could provide ideas about the notion of harmony. Could icosatetrahedral harmony possessing additional 13th note very near to the fourth of basic major chord provide a better view about harmony?

1. The extension of the ideas about harmony to the case of isosatetrahedron is a non-trivial task. If one assumes that the extended Hamiltonian cycle is obtained by deforming tetrahedral Hamiltonian cycle according to the proposal made earlier, one ends up with a problem since the cycle makes a wedge while making a side track of two steps via the new vertex. The two steps must give one quint so that the new vertex must correspond to either minor or major third of note where it started from (and ended to). This would add to the scale a chord of type CGD a chord of type CEG or $CE\flat G$ (plus two other chords containing major or minor third. Depending on the orientation of the cycle one would obtain major or minor key. The remarkable feature of icosahedral harmonies is that they often lack a unique basic chord. Could it be that the addition of tetrahedron breaks the symmetry and fixes the key?

2. The added third could be slightly different from the icosahedral third and this could allow to resolve the problems due to the fact that quint cycle does not quite close ($(3/2)^1 2 = 2^7$ does not hold true exactly. The problems can be of course solved by introducing well-tempered scale defined in terms of powers of $2^{1/12}$: for this choices the topologically induced by these scalings is same as that induced by real topology in frequency space. Algebraically this means introduction of an algebraic extension of rationals. The problem is that persons with absolute ear prefer rational number based scale and experience tempered scale as unaesthetic.

The problem with 3-adic distance of notes was already described: the distance is 4 quints for major third (C-E) and 3 quints for minor third ($C - E\flat$). A smaller distance is suggestive for major third.

1. The proposed extension of the scale would break symmetry by bringing a third which is indeed nearest neighbor of the basic note plus two other notes, which are in corners of a *1-quint* triangle in the biological realization. Thus chord CEGandchord containing EG and third note would be introduced.

2. Using the general results one can readily find the possible extensions of harmony if one assumes that both major and parallel minor with same number of $\sharp$s or $\flat$s are obtained. The chord chosen for extension must be CGA, which an be seen as part of $C6$ or $Am7$. If the added vertex corresponds to E one obtains $C = CEG$, $Am = CEA$, and the GEA which is part of $C6/Am7$ as also the lost chord. In amino-acid analog CGA would become "empty" amino-acid, punct, and would be replaced with GEA contained also in C6. One

can perform this kind of realization for all 11 harmonies and/or their mirror images. The modification induces symmetry breaking and defines a key which is otherwise not obvious for the icosahedral harmonies. Also half-octave symmetry is broken.

3. One can perform the modification also for the inverted harmony. The transformation to reverted harmony $X \to Y$ corresponds to $X7 \leftrightarrow Y6$ and vice versa so that the presence of $X7$ type chords in harmony guarantees the existence of the required type extension in the reverted harmony. One can of course define extension also using X^7 type chords. This would generate besides CEG two dissonant chords of type $GEE\flat$ and $CEE\flat$.

4. In maximally symmetric harmony (2, 12, 6) with 6-fold rotation symmetry, there are as many as 6 manners to perform this modification so that any note of the 6-note scale spanning "impressionistic" octave can define the key. The key is either F, G, A or $Dm, E, F\sharp m$. The harmony contains however no $X7$ type chords and since the transition to the reverted harmony acts as $X6 \leftrightarrow Y7$, it does not allow a modification generating both major and parallel minor. There are also other harmonies possessing no $X6$ type chords such as $(2, 12, 6)$ and bio-harmony $(4, 8, 8)$ with 2-fold rotational symmetry so that the extension in the simplest form can be performed only for their reversals.

5. For the two harmonies with 4-fold reflection symmetry there are 2 manners to perform the modification and modified chords are related by half-octave shift. With the conventions of Table **??** the modification introduces key which is either A ($F\sharp m$) or $D\sharp$ (Cm) for both harmonies (second one is bio-harmony $(4, 8, 8)$).

About the interpretation of bio-harmonies

1. How ideas about harmony evolved?

A brief summary about the evolution of the notion of bio-harmony is in order.

1. The first guess [L16] was that amino-acids could be understood as chords of icosahedral bio-harmony characterized by 3-tuples (3, 10, 7), where the integers tell the numbers of icosahedral triangles with 0, 1, or 2 edges of the Hamiltonian cycle and identifiable as 3-chords with 0, 1, or 2 quints. The interpretation was that 3 0-quint chords correspond to 3 basic polar amino-acids, 10 1-quint chords to the 10 non-polar amino-acids, and 7 2-quint triangles to the 7 polar and acidic polar amino-acids. It turned out however that (3, 10, 7) does not appear as Hamiltonian cycle although it satisfies the necessary conditions.

2. I introduced also a model of genetic code motivated by the properties of the code table suggesting that 60 DNA codons are grouped into 3 groups of 20 codons. The idea that DNA codons coding for a given amino-acid form an orbit of a subgroup of icosahedral group with order which is not smaller than the number of these DNAs and has the aminocid at it. Three subgroups Z_6, Z_4, and Z_2 would predict 3 amino-acids coded by 6 codons and two amino-acids coded by 1 codon, 5 amino-acids coded by 4 codons, and 10 amino-acids coded by 2 codons. The total number of codons would be $3 \times 6 + 2 + 4 \times 5 + 10 \times 2 = 20 + 20 + 20 = 60$ rather than 64. The number of doublets is 10 instead of 9. Could one Z_2 orbit corresponds to punct coded by two stopping codons? But what about the codon triplet associated with Ile? Something is clearly missing.

   There is also second problem: a really realistic model of genetic code should include also 21st and 22nd amino-acids (Pyl and Sec). Pyl or pyrrolysine is modification of Lys and is basic polar amino-acid so that the number 3 of basic polar amino-acids increases to 4. Contrary to the original naive extrapolation Sec (selenocystein) is acidic polar rather than non-polar so that the number 2-quint triangles increases from 7 to 8. For the properties of amino-acids see `http://tinyurl.com/y8b7fumq`. The notion of hydrophobicity is discussed at `http://tinyurl.com/9qr8e7q`).

3. The solution of the problems came from the extension of icosahedral code with tetrahedral code bringing 4 additional codons and 3 amino-acids assigned with the external faces of the tetrahedron (Ile, Pyl, and some standard non-polar amino-acid), and increasing the number

of stopping codons from 2 to 3. This gives 60+3+1=64 codons but one should code also Pyl and Sec. The solution of the problem would be that stopping codons code also these under some conditions. Are DNA codons or their mRNA counterparts pairing with tRNAs - perhaps their magnetic body - modified somehow?

For instance, Pyl and Sec could correspond to icosahedral codons before fusion. After fusion they cease to be coded - most naturally because the group orbits containing punct are replaced with those associated with tetrahedron. The 3 ordinary amino-acids represented by tetrahedron are Ile, 1-quint amino-acid and 2-quint amino-acid. As fusion is broken temporarily Pyl and Sec are coded.

4. The geometric correlate for the fusion of the codes is gluing of tetrahedron to icosahedron along one face which corresponds to "empty" face identifiable as punct coded by stopping codons. The icosahedral Hamiltonian cycle (4, 8, 8), which exists as two variants, is extended to (4, 10, 8) with two new amino-acids.

5. The music analogy for the fusion of tetrahedron is symmetry breaking bringing in a definite key by introducing the major and minor chords as 1-quint chord (but with 2-edges since tetrahedral edges correspond to major and minor thirds).

2. Understanding the misunderstanding

This was the picture as I started to work again with the notion of bio-harmony. Just when I thought that I understand the notion, I realized that something very essential is missing and even wrong.

1. One could argue that the assumption about the correlation of forms of amino-acid polarity with character of Hamiltonian cycle leading to (4, 4, 8) identification is ad-hoc: why not allow all harmonies? One can also wonder whether the group structure behind the genetic code leading to the identification of sets of DNA codons coding for a given amino-acid as orbit of the corresponding triangle can be totally dependent on the group structure emerging from the construction of the Hamiltonian cycles.

2. The question whether the group structures associated with genetic code and with the Hamiltonian cycles might have something to do with each other leads to the realization of the obvious: the groups involved are the same: Z_6, Z_4, and Z_2! The symmetries of DNA are the symmetries of cycles. DNA code would be inherent to the Hamiltonian cycles, and the triangles of the icosahedron representing the harmony would correspond to DNA codons! 20+20+20 icosahedral triangles to 60 genetic codons and 4 icosahedral triangles the remaining 4! The three 20-plets corresponds to 3+1 amino-acids coded by 6 (resp 2) codons, to 5 amino-acids coded by 4 codons, and to 10 amino-acids coded by two codons.

   By direct inspection of the illustrations of the appendix one can indeed convince oneself that the groups in question map chords to chords of same type and one obtains appropriate number of orbits. This of course follows from group theory alone.

3. One must give up the assumption that the integers $n = (n_0, n_1, n_2)$ correspond to the numbers of the basic polar, non-polar, and polar and acidic polar implying that only $n = (4, 4, 8)$ would define bio-harmony. All Hamiltonian cycles with symmetries define bio-harmonies and both Z_2^{rot} and Z_2^{refl} define Z_2 type bio-harmonies assignable to 10 amino-acids coded by 2 codons. This is somewhat frustrating outcome, since just this correspondence served as guideline leading to the extension of the icosahedral code. The extension as such is however independent of this identification and needed in order to get the 4 missing DNA codons and to understand the coding of 21st and 22nd amino-acids Pyl and Sec.

   What do the Hamiltonian triplets n then correspond? Harmonies correlate with moods in music: maybe the serve as mathematical correlates for emotions and moods.

4. Harmonies are not for amino-acids but for DNAs coding them. One can however identify amino-acids as specific triangles the orbits and the chords associated with the amino-acids define much more restricted notion of harmony involving one representative of each basic type of chord. Perhaps the additional chords correspond to modulations of the harmony.

5. The rules of harmony generalize as such to transitions between DNA codons regarded as chords. If chords are near to each other with respect to the distance measured as quints, the transition between the chords respects harmony. One must think that DNA codons form a singular fiber space such that the union of fibers for type n gives the space of 20 amino-acids. The "gauge group" Z_n acting in the fiber is different in the 3 regions of the amino-acid space and the number of elements in the fiber is factor of n actually equal to n for $n \neq 6$ and having values 6 and 2 for $n = 6$. Each choice for the 3 Hamilton cycles of type Z_n, $n = 6, 4, 2$ defines a variant of this fiber space. The distance along the fiber isomorphic to the space of amino-acids is measured as minimal quint distance.

   Note that the DNA codons for two different variants of the fiber space need not define same kind of chord so that also given amino-acid can correspond to several different chords. It is enough that the notes of the chords are specified - as they indeed are. The Z_n, $n = 6, 4, 2$ in turn can correspond to any Hamilton cycle with symmetry Z_n so that for $n = 1, 4, 2$ one can have $1, 2, 3 + 5 = 8$ different fiber spaces. The hierarchy of Fibonacci numbers is involved. A hierarchy of symmetry breakings is highly suggestive and leads to increasingly richer harmonies.

   Z_6has maximal symmetry but Z_4 is not a subgroup of Z_6 so that only the symmetry breakings $Z_4 \to Z_2^{rot}$ and $Z_4 \to Z_2^{refl}$ can be said to occur. Note that transition between different realizations of the covering space has interpretation as a phase transition and that it could occur at RNA rather than DNA level. These phase transitions need not relate to the biochemistry but to serve as correlates for emotions and moods. Also the degeneracy due to the existence of several DNAs coding given amino-acid could have similar interpretation.

   One can of course play with more stringent scenarios for the transitions between DNAs or RNAs). For instance, the assumption that transitions can occur between chords of same type, leads to contradiction since the $Xaug$ chords of Z_6 harmony do not appear in any other harmony.

   In any case, the quint-rule in its various forms is readily testable for DNA sequences.

6. An open question concerns the change of the key. The convention of the illustrations is that 1-2 edge corresponds to C-G quint. Should one allow the DNAs at various sheets of covering space to be in different keys? Change of the key could be identified as a rotation by some number of quints. It would change the graph representing icosahedron and change the chords. Z_{12} would allow to realize all keys. Z_{12} is not however a subgroup of the icosahedral isometries (whereas $Z_6 = Z_3 \times Z_2^{rot}$ is) so that the transformation should be interpreted as a translation in quint space acting as coordinate transformation.

   The active transformations induced by isometries of icosahedron do not change the graph and would map chords to new ones. The action of Z_6 is well-defined also for other harmonies than Z_6 symmetric ones. Could the modulations of the basic key correspond to Z_6 transformations. If so, one would have 6 keys. Unfortunately, the most common modulation by quint ($G \to G$) would be missing.

   The change of key could correspond also the change of the chords defined by the extension to tetra-icosahedral harmony. One can choose the chord for extension in several manners for Z_2^{rot} and Z_2^{refl} and these choices could define the allowed modulations of the key.

7. What would be the correlates of different keys the level of DNA? An attractive assumption is that notes are realized in terms of dark photons, which could also transform to ordinary sound since living matter is piezo-electric system. The general hypothesis is that dark photons have universal energy spectrum, which is that of bio-photons. Change of key corresponds to a change of frequency scale and would correspond the change of either Planck constant or of magnetic field strength the flux tubes of the magnetic body associated with DNA codon (or amino-acid perhaps). This would mean that 12-note scale would correspond to 12-note scale for the magnetic fields strength to which cyclotron frequency is proportional or equivalently for the thickness of the flux tube since magnetic flux is quantized if monopole fluxes are in question. 12-note scale could mean in biology a standardization of frequencies used.

One must modify the extension of the icosahedral Hamiltonian cycles to tetra-icosahedral ones appropriately.

1. The Z_6 symmetric 20-plet contains 3 6-plets and 1 doublet and the Z_2 symmetric code contains 10 doublets so that here is one 11 DNA doublets in the icosahedral code. "Ordinary" amino-acids have only 9 doublets. The interpretation is that the Z_6 doublet corresponds to ile and the additional ile is coded by tetrahedral codon. The second surplus doublet can be identified as 2 codons coding for punct, "punct". This gives 4+5+ 10 =19 amino-acid if "punct" is counted.

2. What is lacking is one ile, met, trp, plus Pyl and Sec. Also 4 DNA codons are needed. One of them must code ile, one met, one for punct, and one for trp. The tetrahedral codons would thus correspond to orbits of Z_1. This is actually the only possible subgroup since for the choices $Z_n = 2, 3, 4$ the numbers of codons and amino-acids are not correct. This exhausts all DNA codons.

3. The only manner to proceed is to assume that icosahedral and tetrahedral codes can appear also as unfused versions. This would naturally occur for Z_2^{ref} for which all cycles contain $X6$ type chord but can occur also for Z_2^{rot} if the completion is done for the inverse harmony and then mapped to the harmony back. The icosahedral code would be as already described. The "free" tetrahedral codes would correspond to Z_1 and the faces coding punct in the two codes would code for Pyl and Sec. The fusion of the tetrahedral and icosahedral codes codes gives just the ordinary genetic code so that the proposal is consistent with the proposal that dark proton sequences realize genetic code [K24].

4. Note that geometrically this extension means only that the amino-acid sheet of the fiber space is extended by tetrahedral sheet.

The challenge is to construct the covering space of the icosahedron representing amino-acids.

1. The has as a local fiber the orbit under Z_n associated with the amino-acid defining base point. The space of amino-acids decomposes to disjoint regions corresponding to the 20+20-20 DNA codons. Z_n is the analog of gauge group and by symmetry breaking is different from three different regions of amino-acid space. There are $1 \times 2 \times 8 = 16$ variants of this space due to existence of several harmonies for given symmetries. There are actually only three different options for n given by $n = (0, 16, 4)$, $(2, 12, 6,$ and $(4, 8, 8)$.

2. The Z_n orbits of the three disjoint amino-acid regions (containing 3+1=4, 5, resp. 10 amino-acids) intersect each other. The challenge is to choose the representative amino-acids from the orbits of Z_n in such a manner that the chosen amino-acids belong to the three disjoint regions. It remains to be proven that this is possible. One must also understand how uniquely this can be done.

3. One could think of choosing a set P_2 of 10 representatives from the 10 orbits of Z_2 related by 6-quint scaling along Hamiltonian cycle. The 3+1+5=9 amino-acids associated with Z_6 and Z_4 would belong to the mirror images $P(S)$ of this 10-element set. $P(S)$ decomposes into set P_6 of 3+1 triangles and set P_4 of 5 triangles and there are 2-element, 4-element and 6-element orbits connecting the elements of the sets P_2, P_4, and P_6.

The following observations lead to a rather detailed and surprisingly simple picture.

1. The key observation is that the construction of the covering space - that is identifications of amino-acids at the orbits of the groups involved - depends only on whether the choice of Z_2 as Z_2^{rot} or Z_2^{refl}! Thus the two codes (ordinary one and code with Pyl and Sec coded by stop codons) are distinguished by different DNA-amino-acid covering spaces. The details of the Hamiltonian cycle do not matter. Only the structures and mutual relationships of the groups $Z_6 = Z_3 \times Z_2^{refl}$, $Z_4 = Z_2^{rot} \times Z_z^{refl}$ and Z_2^{rot} and Z_2^{refl} matter. Furthermore, the actions of the groups Z_2^{rot}, Z_3 and Z_2^{refl} determine also the actions of Z_6 and Z_4. Only Z_2^{rot} and Z_3 are non-commuting actions.

2. One can decompose amino-acids to 10 pairs of Z_2^{ref} orbits and visualize the 20 codons involved as two layers on top of each other such that two on top of each other correspond to the same 2-orbit - 2 boxes on top of each other. The choice of the two layers is not unique since one can permute the members of any vertical box pair.

Table 9.4: The representations of the associations of amino-acids to the orbits of of Z_n, $n = 6, 4, 2$ for $Z_2 = Z_2^{refl}$ (upper two rows) and $Z_2 = Z_2^{rot}$ (lower two rows). The integer n in box tells that the amino-acid associated with that box corresponds to Z_n type amino-acid. "(2)" tells that the Z_6 orbit in question consists of 2 codons.

4	6	4	6	4		4	6	4	6(2)
2	2	2	2	2	2	2	2	2	2
2	6	2	6	2		2	6	2	6(2)
4	2	4	2	4	2	4	2	4	2

3. By a suitable choice of the members of vertical box pairs one can arrange that Z_3 and Z_2^{rot} act along the two layers horizontally. Z_2^{rot} orbits divide each layer to 5 pairs of horizontal boxes. One can also permute the vertical pairs horizontally in such a manner that the 5+5 Z_2^{rot} orbits correspond to neighboring horizontal boxes along upper and lower layer giving 2+2+2+2+2 decomposition. This still leaves the possibility to permute these 5+5 horizontal pairs defining 4-orbits of Z_4 horizontally with each other.

   Simply by drawing one find that Z_3 orbits divide each layer to 3 triplets and 1 singlet and by a suitable choice Z_3 singlets correspond to the 10th box on the right for both layer. The Z_3 orbits and Z_2^{rot} orbits overlap in such a manner that the middle Z_3 orbit contains entire Z_2^{rot} orbit.

4. It is clear how to choose amino-acids from the orbits.

   (a) Consider first the $Z_2 = Z_2^{refl}$ case. The lower layer corresponds to the 10 Z_2^{refl} amino-acids (punct included) coded by 2 codons. One must choose from each Z_4 orbit consisting of a square of 4 boxes one upper box to represent Z_4 amino-acid (ala, val, gly, pro, thr). Each 4-unit contains one free upper box to which one can assign 1 Z_6 amino-acid. One cannot however put two amino-acids on 3-orbit. There are 3+1 Z_6 amino-acids and 5 boxes so that one box remains unused. This must be the case. The used box must belong to either second or third horizontal Z_2^{rot} 2-box: if it were filled, the middle Z_3 3-orbit would contain 2 Z_6 amino-acids and the fiber space-structure would fail.

   Contrary to the original intuition, the unfilled box is *not* at the 2-orbit of Z_6 containing as Ile but at the middle upper 3-orbit, which would contain 2 amino-acids if filled. It is associated with one of the 10 amino-acids coded by two codons and is same for both Z_2^{rot} and Z_2^{refl}. One expects that this amino-acid is somehow special: maybe it is punct. Also the corresponding 6-amino-acid (Ser, Arg, or Leu) might be somehow special.

   (b) $Z_2 = Z_2^{rot}$ can be treated similarly. The upper row of boxes is filled in the same manner as in the previous case. The horizontal box pairs in the lower row contain one $Z_2 rot$ box and one Z_4 box. The difference to the previous case is that Z_2 boxes are now shared by the both rows: in the previous case they belonged to the lower row.

5. The assignment of amino-acids to the orbits is not unique: for n similar orbits there are n! different assignments. Inside orbit there is also some non-uniqueness.

Table 9.4 represent the two situations graphically.

3. Music and physical correlates of emotions

Peptides are regarded as molecules of emotion and also information and positive/negative coloring of emotions would naturally correlate with the increase/reduction of negentropic resources of the system as negentropy is transferred to or from it away or increases as a whole. Music induces and expresses emotions. Therefore the idea that music in generalized form - say represented by dark photons with ELF frequencies and having energy spectrum in visible and UV energy range of bio-photons- could be the fundamental correlate of emotions and whether tetra-icosahedral music

could be in special role (note that one can associated Hamilton's cycles and "music" with any graph).

There are 11 candidates for the icosahedral harmony and its extensions. The candidates have either Z_6 (**Fig. 9.4**, Z_4 reflection symmetry (**Figs. 9.5**, **9.6**), or Z_2 rotation symmetry (**Figs. 9.7**, **9.8**, **9.9**), and Z_2 reflection symmetry (**Figs. 9.10**, **9.11**, **??**, **??**, **??**). For the first case Z^2 reflection symmetry and for the second case Z_2 rotation symmetry are represented as as half-octave shift. Second reflection symmetry corresponds geometrically to reflection in horizontal direction. The extension assigns to them definite key and adds to 1-quint chords minor and major chords absent for the icosahedral bio-harmonies. The question is whether one of these harmonies is selected in biology or whether all three can appear and are perhaps realized at the level of magnetic bodies of amino-acids.

The reversal of the harmony differs from the original one and major-minor transformation takes place. Could it be that both "moods" are realized at the level of magnetic body and even serve as the physical correlates of moods and emotions? Could emotions be realized at the level of amino-acid magnetic bodies as phase transitions affecting parts of organism or even entire organisms and in this manner changing the mood. Peptides are regarded as molecules of emotion: could these phase transitions occur only for peptides and other information molecules involving proteins? Could peptides also serve as seeds of these phase transitions? Could even the Hamiltonian cycle be changed for the magnetic body of the entire organism and correspond to some importance two-valued characteristic of emotional profile?

Could orientation reversal relate to time reversal, which in Zero Energy Ontology (ZEO) corresponds to state function at opposite boundary of causal diamond (CD)? This reversal would occur in volitional acts: the subsequent reduction would not affect the quantum state in positive energy but in TGD framework they affect the state at opposite boundary CD and in this manner give rise to the experience flow of time.

The simplest extension of the harmony in the proposed form requires that harmony possesses X_6 chord. It does not exist for for the candidate with Z_2^{rot} symmetry but for its reversal 4 of them are present as images of $D7, E7$ and $G\sharp 7, B\flat 7$ which are chords of type X^6. One can however map the harmony to its reversal, perform the completion for it, and perform the reversal back to the original harmony. The reversal depends on what note remains invariant in the reversal. One can require that it is the basic note of the chord to itself: with this condition one would obtain $Dm, Em, G\sharp m, B\flat m$ and major keys $C\sharp, F, A, H$. 4 different harmonies would result. Without the restriction the number of harmonies is different and each has different emotional characteristics.

4. Religious myths, music, and biology

These symmetries define a hierarchy of symmetry breakings. This hierarchy has amazing connections with the myths, which I believe to reflect deep facts about consciousness and biology at fundamental level expected if also consciousness is fractal. The story of genesis is a good representative in this respect.

1. The hierarchy of symmetry breakings proceeding from Z_6 down to Z_2^{refl} brings strongly in mind evolution as loss of innocence. For Z_6 one as 4 orbits. One orbit contains 2 triangles (chords, DNA codons assignable to ile). The other orbits correspond to six codons assignable to amino-acids ser, arg, and leu. The chords at the orbits are major chords and 7-chords, and minor chords and 6-chords for the inverse of the harmony.

   There are no dissonant chords in 0-quint sector: dissonances appear only for the remaining groups as 0-quint chords. This is musical representation of paradize. This harmony is based on 6-note scale for the basic notes of the chords and used by impressionistic composers. Amino-acids correspond to selections of preferred chord from each orbit and there are only four different chords: this sub-harmony is very simple. Life in paradize is simple!

2. Next comes an intriguing observation. The number of amino-acids obtained as projections of the icosahedral DNA orbits is 19, not 20. Could it be impossible to have 20 amino-acids as projections of the orbits and that 19 is the maximum number? The reason for 19 is that the number of amino-acid of type Z_6 is $3 + 1 = 4$ rather than 5. Therefore there is one "non-playable" chord - located at some "paradize orbit" -, which does not correspond to any amino-acid.

The first guess for the non-playable chord is as one of the *aug* type chords (say $CEG\sharp$, which is the last breath in many finnish tangos telling about unhappy love end - it is something between happy CM and sad Am, "raueta" is finnish word for this manner to come to an end: "expire" might be the nearest english counterpart). This chord is located at the 2-chord orbit related to the other chord of the orbit by half-octave shift (chords could be $CEG\sharp$ and $F\sharp B\flat D$), the tritonus denied by church.

Unfortunately, this identification is not consistent with the argument identifying the amino-acid chords at Z_n orbits (see table **??**) the non-playable chord must belong to an intersection of 6-orbit and 4-orbit and is not completely unique without further assumptions. It belongs to a 2-orbit of Z_2^{refl}: if it is somehow special, it could belong to the 2-orbit assignable to punct. If the chords at the 2-orbit have basic notes differing by tritonus, the inspection of the Table **??** shows that it is possible to find a unique chord pair having this property for all 5 Z_2^{refl} cycles.

One cannot avoid the associations between non-playable chord and the denied fruit hanging in the tree of good and bad knowledge in the story of Adam and Eve, and its analog in many fairy tales. The non-playable chord also brings in mind the hilarious story of Gödel-Escher-Bach about non-playable record (a truth unprovable in given axiom system).

3. The hierarchy of symmetry breakings leading from Z_6 to Z_2^{refl} encourages one to continue with the biblical analogies. Z^6, Z_4 and Z_2^{rot} cycles have half-octave shift as a symmetry: good and evil do not exist in paradise, but dissonances are already there for Z_4 and Z_2 harmonies - the evil snake! These states correspond to the consciousness of animals, children, and saints. Note that bio-harmony corresponds to the presence of one sub-harmony of type Z_n, $n = 6, 4, 2$.

4. The banishing from the paradize takes place as Z_2^{refl} symmetric harmony replaces Z_2^{rot} harmony: half-octave shift is not a symmetry anymore, and one can tell between good and evil, and eventually church decides to deny tritonus as a symbol of evil! Paradise is left as icosahedral and tetrahedral code are fused to form the tetra-icosahedral code - the ordinary genetic code leading to the breaking of Z_2^{refl} symmetry.

5. In banishment punct ("empty" amino-acid) as a counterpart of chord shared by tetrahedron and icosahedron emerges and means stopping of the music piece altogether. Death of the sinner! For unfused codes this chord is playable as Sec/Pyl and the music piece is never-ending: life is eternal in paradise! No notion of time, no sin, no death! Amusingly, impressionist music with 6-note scale is music of "now", attempt to catch this moment.

6. Also the holy trinity finds an analog as $Z_6 - Z_4 - Z_2$ trinity of the bio-harmony. Holy Spirit, Father, Son: perhaps in this order. Even more, Z_2^{rot} can be associated with Son in Heaven and $Z_2 refl$ with Son at Earth as ordinary mortal!

5. What do DNAs/amino-acids sound like?

If DNA/amino-acid sequences correspond to chord sequences of tetra-icosahedral harmony, one can ask what they sound like. The best manner to study this question is to build concrete simulations of the DNA/amino-acid sequences.

1. This requires specification of harmony by selecting one Hamiltonian cycle from the cycles belonging to the groups of cycles with Z_n, $n = 6, 4, 2$ symmetry and decomposing amino-acids to 3 groups correspondingly (those coded by 6, 4, and 2 codons). One must include tetrahedral codons and amino-acids.

2. The basic rule of harmony would be the minimization of quint distance between initial and final chords of the transition. One can consider probabilistic versions of this rule or pose strict form of the rules stating in the most stringent form that only transitions with vanishing quint distance (between neighboring triangles) are possible.

3. The transitions between different amino-acid regions would be governed by this rule. Aso the transitions between different variants of the DNA-amino-acid space defined by different choices of the Hamilton cycles would be governed by the same rule

4. The most plausible looking model considers only transitions between DNA codons since DNA sequences induce amino-acid sequences.

Appendix represents an example about randomly generated chord sequence assignable to bio-harmony defined as a composite of 3 harmonies - one from each symmetry type and $Z_2 = Z_2^{refl}$ involving tetra-icosahedral extension. Anyone having garage band skills in guitar playing can check what these chord sequences sound like and maybe try to build a melody on the background. One could also test the proposal that codons at the orbit of amino-acid define the melody by finding a concrete representation for the orbits and building random melodies defined by DNA sequences coding for the chord sequence.

Magnetic body, bio-harmonies, morphogenesis, and epigenetics

What TGD can possibly give to biology is the vision about magnetic body as an intentional agent using biological body as a sensory receptor and motor instrument and about various mechanism used by magnetic body for control and communication purposes. A new element is brought in by Zero Energy Ontology: magnetic body is 4-dimensional and thus correlate for a behavioral pattern rather than 3-D state for part of organism. Also the notion of bio-harmony suggests itself as a correlate for quantum coherence at the level of basic bio-molecules. The discussion below raises and tries to answer general questions.

The finding that behavioral patterns of planaria can be remembered also by the piece of split planaria without brains is consistent with the idea that replication of magnetic body coding for behaviors is behind biochemical replication. That alleles of the same gene have different expression could be understood if the bio-harmony assignable to gene carries additional information besides the biochemical information. An alternative explanation is that emotional memories associated with conditioning are realized at the level of the body of planaria.

These notions might also provide a fresh approach to epigenetics. Histone modification and DNA methylation are believed to induce kind of geometric locking preventing transcription. They could also affect the frequency assignable to DNA codon or some key unit so that the resonance condition making possible reconnection of U-shaped flux tubes allowing biomolecules to get in contact fails and transcription cannot proceed. Epigenetic inheritance could reduce to the inheritance of bio-harmony: the magnetic bodies of cells of offspring get in tune with those of parent. To how high degree magnetic body and bio-harmony are inherited? This becomes the key question.

1. Basic ideas related to magnetic body

Recall first some key ideas of TGD inspired quantum biology.

1. In TGD framework magnetic body extends the pair formed by organism and environment to a kind of holy trinity. Magnetic flux tubes and the realization of genetic code in terms of dark proton sequences has been the key hypothesis. The model for cold fusion [L17] suggests that also more general dark nuclei must be allowed. Dark neutron sequences could correspond to genes separated by dark protons. Dark weak interactions with large value of h_{eff} effectively massless below neuron size scale would play central role and induce large parity breaking effects (chiral selection).

   The chemistry would not be all that matters. DNA-nuclear/cell membrane as topological quantum computer with braided magnetic flux tubes would explain why organisms with virtually identical genomes are so different (we and our ancestors for instance). The hierarchy of magnetic bodies would be responsible for the development of intelligence and for cultural evolution. Flux tubes connecting DNA and mRNA as well as mRNA and tRNA molecules are present but it is difficult to say anything concrete.

2. Ontogeny could be seen as a kind of editing process for the text defined by the DNA. Control of control of... is involved so that situation is very complex. Who performs the editing? Does DNA edit itself and is the editing process defining evolution of genome coded by genome? Or is the editing performed by Darwinian selection at cell level (see `http://tinyurl.com/nd9a9ks`)? Or is the magnetic body the editor using genome also as its tool as TGD would suggest? What is important that in TGD framework self-organization

in 4-D sense implied by Zero Energy Ontology replaces ordinary self organization leading to asymptotic spatial patterns and select spatiotemporal patterns as asymptotic behavioral patterns defining various biological functions. The role of magnetic body is central in this process.

3. Magnetic body contains cyclotron Bose-Einstein condensates and cyclotron frequencies determined by the strength of magnetic field would give for DNA and other biomolecules additional characteristics. In TGD based model for musical harmony DNA codons would correspond quite concretely to 3-chords but played using dark photons (also ordinary music represented as sounds could be transformed to dark photon music). If one accepts the icosahedral model of bio-harmonies predicting genetic code correctly, there would be 256 fundamental harmonies characterised by the allowed collection of 3-chords and they would add to the information carried by DNA molecules. I have constructed a program building random sequences of the allowed chords using the additional harmonic rule that two subsequent chords contain at least one common note and this music sounds rather harmonic (albeit boring in absence of any other elements!)

4. Could one distinguish between different states/phases of DNAs, mRNAs, tRNAs, and amino acids in terms of harmony? Could their functioning depend on the harmony? With the inspiration coming from the connection of emotions and musical harmonies I have proposed that the harmony associated with a gene or organ could correlate with something analogous to an emotional state or mood - maybe micro-mood or microemotion could be the proper notion. Could amino-acids be happy, hilarious, melancholic, sad, depressed? Could one distinguish between different phases of DNA, RNA, tRNA, aminoacid collections characterized by the harmony in turn characterizing the of a cell, organelle, organ, or even organism? tRNA defines the map of the harmony associated with DNA codons to amino-acid harmony. Is the information about DNA codon and about corresponding 3-chord represented at the level of magnetic body of amino-acid- that is as the 3-chord, which it represents, and realized as the rules telling with which tRNAs amino-acid can reconnect?

   In contrast to DNA codons, which represent local information, harmony could represent holistic information and characterize entire genes or their intronic portions.

2. Problem

There is however a problem. DNA codons coding for the same amino-acid correspond to different 3-chords of harmony. One of these chords corresponds to amino-acid itself and the codons coding for amino-acid correspond to the orbit of this chord under subgroup of isometries of icosahedron moving the triangles of icosahedron along the orbit. This would apply also to mRNA and maybe also to tRNA. The chords at the orbit of amino-acid are isomorphic (intervals are same) and obtained as transposes of each other.

The chords are isomorphic but not identical and this leads to the problem with resonance paradigm unless one gives up the idea that amino-acid corresponds to a unique DNA codon and assumes that there is analog of gauge invariance allowing to choose the preferred codon freely.

1. The assumption about preferred DNA codon could be given up if one can choose the preferred DNA codon freely so that also the magnetic bodies of amino-acids are characterized by 3-chords and thus carry information about what DNA codon coded them. This is possible if one has the analog of fiber space structure with DNA codons coding for amino-acid defining the fiber and amino-acids defining the base. This fiber structure with discrete gauge invariance is strongly suggestive and I have proposed it for two decades ago but it seems that it poses strong conditions on the orbits of the subgroups of isometries of icosahedron.

   This condition is very restrictive. Simplifying somewhat: one considers 60 codons decomposing into 20+20+20 codings and each group of 20 codons codes for amino-acids belonging to different groups. There are twenty of them. The 20 triangles of icosahedron correspond to 3 DNA codons each and each of them corresponds to one and only one amino-acid. One has 3 subgroups of isometries corresponding to 20+20+20 decomposition.

Can one perform a global gauge transformations realized as isometries and moving triangles along the orbits of one of the 3 subgroups involved - say isometry g_1 of G_1? These transformations would move the entire orbits of 2 subgroups involved - call them G_2 and G_3. What happens to the chords of G_2 and G_3: is their character changed completely so that these harmonies would be destroyed? It seems that this cannot work. Should one replace G_2 and G_3 with their automorphs $g_1 G_2 g_1^{-1}$ and $g_1 G_3 g_1^{-1}$. Does this make sense? 3-chords defining give orbit should be invariant under automorphisms of G_i? This does not seem to be a realistic condition.

2. Could different automorphs correspond to different collections of chords physically just as global gauge transformations generate different physical situations? Isometries of groups G_i would therefore define physically different realizations of bio-harmonies such that for each of them only one of the DNA codons coding for given amino-acid could actually perform the coding. Ordinary genetic code with many-to-one correspondence would make sense in statistical sense only. If this is true, the cyclotron frequency 3-chord assignable to amino-acid depends on the DNA coding it and implies physical distinctions.

3. One can consider also a third alternative. DNA codon with same 3-chord as coding for amino-acid is in special role in that only it can resonate with the amino-acid! Could DNA codons codons correspond to same cyclotron frequency triplet (magnetic fields) but different value of h_{eff} so that one would have chord with respect to energy rather than frequency. Different values of h_{eff} for DNA codons coding for the same amino-acid would scale their cyclotron frequencies to the same amino-acid frequency while keeping cyclotron energies invariant? Cyclotron energy ratios for codons correspond to rational valued ratios $E_i/E_j = h_{eff}(i)/h_{eff}(j) = n(i)/n(j)$. Amino-acid would correspond to fixed h_{eff} and this creates a problem: can DNA codon code for amino-acid with different value of h_{eff}. This option does not look attractive.

Second option looks most plausible. Of course, it is early to talk about a prediction: it might well be that I have mis-understood something.

3. Questions about bio-harmony

One can pose a lot of questions about bio-harmony.

1. It is not necessary to assign any interpretation on the harmony. Just the harmony could be enough if it is forced to be same for DNA, corresponding mRNA, tRNA, and aminoacids. One can however make questions. Is the harmony inherited invariant and could it distinguish between different personality types about which we learned in old books of psychology? Or could the harmonies correlate with our own moods?

2. Could differentiation selecting particular genes as expressed genes apply also to harmonies so that given gene would correspond only to a particular harmony and different copies of gene could correspond to different harmonies. Could this selection rely on the same mechanisms as ordinary differentiation realized in terms of epigenetic mechanisms and DNA editing? From the magnetic bodies of genes the harmony would be automatically transferred to the magnetic bodies of mRNA, tRNA and aminoacids since otherwise the transcription and translation do not work since magnetic bodies do not have common resonance frequencies and reconnection and resonant interaction is not possible.

3. Does given harmony characterize given gene or the entire cell? All basic biomolecules associated with a gene would naturally correspond to the same harmony. If the rRNAs associated with ribosomes are in harmony mutually cellular harmony seems to be the only option. If ribosomes have their own harmonies, only certain ribosomes can translate given gene. This would bring in additional control tool. The most plausible picture is that the situation depends on what happens in the self-organization process. Some organs/organisms are more harmonious, others not so harmonious. Harmony need not be given fixed to remain the same: magnetic body can have motor actions changing the cyclotron frequencies. Moods could reflect the character of harmony at gene level.

4. Does magnetic body control the differentiation by posing restrictions on gene expression or vice versa? The idea about magnetic body as intentional agent suggests that the first option is correct. There would be hierarchy of magnetic bodies with magnetic bodies at the higher level controlling bodies at the lower level. The value of Planck constant would label the hierarchy levels and also DNA codons would be characterized by "intelligence quotient" defined by h_{eff}/h. This would be nothing but the analog for the hierarchy of program modules and I have earlier considered the realization of this hierarchy [L18].

5. The selection of harmony could take place and be analogous to cell differentiation. This would be a self-organization process in which magnetic bodies of genes, cells, etc.. tune themselves to resonance with each other by modifying their magnetic fields by controlling their thickness (for monopoles flux the flux is invariant). Something analogous to the development of social skills. This could pose resonance as a constraint on processes like replication, transcription, reverse transcription, silencing, enhancing, editing, etc.... It might induce the differentiation at gene level.

   Editing processes for genome could be seen as being induced by the motor actions of the magnetic body involving reconnection and change of the value of h_{eff} changing the length of the flux tube and bringing biomolecules near to each other or separating them. This selection would also apply to the intronic part of DNA proposed to be responsible for topological quantum computation like processes. The copies of same fragment appearing in intronic portion and copies of genes could correspond to different harmonies.

4. Can the notions of magnetic body and bio-harmony explain something that ordinary genetic cannot?

It would be nice to identify some biological phenomenon difficult to understand in standard framework but having an elegant explanation in terms of magnetic body.

1. The notion of harmony could manifest itself at the level of genes as different expressions for the copies of same gene if they correspond to different notions of harmony. The copies of gene are known as alleles (see `http://tinyurl.com/bpee49t`). The alleles can indeed give rise to different phenotypic traits such as different pigmentation.

2. Morphogenesis provides examples of this kind of phenomena [I120, I121, I137]. The first key idea is that DNA and cell replication is induced by the replication of magnetic bodies serving as information carriers [K62]. The second key idea is that in zero energy ontology (ZEO) magnetic body is 4-dimensional and represents behavioral patterns rather than only 3-dimensional patterns. For instance, memory as behavioral patterns can be inherited by the piece of planaria worm not containing the brain. The explanation could be that the magnetic body carries behavioral patterns replicated in the splitting of the worm.

3. Epigenetics (see `http://tinyurl.com/4xpwcm`) studies changes of gene expression not caused by the change of DNA itself. Epigenome (see `http://tinyurl.com/y9xkfb2u`) is the highly dynamic part of DNA controlling expression of the rather stable part of genome. One might regard stable part of genome as hardware and epigenome as topological quantum computer programs assignable to magnetic body and modifying gene expression epigenetically. Comment sign in computer code serves as a computer scientific metaphor for epigenetic control by repression.

The modelling of epigenesis in terms of magnetic body and bio-harmonies deserves a separate discussion.

1. The modification of transcription rate is the basic tool of epigenetic regulation. There are two basic mechanisms involved. Histone modification (see `http://tinyurl.com/y8ywse5v` affects the histones of chromatin so that the transcription is repressed or activated. Histone modification takes place by several mechanisms. DNA methylation occurs for CpG pair and if it occurs for a promoter region it represses the transcription and serves as a kind of gene lock. The degree of methylation serves as a measure for the effectiveness of repression. I do not know whether the locking is absolute at the level of single gene or whether only the

transcription rate is reduced. Two mechanisms are mentioned in the Wikipedia article (see http://tinyurl.com/y9kwrvwx). Methylation can impede geometrically some step in the transcription. Methylated site can be also accompanied by proteins affecting histones in chromatin and in this manner impede transcription.

2. The notions of magnetic body and bio-harmony suggest an alternative - one might even hope fundamental - mechanism of repression. Methylation (histone modification) could affect some cyclotron frequency associated with DNA codon (histone). In the optimal situation for transcription the DNA and protein catalyzing the transcription or mRNA are in resonance. When cyclotron resonance condition is not exactly satisfied, the reconnection rate for the U-shaped flux tubes associated with the molecules involved in the process is reduced and also transcription is repressed.

   I have considered also the radical possibility that the dynamics at the level of magnetic body is fundamental for biology and that magnetic body defines templates for the bio-molecular self-organization making dark matter dynamics visible. This is probably too extremist view and it would seem that biochemistry affects the cyclotron frequencies assignable to the magnetic body by affecting the strengths of magnetic fields also at dark magnetic flux tubes.

3. The notions of epigenetic code (see http://tinyurl.com/y8ztzzza) and histone code (see http://tinyurl.com/y854w58p) have been proposed. Epigenetic code would consist of histone modifications and additional modifications such as DNA methylation. The codeword of the epigenetic code could code for some larger unit than protein: say gene or entire cell. The hypothesis is that the chromatin-DNA interactions are induced by histone tail modifications (such as methylation, acetylation, ADP-ribosylation, ubiquitination, citrullination, and phosphorylation). There are 4 histones and the position of modification varies as well as the modifier (the above modifications are not the only ones) so so that the number of modifications is very large.

   The addition of bioharmonies to the genetic information could simplify the situation dramatically since the modifications could be seen as defining of of the 256 bio-harmonies with 64 chords each (this for fixed scale which varies if the value of magnetic field strength is varied: biophoton spectrum in visible is proposed to represent the range of values of magnetic field). The most plausible starting hypothesis is that given harmony characterizes the gene. Much simpler option would be that the harmony characterizes entire cell or even group of cells.

   If the modification by kicking cyclotron frequency out of harmony is enough to repress transcription, almost endless number of bio-chemical manners to achieve would exist but the epigenetic code could be very simple at the basic level as TGD would predict. Each bio-harmony [L12] [K43] would provide a representation of genetic code in terms of 3-chords predicting correctly the DNA-amino-acid correspondence (there are actually two slightly differing codes explaining the presence of 21st and 22nd amino-acid and deviations from the standard code). The states of dark protons (or neutrons) are also proposed to realize genetic code [L2, K24]: it is an open question whether these codes imply each other as they should.

4. The understanding of transgenerational epigenetic inheritance (see http://tinyurl.com/h6qg64c) raises difficult challenges. One should understand how histone modification and DNA methylation are transferred to daughter cells in cellular division or inherited by the offspring. Transgenerational interaction of the genomes seems necessary. In TGD framework the interaction of magnetic bodies of via resonance mechanism could transfer the epigenetic programs to the offspring. Offspring could "learn" the epigenetic programs of the mother by tuning.

5. Gregory Carey (see http://tinyurl.com/ydyznsaq) gives nice real life examples about the complexities of epigenesis identified quite generally as gene regulation (see http://tinyurl.com/zb97cgs). He compares the gene regulation involved with the handling of a stressful situation to "nightmarish Rube Goldberg mousetrap" and sees the process as extremely ineffective from engineering point of view. For instance, the hormones secreted to blood circulation are distributed to the entire body. The whole thing could be carried out in brain! He also wonders why evolution is so inefficient. All cells have same genome although most of

the genes are silenced. Second strand of DNA is totally un-used and most of DNA consists of introns. His explanation is that evolution does not make long term plans but finds just a solution to a particular without thinking it from a wider perspective: "If it ain't broke, don't fix it".

I tend to see this differently. If entire body is coherent quantum entity, engineering based thinking does not make sense. Entire body and also magnetic body must be informed from the stress situation since the reaction is holistic. The genes which are not used for gene expression might be used for other purposes. Topological quantum computation could be this purpose in TGD framework and repressed genes could be thus used for quantum information processing. Information processing could be actually the dominating function of the DNA of higher vertebrates.

To sum up, magnetic body could be seen as the "boss" controlling the gene expression and also the evolution of genome in longer scales. Magnetic body would use bio-molecular mechanisms for its purposes. This would bring in a new kind of inheritance: bio-harmony would be inherited. The most spectacular almost-prediction would be that genetic code is many-to-one only in statistical sense.

5. RNA is transferred between soma cells and germ cells

The basic question of epigenesis is how the information between soma cells and germ cells is transferred. In standard genetic the transfoer RNA or DNA molecules is necessary to achieve this. In TGD dark DNA, RNA, tRNA, and aminocids consisting of dark nucleons realized as nuclear strings and accompanied by the corresponding biomolecules is one possibility. The extremist view would be that the dynamics of the dark variants of basic bio-molecules induces the dynamics of their molecular shadows making them only visible. Also the transfer of information as cyclotron radiation can be considered in TGD framework and cyclotron resonance could serve as a fundamental mechanism of epigenetic control. The above model suggest that epigenetic control mechanisms rely on resonance mechanism for 3-chords associated with DNA codons and other biomolecules giving them "names" is also at work besides purely geometrical silencing.

The popular article "No Sex Required: Body Cells Transfer Genetic Info Directly Into Sperm Cells, Amazing Study Finds" (see `http://tinyurl.com/hhdth5j`) summarizing the findings discussed in the article [I75] (see "Soma-to-Germline Transmission of RNA in Mice Xenografted with Human Tumour Cells: Possible Transport by Exosomes" (see `http://tinyurl.com/yde7wb55`) as very interesting concerning this basic question.

The abstract of the article gives for a professional a readable summary.

Mendelian laws provide the universal founding paradigm for the mechanism of genetic inheritance through which characters are segregated and assorted. In recent years, however, parallel with the rapid growth of epigenetic studies, cases of inheritance deviating from Mendelian patterns have emerged. Growing studies underscore phenotypic variations and increased risk of pathologies that are transgenerationally inherited in a non-Mendelian fashion in the absence of any classically identifiable mutation or predisposing genetic lesion in the genome of individuals who develop the disease. Non-Mendelian inheritance is most often transmitted through the germline in consequence of primary events occurring in somatic cells, implying soma-to-germ line transmission of information. While studies of sperm cells suggest that epigenetic variations can potentially underlie phenotypic alterations across generations, no instance of transmission of DNA- or RNA-mediated information from somatic to germ cells has been reported as yet.

To address these issues, we have now generated a mouse model xenografted with human melanoma cells stably expressing EGFP-encoding plasmid. We find that EGFP RNA is released from the xenografted human cells into the bloodstream and eventually in spermatozoa of the mice. Tumor-released EGFP RNA is associated with an extracellular fraction processed for exosome purification and expressing exosomal markers, in all steps of the process, from the xenografted cancer cells to the spermatozoa of the recipient animals, strongly suggesting that exosomes are the carriers of a flow of information from somatic cells to gametes. Together, these results indicate that somatic RNA is transferred to sperm cells, which can therefore act as the final recipients of somatic cell-derived information.

Some background is needed to understand this rather technical summary.

1. Darwinism has dominated biology since Darwin. The rules of classical Mendelian inheritance conform with the Darwinian view and can be reduced to genetic level. Various traits are inherited genetically by sexual reproduction and genome would change during lifetime only through mutations. Genome changes exremely slowly by random changes for offspring from which selection pressures choose the survivors.

   Lamarckian view in turn assumed that the external circumstances experienced by organism leave a trace, which can be inherited but it could not be formulated in terms of modern molecular biology whereas the Darwinian dogma could be formulated in terms of Weissman's genetic barrier. Information flows from germ cells to soma but never in opposite direction. If it would do so, the soma interacting with environment could transfer information to germ cells and the experiences during lifetime could leave inheritable trace to germ cells.

   An analogous dogma is that information is always transcribed from DNA to RNA to proteins but never in opposite direction. It is now known that this takes place in case of viruses and retroviruses: there are so called jumping genes which can also make copies of themselves. 5 per cent of human genome conists of endogenous retroviruses capable of doing the same. The huge genome of maize is due to this kind of proces.

2. The development epigenetics has started to shatter the belief on Wessimann's genetic barrier. Gene expression is not fixed by genome alone and can be change even when genes are unaffected. Silencing of genes by DNA methylation and histone modification allow to modify gene expression. Silencing is essentially a locking of gene preventing its expression by transcription followed by translation.

   It is now known that epigenetic changes in the gene expression can be inherited. The mechanisms are still poorly understood. What seems however clear the genome is more like a slowly changing hardware and gene expression or whatever is behind it is the software and programs can change very rapidly by just adding or deleting comment signs in the code. A deeper understanding of this software is needed.

3. Epigenetic inheritance requires that genetic information is transferred from soma cells to germ cells. If only DNA or RNA are capable of representing genetic information, then DNA or RNA must be transferred from soma cells to germ cells. No instance of direct DNA or RNA mediated information from soma to germ cells had been observed before the above mentioned experiments. One can of course challenge the assumption about DNA and RNA as the only representations of genetic information.

The basic idea of the experiment was simple. Use a marker for RNA by using plasmids (DNA strands not belonging to chromosomes) genetically engineered to code for a marker protein making itself visible by fluorescence. Then one just follows the fate of these proteins generated in soma cells and looks whether they end up inside germ cells and how this happens.

More technically: mouse model was xenografted with human melanoma cells stably expessing EGFP-coding plasmid (expressed in a manner possibly evoking emotions: human melanoma cancer tissue was implanted in mouse). EGFP-RNA is released from xenografted human cells to blood. One just looks whether it eventually ends up to the sperm cells of mice and tries to identify the transfer mechanism. Only transfer to sperm cells was studied. One might expect that the transfer of RNA can happen also to ovum. I guess that the sperm cells are easier to study.

What was observed?

1. The transfer of RNA from soma cells to sperm cells was indeed found to occur. The transferred RNA can in turn induce epigenetic effects in germ cells known to be inherited by a mechanisms, which however remain poorly understood. Epigenetic mechanisms seem to be involved in the cases considered so that DNA is not changed, only its expression.

2. The transfer mechanism was identified. The transferred RNA is contained by exosomes analogous to synaptic vesicles transferring neurotransmitters from presynaptic to postsynaptic cell. Transfer of RNA takes place via fusion of the membranes just like transfer of neurotransmitters. Maybe genetic engineering using exosomes or analogous structures to transfer the needed material to cells has been tried.

The implications of the findings are dramatic but already implied by the earlier work in epigenetics. What is important that Lamarckian view can be now defended by a concrete genetic mechanism. Lamarckism implies that the time scale of inheritance becomes the time scale for the appearence of a new generation. Nutrition, environment, lifestyle and even meditation and similar practices, are already now known to affect gene expression on daily basis: we are not victims of genetic determinism and are epigenetically responsible for our own well-being. Epigenetic information can be transferred also to germ cells so that we responsible also for the well-being of our children. Our children suffer our sins and share our sufferings.

The precise mechanism of inheritance of epigenetic modifications remains still poorly understood although it seems that the transfer or RNA to germ cells occurs. There are also other hints: it is known that alleles (variants of game gene) can express themselves differently. One allele can also induce other allele to express in the same manner. Somekind of "social pressure" like interaction seems to be involved.

As explained, TGD suggests the notion of magnetic body and cyclotron resonance as this interaction. The DNA of offspring get tuned to the DNA of mother during pregnancy and this gives to epigenetic inheritance. Various epigenetic mechanisms such as methylation and histone modification could affect cyclotron frequencies besides purely geometric modifications of DNA and locking at the level of gene could be accompanied kicking out of tune at the level of magnetic body. In this framework the transfer of RNA to germ cells would be necessary to affect the cyclotron frequencies.

$\mathbf{E}_8$ symmetry, harmony, and genetic code

Bee gave in Facebook a link to an article about a connection between icosahedron and E_8 root system [B18] (see `http://tinyurl.com/zotpm4b`). The article (I have seen an article about the same idea earlier but forgotten it!) is very interesting.

The article talks about a connection between icosahedron and E_8 root system (see `http://tinyurl.com/y7csb6uh`). Icosahedral group has 120 elements and its double covering $2\times 120 = 240$ elements. Remarkably, E_8 root system has 240 roots. E_8 Lie algebra is 248 complex-dimensional contains also the 8 commuting generators of Cartan algebra besides roots: it is essential that the fundamental representation of E_8 co-incides with its adjoint representation. The double covering group of icosahedral group acts as the Weyl group E_8. A further crucial point is that the Clifford algebra in dimension $D = 3$ is 8-D.

One starts from the symmetries of 3-D icosahedron and ends up with 4-D root system F_4 assignable to Lie group and also to E_8 root system. E_8 defines a lattice in 8-D Euclidian space: what is intriguing that dimensions 3,4, 8 fundamental in TGD emerge. To me this looks fascinating - the reasons will be explained below.

1. What I might have understood

I try to explain what I have possibly understood.

1. The notion of root system is introduced. The negatives of roots are also roots but not other multiples. Root system is crystallographic if it allows a subset of roots (so called simple roots) such that all roots are expressible as combinations of these simple roots with coefficients having the same sign. Crystallographic root systems are special: they correspond to the fundamental weights of some Lie algebra. In this case the roots can be identified essentially as the quantum numbers of fundamental representations from which all other representations are obtained as tensor products. Root systems allow reflections as symmetries taking root system to itself. This symmetry group is known as Coxeter group and generalizes Weyl group. Both H_3 and H_4 are Coxeter groups but not Weyl groups.

2. 3-D root systems known as Platonic roots systems (A_3, B_3, H_3) assignable to the symmetries of tetrahedron, octahedron (or cube), and icosahedron (or dodecahedron) are constructed. The root systems consist of 3 suitably chosen unit vectors with square equal to 1 (square of reflection equals to one) and the Clifford algebra elements generated by them by standard Clifford algebra product. The resulting set has a structure of discrete group and is generated by reflections in hyper-planes defined by the roots just as Weyl group does. This group acts also on spinors and one obtains a double covering SU(2) of rotation group SO(3) and its

discrete subgroups doubling the number of elements. Platonic symmetries correspond to the Coxeter groups for a "Platonic root system" generated by 3 unit vectors defining the basis of 3-D Clifford algebra. H_3 is not associated with any Lie algebra but A_3 and B_3 are.

Pinors (spinors) correspond to products of arbitrary/even number of Clifford algebra elements. Spinors induced orientation preserving transformations and pinos also orientation reversing ones. They mean something else than usually a bein identified as elements of the Clifford algebra acting and being acted on from left or right by multiplication so that they always behave like spin 1/2 objects since only the left(right)-most spin is counted. The automorphisms involve both right and left multiplication reducing to SO(3) action and see the entire spin of the Clifford algebra element.

3. The 3-D root systems (A_3, B_3, H_3) are shown to allow an extension to 4-D root systems known as (D_4, F_4, H_4) in terms of 3-D spinors. D_4 and F_4 are root systems of Lie algebras (see `http://tinyurl.com/y97dzqc2`). F_4 corresponds to non-simply-laced Lie group related to octonions. H_4 is not a root system of any Lie algebra.

4. The observation that the dimension of Clifford algebra of 3-D space is $2^3 = 8$ and thus allows imbedding of at most 8-D root system must have inspired the idea that it might be possible to construct the root system of E_8 in 8-D Clifford algebra from 240 pinors of the double covering the 120 icosahedral reflections. Platonic solids would be behind all exceptional symmetry groups since E_6 and E_7 are subgroups of E_8 and the construction should give their root systems also as low-dimensional root systems.

2. McKay correspondence

The article explains also McKay correspondence stating that the finite subgroups of rotation group SU(2) correspond to simply laced affine algebras assignable with ADE Lie groups.

1. One considers the irreducible representations of a finite subgroup of the rotation group. Let the number of non-trivial representations be m so that by counting also the trivial representation one has $m + 1$ irreps altogether. In the Dynkin diagram of affine algebra of group with m-D Cartan algebra the trivial representation corresponds to the added node. One decomposes the tensor product of given irrep with the spin 2 representation into direct sum of irreps and constructs a diagram in which the node associated with the irrep is connected to those nodes for which corresponding representation appears in the direct sum. One can say that going between the connected nodes corresponds to forming a tensor product with the fundamental representation. It would be interesting to know what happens if one constructs analogous diagrams by considering finite subgroups of arbitrary Lie group and forming tensor products with the fundamental representation.

2. The surprising outcome is that the resulting diagram corresponds to a Dynkin diagram of affine (Kac-Moody) algebra of ADE group with Cartan algebra, whose dimension is m. Cartan algebra elements correspond to tensor powers of fundamental representation: can one build any physical picture from this? For $m = 6, 7, 8$ one obtains E_6 , E_7 , E_8. The result of the article implies that these 3 Lie-groups correspond to basis of 3 3-D unit identified as units of Clifford algebra: could this identification have some concrete meaning as preferred non-orthogonal 3-basis?

3. McKay correspondence emerges also for inclusions of hyper-finite factors of type II_1 [K57] The integer m characterizing the index of inclusion corresponds to the dimensions of Cartan algebra for ADE type Lie group. The inclusions of hyperfinite factors (HFFs) are characterized by integer $m \geq 3$ giving the dimension of Cartan algebra of ADE Lie groups (there are also C, F and G type Lie groups). m= 6,7,8 corresponds to exceptional groups E_6 , E_7 , E_8 on one hand and to the discrete symmetry groups of tetrahedron, octahedron, icosahedron on the other hand acting as symmetries of corresponding 3-D non-crystallographic systems and not allowing interpretation as Weyl group of Lie group.

3. Connection with the TGD based model of harmony

These findings become really exciting from TGD point of view when one recalls that the model for bioharmony [K43] [L12] (see `http://tinyurl.com/yad4tqwl`) for 12-note harmonies central in classical music in general relies on icosahedral geometry. Bioharmonies would add something to the information content of the genetic code: DNA codons consisting of 3 letters A,T,C,G would correspond to 3-chords defining given harmony realized as dark photon 3-chords and maybe also in terms of ordinary audible 3-chords. This kind of harmonies would be roughly triplets of 3 basic harmonies and there would be 256 of them (the number depends on counting criteria). The harmonies could serve as correlates for moods and emotional states in very general sense: even biomolecules could have "moods". This new information should be seen in biology. For instance, different alleles of same gene are known to have different phenotypes: could they correspond to different harmonies? In epigenetics the harmonies could serve as a central notion and allow to realize the conjectured epigenetic code and histone code. Magnetic body and dark matter at them would be of course the essential additional element.

The inspiring observations are that icosahedron has 12 vertices - the number of notes in 12-note harmony and 20 faces- the number of amino-acids and that DNA codons consist of three letters - the notes of 3-chord.

1. Given harmony would be defined by a particular representation of Pythagorean 12-note scale represented as self-non-intersecting path (Hamiltonian cycle) connecting the neighboring vertices of icosahedron and going through all 12 vertices. One assumes that neighboring vertices differ by one quint (frequency scaling by factor 3/2): quint scale indeed gives full octave when one projects to the basic octave. One obtains several realizations (in the sense of not being related by isometry of icosahedron) of 12-note scale. These realizations are characterized by symmetry groups mapping the chords of harmony to chords of the same harmony. These symmetry groups are subgroups of the icosahedral group: Z_6, Z_4, and two variants of Z_2 (generated by rotation of π and by reflection) appear. Each Hamiltonian cycle defines a particular notion of harmony with allowed 3-chords identified by the 20 triangles of icosahedron.

2. Pythagoras is trying to whisper me an unpleasant message: the quint cycle does not quite close! This is true. Musicologists have been suffering for two millenia of this problem. One must introduce 13th note differing only slightly from some note in the quint cycle. At geometrical level one must introduce tetrahedron besides icosahedron - only four notes and four chords and gluing along one side to icosahedron gives only one note more. One can keep tetrahedron also as disjoint from icosahedron as it turns out: this would give 4-note harmony with 4 chords something much simpler that 12- note harmony.

3. The really astonishing discovery was that one can understand genetic code in this framework. First one takes three different types of 20-chord harmonies with group Z_6, Z_4, and Z_2 defined by Hamiltonian cycles: this can be done in many different maners (there are 256 of them). One has 20+20+20 chords and one finds that they correspond nicely to 20+20+20=60 DNA codons: DNA codons coding for a given amino-acid correspond to the orbit of the triangle assigned with the amino-acid under the symmetry group of harmony in question.

   The problem is that there are 64 codons, not 60. The introduction of tetrahedron brings however 4 additional codons and gives 64 codons altogether. One can map the resulting 64 chord harmony to icosahedron with 20 triangles (aminoacids) and the degeneracies (number of DNA codons coding for given amino-acid in vertebrate code) come out correctly! Even the two additional troublesome amino-acids Pyl and Sec appearing in Nature and the presence of two variants of genetic code (relating to two kinds of Z_2 subgroups) can be understood.

4. What could the interpretation of the icosahedral symmetry?

An open problem is the proper interpretation of the icosahedral symmetry.

1. A reasonable looking guess would be that it quite concretely corresponds to a symmetry of some biomolecule: both icosahedral or dodecahedral geometry give rise to icosahedral symmetry. There are a lot of biomolecules with icosahedral symmetry, such as clathrate molecules at the axonal ends and viruses. Note that dodecahedral scale has 20 notes - this

might make sense for Eastern harmonies - and 12 chords and there is only single dodecahedral Hamiltonian path found already by Hamilton and thus only single harmony. Duality between East and West might exist if there is mapping of icosahedral notes and to dodecahedral 5-chords and dodecahedral notes to icosahedral 3-chords and different notions of harmony are mapped to different notions of melody - whatever the latter might mean!).

2. A more abstract approach tries to combine the above described pieces of wisdom together. The dynamical gauge group E_8 (or Kac-Moody group) emerging for m=8 inclusion of HFFs is closely related to the inclusions for the fractal hierarchy of isomorphic sub-algebras of super-symplectic subalgebra. $h_{eff}/h = n$ could label the sub-algebras: the conformal weights of sub-algebra are be n-multiples of those of the entire algebra.

   The integers n_i resp. n_f for included resp. including super conformal sub-algebra would be naturally related by $n_f = m \times n_i$. $m = 8$ would correspond to icosahedral inclusion and E_8 would be the dynamical gauge group characterizing dark gauge degrees of freedom. The inclusion hierarchy would allow to realize all ADE groups as dynamical gauge groups or more plausibly, as Kac-Moody type symmetry groups associated with dark matter and characterizing the degrees of freedom allowed by finite measurement resolution.

3. E_8 as dynamical gauge group or Kac-Moody group would result from the super-symplectic group by dividing it with its subgroup representing degrees of freedom below measurement resolution. E_8 could be the symmetry group of dark living matter. Bioharmonies as products of three fundamental harmonies could relate directly to the hierarchies of Planck constants and various generalized super-conformal symmetries of TGD! This convergence of totally different theory threads would be really nice!

5. Experimental indications for dynamical E_8 symmetry

Lubos (see `http://tinyurl.com/htjp55h`) (thanks to Ulla for the link to the posting of Lubos) has written posting about experimental finding of E_8 symmetry emerging near the quantum critical point of Ising chain at quantum criticality at zero temperature. Here is the abstract (see `http://tinyurl.com/zulzk9y`):

Quantum phase transitions take place between distinct phases of matter at zero temperature. Near the transition point, exotic quantum symmetries can emerge that govern the excitation spectrum of the system. A symmetry described by the E_8 Lie group with a spectrum of eight particles was long predicted to appear near the critical point of an Ising chain. We realize this system experimentally by using strong transverse magnetic fields to tune the quasione-dimensional Ising ferromagnet CoNb2O6 (cobalt niobate) through its critical point. Spin excitations are observed to change character from pairs of kinks in the ordered phase to spin-flips in the paramagnetic phase. Just below the critical field, the spin dynamics shows a fine structure with two sharp modes at low energies, in a ratio that approaches the golden mean predicted for the first two meson particles of the E8 spectrum. Our results demonstrate the power of symmetry to describe complex quantum behaviors.

Phase transition leads from ferromagnetic to paramagnetic phase and spin excitations as pairs of kinks are replaced with spin flips (shortest possible pair of kinks and loss of the ferromagnetic order). In attempts to interpret the situation in TGD context, one must however remember that dynamical E_8 is also predicted by standard physics so that one must be cautious in order to not draw too optimistic conclusions.

In TGD framework $h_{eff}/h \geq 1$ phases or phase transitions between them are associated with quantum criticality and it is encouraging that the system discussed is quantum critical and 1-dimensional.

1. The large value of h_{eff} would be associated with dark magnetic body assignable to the magnetic fields accompanying the E_8 "mesons". Zero temperature is not a prerequisite of quantum criticality in TGD framework.

2. One should clarify what quantum criticality exactly means in TGD framework. In positive energy ontology the notion of state becomes fuzzy at criticality. For instance, it is difficult to assign the above described "mesons" with either ferromagnetic or paramagnetic phase since

they are most naturally associated with the phase change. Hence Zero Energy Ontology (ZEO) might show its power in the description of (quantum) critical phase transitions.

Quantum criticality could correspond to zero energy states for which the value of h_{eff} differs at the opposite boundaries of causal diamond (CD). Space-time surface between boundaries of CD would describe the transition classically. If so, then E_8 "mesons" would be genuinely 4-D objects - "transitons" - allowing proper description only in ZEO. This could apply quite generally to the excitations associated with quantum criticality. Living matter is key example of quantum criticality and here "transitons" could be seen as building bricks of behavioral patterns. Maybe it makes sense to speak even about Bose-Einstein condensates of "transitons".

The finding suggests that quantum criticality is associated with the transition increasing $n_{eff} = h_{eff}/h$ by factor $m = 8$ or its reversal - maybe the standard value $n_{eff}(i) = 1$. $n_{eff}(f) = 8$ could correspond to the ferromagnetic phase having long range correlations. Could one say that at the side of criticality (say the "lower" end of CD) the $n_{eff}(f) = 8$ excitations are pure gauge excitations and thus "below measurement resolution" but become real at the other side of criticality (the "upper" end of CD)?

3. The 8 "mesons" associated with spin excitations naturally correspond to the generators of the Cartan algebra of E_8. If the "mesons" belong to the fundamental (= adjoint) representation of E_8, one would expect 120+120 additional particles with non-vanishing E_8 charges. Why only Cartan algebra? Is the reasons that Cartan algebra is in preferred role in the representations of Kac-Moody algebras in that charged Kac-Moody generators can be constructed from Cartan algebra generators by standard construction used also in string models. Could this explain why one expects only 8 "mesons". Are charged "mesons" labelled by the elements of double covering of icosahedral group more difficult to excite?

9.8.3 Icosahedral Harmonies

In the following the icosahedral harmonies are discussed in detail. This includes overall summary and tables giving the 20 3-chords of the harmonies and illustrations of the Hamiltonian cycles.

About symmetries of the icosahedral harmonies

Some words about the symmetries associated with the icosahedral harmonies and genetic code are in order.

There are 3 different kind of bio-harmonies characterized partially by the symmetry group which can be Z_6, Z_4 or Z_2 which acts either as rotations or reflections.

1. The first variant as $Z_3^{rot} \times Z_2^{refl}$ subgroup of icosahedral group as symmetries and its orbits correspond to 3 6-plets and 1 2-plets for which Z_3 leaves the triangle invariant. The counterparts for the orbits are 3 DNA 6-plets and one 2-plet.

2. The second variant has Z_4 symmetry generated by two commuting reflection as symmetries as is obvious from figures **??**, **??**: the reflections act on vertical and horizontal coordinates. The orbits are five 4-plets of chords. Vertical reflection induces half-octave shift and horizontal one permutes the note sequences $B\flat CDG\sharp F\sharp E$ and $D\sharp C\sharp HFGA$.

3. Z_2^{rot} or Z_2^{refl} acts as symmetries of the remaining 3+5 cycles. The covering space of 10 amino-acids involved defined by 20 DNA codons decomposes to 10 2-plets.

   The 2-fold rotation symmetry of the Hamiltonian cycles is obvious from the illustration **??**: it corresponds to 6-quint rotation and the chord sets must be invariant under this rotation. This rotation corresponds to the 1/2 octave shift realized as rotation. These symmetries are realized as "coordinate transformations" for the cycle - a curve in the "imbedding space" defined by icosahedron but induced from the "imbedding space symmetries" acting as isometries of icosahedron.

DNA codons have also almost exact Z_2 symmetry discussed in [K53, K17, K19].

1. For the last codon the reflection A-T, C-G is an almost symmetry broken only for special cases. This approximate symmetry could be understood as following from the fact that the number of DNAs coding given amino-adic is even in most cases. The exceptions are ile, met, trp coded by odd number of DNA codons. By mapping DNAs to binary sequences one can order the situation so that the 6: th binary digit is the almost-symmetry digit.

2. What is trivial is that RNA has chosen the third bi-digit to be the almost symmetry digit with the ordering UCAG of the nucleotides so that a genuine physical symmetry is in question. An interesting question is how this symmetry relates to the model of genetic code based on tetra-icosahedral orbits.

   The restriction of DNAs to 60 icosahedral DNAs demonstrates that this symmetry originates from the icosahedral Z_2. The tetrahedral extension of the code breaks this symmetry by extending ile and punct multiples by one codon and introducing also 4 singlets met, trp, Pyl, and Sec.

The detailed correspondence between chords of the harmony and DNA codons is also a problem to be solved.

1. The correspondence matters in the proposed scenario since the chords at at the orbits are different and the gluing of tetrahedron breaks the symmetry in Z_2 sectors so that quint rule determining harmonic DNA sequences is different.

2. The common face of tetrahedron and icosahedron corresponds to punct so that the quint rule for different representations says something about the pairs of form codon-stop codon that is about the codon preceding the last codon of gene! This codon could allow to recognize what Hamiltonian cycle is in question. If C-major is one of the added chords, stop codons correspond to what was $C6 = CGA$ chord and its Z_2 image, which is $X7$ type chord. By the strongest form of the quint rule only the chords having common notes with these chords would correspond to DNA codons of Z_6 and Z_4 cycles which can precede stopping codon.

3. There are some restrictions on the correspondence. Z_2^{refl} symmetry would correspond to the flipping of the 6th bit for the bit representation defined by nucleotides representing 2-bits in the case of $Z^3 = Z_3 \times Z_2^{refl}$. $Z_4 = Z_2^{rot} \times Z_2^{refl}$. For $Z_2 = Z_2^{rot}$ the role of Z_2^{refl} must be taken by Z_2^{rot}. One can of course ask whether Z_2^{rot} cycles are realized at all. For Z_4 cycles Z_2^{rot} would correspond to symmetry permuting the AT, CG doublets for the first nucleotide. For Z_6 subgroup Z_3 would cyclically permute the 3 doublets with respect to third nucleotide. These constraints do not fix the correspondence completely.

To sum up, there is a connection between genetic code and the groups acting along the Hamiltonian cycle. The simplest option fixes the orbits of the triangles and therefore also the representation of genetic code.

Summary of the basic results

One can find the list of Hamiltonian cycles at `http://tinyurl.com/yacgzm9x`. The edge $\{1, 2\}$ is fixed and cycles are oriented so that there are 1024 of them. All of them are relevant from the point of music interpretation and the change of orientation corresponds to major-minor duality, albeit not in the simplest sense. Note that this duality does not affect the characteristics listed above.

The general following general results hold true as one can learn at `http://tinyurl.com/pmghcwd`. One can classify the cycles using their symmetries which can correspond to isometries of icosahedron leaving them fixed or to a reflection taking the vertex n at the cycle to vertex $12 - n$. This symmetry is not same as change of orientation which is purely internal operation and cannot change the cycle.

One can even find images of the cycles possessing symmetries at `http://tinyurl.com/y8ek7ak8` and deduce the triplets n and p characterizing them by visual inspection. Also one can write explicitly the 3-chords defined by the three kinds of faces. I have deduced the triplets n and the 3-chords defining the harmony by the inspection of the images. "Bio-harmony" (4, 8, 8) forced by the model of extended genetic code involving also the 21st and 22nd amino-acids is of

Table 9.5: Notation of chords inspired by popular music notations.

$$\begin{array}{llll} CEG \equiv C\ , & CD\sharp G \equiv Cm\ , & CD\sharp F\sharp \equiv C^o\ , & CEG\sharp \equiv Caug\ , \\ CFG \equiv C4\ , & CF\sharp G \equiv C4_+\ , & CGG\sharp \equiv C6_-\ , & CGA \equiv C6\ , \\ CGB\flat \equiv C7\ , & CGB \equiv Cmaj7\ , & CGC\sharp \equiv C9_-\ , & CGD \equiv C9\ . \end{array} \tag{9.8.1}$$

special interest.The classes of cycles with symmetries 6-fold rotational symmetry and two distinct reflection symmetries realize it.

Before continuing some terminology and notation is in order. Take C as the major key. Submediant or relative minor corresponds to Am, subdominant (sharp or flat) to F major (F) or Fminor (Fm), dominant to G. The notation for chords is such that quints correspond to subsequent notes in the chord. For 1-quint chords this means that first two notes define the quint. **Table 9.5** the notation inspired by the popular music notation. The basic different is that the third is in most cases excluded so that the emotional character of the chord is not fixed.
Besides these notions it is convenient to introduce additional notations for various dissonant chords appearing as 0-quint chords.

$$\begin{array}{llll} CC\sharp D \equiv Cex1\ , & CC\sharp D\sharp \equiv Cex2\ , & CDD\sharp \equiv Cex3\ , & CDE \equiv Cex4\ , \\ CD\sharp E \equiv Cex5\ , & CC\sharp E \equiv Cex6\ , & CDF\sharp \equiv Cex7\ , & CDG\sharp \equiv Cex8\ . \end{array} \tag{9.8.2}$$

Clearly, the sets {ex1}, {ex2, ex3}, {ex4, ex5, ex6}, {ex7}, {ex8}, corresponds to the span of 2, 3, 4, 6, 8 half notes for the chord. The following summarizes the results. Note that $Cex7$ can be seen as part of $D7$ chord.

1. There are 6 collections of cycles without any symmetries containing 48 cycles each: these 48 cycle are mutually isometric so that one can say that there 6 different harmonies.

2. There is a collection with 6-fold rotational symmetry, 48/6=8 examples. $n = (2, 12, 6)$. The chords of this scale define 6-note scale involving only total steps. CDFandits 6 translates by integer number of steps define 6 1-quint chords. $CE\flat G$ (Cm) and its 6 translates (they obviously correspond to the 6-fold rotational symmetry) define also 6 1-quint chords. The reflection transforms these series to those defined by $GB\flat G$ and its translate and byFAC (F major) and its translates. Impressionists like Debussy used 6-note scale of this kind. Half-octave shift is an exact symmetry. 1-chords lack the third so that one cannot assign to 3-chords any emotional quality. The extension to 4-chord can however bring either "happy" or "sad" quality. Clearly, these harmonies have "jazzy" character.

   0-quint chords are $Faug \equiv FAC\sharp$ and $Gaug \equiv GHD\sharp$ are transformed to each other by both half-octave shift and inversion.

3. There are 2 collections with 2 distinct reflectional symmetries with 12=48/4 representatives in each. Half-octave scaling is a symmetry of both these scales as one might guess.

   The first cycle (see **Fig. 9.5**) has $n = (0, 16, 4)$ so that there are no 0-quint chords which in general are dissonant. Second cycle (see **Fig. 9.6**) realizes $n = (4, 8, 8)$ bio-harmony and deserves some comments. It will be discussed in detail later.

   (a) The 8 2-quint chords consist of $B\flat FG \equiv B\flat 9$, C9, F9, G9 and their half-octave scalings. Clearly, the simple four-note scale appears here.

   (b) Using the popular notion introduced earlier 1-quint chords consist of two 4-plets $Dmaj7$, $E9_-$, $A7$, $A6$ and $G\sharp maj7$, $B\flat 9_-$, $D\sharp 7$, $D\sharp 6$ related by half-octave shift. The harmony contains no "simple" major or minor chord and only the extension to tetrahedral harmony can provide them. The same is true for the second bio-harmony.

   (c) The 4 0-quint chords are $Cex3 \equiv CDD\sharp$ and $Eex2 \equiv EFG$ and their half-octave scalings $F\sharp ex3 \equiv F\sharp G\sharp A$ and $B\flat ex2 \equiv B\flat BC\sharp G$.

4. There are 3 collections with Z_2 rotational symmetry with $48/2 = 24$ representatives in each. The triplets n are $(0, 16, 4)$ (see **Fig. 9.7**), $(2, 12, 6)$ (see **Fig. 9.8**), and $(4, 8, 8)$ (see **Fig. 9.9**). All these harmonies are symmetric with respect to half-octave shift (tritonus), which obviously corresponds to the Z_2 rotation. Tritonus would not have been tolerated by catholic church! This symmetry characterizes all 3 harmonies. Basic 3-chords do not contain pure minor and major chords. The reflection of the scale does not leave the collection of chords invariant but it is not clear whether this corresponds only to a change of scale, probably not.

   Consider the (4, 8, 8) case (see **Fig. 9.9**).

   (a) The 8 2-quint chords appear as four-plet $H9, C\sharp 9, D\sharp 9, F9$ and its half octave shift (tritonus interval) acting as a symmetry of the harmony. 2-quint chords are always of type X^9 (note that the third is missing) but also 1-quint chord can be of form X^9 as explicit construction of chords demonstrates: I have denoted these 1-quint chords by symbol $X4$ (CDG is obviously equivalent with CDG).

   (b) Using the popular music notation introduced earlier, the 8 1-quint chords are $D7, Amaj7, A4_+, E7$ and their half-octave shifts $G\sharp 7$, $D\sharp 7, D\sharp 4_+, B\flat 7$.

   No major and minor chords are included and only the extension to tetra-icosahedral harmony can provide them and also break the symmetry giving rise to well-defined key.

5. The four 0-quint chords appear in two types. $D\sharp ex2 \equiv D\sharp EF\sharp$ and its half-octave shift $Aex2 \equiv AB\flat C$ plus $Hex3 \equiv HC\sharp G$ and its half-octave shift $Fex3 \equiv FGC\sharp$. According to usual thinking these chords involve dissonances. This dissonance character is a rather general phenomenon for the harmonic loners and classical views about harmony would exclude them as asocial cases! In the case of maximally symmetric harmony the loners are diminished chords and thus not so dissonant. In some cases there are no 0-quint chords.

There are 5 collections with Z_2 reflection symmetry having 24 representatives in each (see **Figs. 9.10**, **9.11**, **9.12**, **9.13**, **9.14**). The integer triplets n are $(2, 12, 6), (2, 12, 6), (4, 10, 6), (2, 12, 6), (2, 12, 6)$. Bio-harmony has representative also in this class (see **Fig. 9.12**). The half-octave scaling symmetry is broken for these harmonies. I have not found simple characterization for the symmetry which corresponds to reflection in the direction of x-axis since it changes the interval structure of the chords.

Some comments $(4, 8, 8)$ case are in order (see **Fig. 9.12**).

1. 2-quint chords appear as reflection related multiplets $C9, D9, H\sharp 9, D\sharp 9$ and $C\sharp 9, H9, F9, B\flat 9$.

2. 1-quint chords appear as symmetry related mutiplets $G, D7, Amaj7, E7$ and $C\sharp m, F\sharp 6, H6_-, E6$. Key G major and $C\sharp$ minor would be natural looking keys even without tetrahedral extension. For the mirror image $B\flat$ minor and E major would be the natural looking keys. For extension E major would be the key.

To sum up, half octave shift is a symmetry of all harmonies expected those having only Z_2 reflection symmetry, and fails thus also for the corresponding bio-harmonies.

Tables of basic 3-chords for the icosahedral harmonies with symmetries

The tables below give list for the three types of 3-chords for the 11 harmonies possessing symmetries. One must remember that the reversal of the orientation for the cycle induces the transformation $C \leftrightarrow C$, $F\sharp \leftrightarrow F\sharp$, $H \leftrightarrow C\sharp$, $F \leftrightarrow G$, $D \leftrightarrow B\flat$, $E \leftrightarrow G\sharp$, $A \leftrightarrow D\sharp$ and produces a new scale with minor type chords mapped to major type chords and vice versa. Also one must remember that all 3-chords except those which are simple majors or minors lack the third so that their emotional tone remains uncharacterized. For instance, $C6$ does could be replaced with $Cm6$ and $G7$ with $Gm7$. The reader can check the chords by direct inspection of the figures. The convention used is that vertex number one corresponds to C note.

Table 9.6: Table gives various types of 3-chords for harmonies with Z_6 rotational symmetry. Note that half-octave shift is an exat symmetry. Note that $G^{aug} = CEG\sharp, F^{aug}$ act as bridges between the groups related by half octave shift. The chords have been arranged so that they form orbits of Z_6. "Amino-acid chords" correspond to preferred chords at the orbits.

$(\mathbf{n_0}, \mathbf{n_1}, \mathbf{n_2})$	**0-chords**	**1-chords**	**2-chords**
(2, 12, 6)	$(Faug, Gaug)$	$(Cm, Dm, Em, F\sharp m, G\sharp m, B\flat m)$,	$(C9, D9, E9, F\sharp 9, G\sharp 9, B\flat 9)$.
		$(F6, G6, A6, B6, C\sharp 6, D\sharp 6)$.	

Table 9.7: Table gives various types of 3-chords for the two harmonies with $Z_4 = Z_2^{rot} \times Z_2^{refl}$ symmetry. 4-plets represent the orbits. First cycle has no harmonic loners. Second cycle gives rise to bio-harmony (4, 8, 8) for which 0-quint chords are dissonant. Both cycles have Z_2 rotation symmetry acting as a vertical reflection symmetry in figures and realized also as half-octave shift so that 4-plets contains chords and their half-octave shifts. The genuine reflection symmetry acts as a horizontal reflection symmetry in figures. The cycles correspond to figures **??**, **??**

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$(\mathbf{n_0}, \mathbf{n_1}, \mathbf{n_2})$	**0-chords**	**1-chords**	**2-chords**
(0, 16, 4)		$(D7, D6, G\sharp 7, G\sharp 6)$,	$(B\flat 9, B9, E9, F9)$.
		$(G4+, A9-, C\sharp 4+, D\sharp 9-)$,	
		$(Emaj7, Gmaj7, B\flat maj7, C\sharp maj7)$,	
		$(C9-, A9-, F\sharp 9-, D\sharp 9-)$.	
(4, 8, 8)	$(Cex3, Eex2, F\sharp ex3, B\flat ex2)$.	$(Dmaj7, E9-, A7, A6)$,	$(B\flat 9, F9, C9, G9)$.
		$(G\sharp maj7, B\flat 9-, D\sharp 7, D\sharp 6)$.	$(E9, B9, F\sharp 9, C\sharp 9)$.

Table 9.8: Table gives various types of 3-chords for harmonies with Z_2 rotation symmetry acting as half-octave shift. The doublets represent 2-chord orbits. The cycles correspond to figures **??**, **??**, and **??**.

$(\mathbf{n_0}, \mathbf{n_1}, \mathbf{n_2})$	**0-chords**	**1-chords**	**2-chords**
(0, 16, 4)		$(Em, B\flat m), (Cm, F\sharp m)$,	$(D9, G\sharp 9)$,
		$(G6, C\sharp 6), (A6, D\sharp 6)$,	$(E9, B\flat 9)$.
		$(D4+, G\sharp 4+), (B4+, F4+)$,	
		$(Cmaj7, F\sharp maj7), (G6-, C\sharp 6-)$.	
(2, 12, 6)	$(Aex4, D\sharp ex2)$.	$(Am, D\sharp m), (G9-, C\sharp 9-)$,	$(C9, F\sharp 9)$,
		$(C4, F\sharp 4), (E4+, B\flat 4+)$,	$(A9, D\sharp 9)$,
		$(Dmaj7, G\sharp maj7)$,	$(D9, G\sharp 9)$.
		$(Bmaj7, Fmaj7)$.	
(4, 8, 8)	$(Aex2, Hex8, D\sharp ex2, Fex8)$.	$(D7, G\sharp 7), (Amaj7, D\sharp maj7)$,	$(G9, C\sharp 9), (A9, D\sharp 9)$,
		$(A4+, D\sharp 4+), (E7, B\flat 7)$.	$(B9, F9), (E9, B\flat 9)$.

Table 9.9: Table gives various types of 3-chords for harmonies with single reflection symmetry. The cycles correspond to figures **??**, **??**, **??**, **??**, **??**.

$(\mathbf{n_0}, \mathbf{n_1}, \mathbf{n_2})$	**0-chords**	**1-chords**	**2-chords**
(2, 12, 6)	$(F\sharp ex3, Hex4)$,	$(Am, D\sharp), (A6, D\sharp 7)$,	$(C9, F9), (B9, F\sharp 9)$,
		$(D7, B\flat 6), (G6-, Fmaj7)$,	$(E9, C\sharp 9)$.
		$(D4+, B\flat 9-), (E9, G\sharp 4+)$,	
(2, 12, 6)	$(Dex4, Hex4)$.	$(F, Fm), (C6-, B\flat maj7)$,	$(C9, D\sharp 9)$,
		$(D7, G\sharp 6), (Gmaj7, D\sharp 6-)$.	$(D\sharp 9, C\sharp 9)$,
		$(C\sharp 4-, A4+), (E4+, F\sharp 6)$.	$(E9, B9)$.
(4, 8, 8)	$(Fex1, D\sharp ex3, G\sharp ex1, Aex2)$.	$(E7, E6), (Amaj7, B9-)$,	$(D9, B9), (C9, C\sharp 9)$,
		$(G, C\sharp m), (D7, F\sharp 6)$.	$(F9, G\sharp 9), (D\sharp 9, B\flat 9)$.
(2, 12, 6)	$(Hex3, Eex7)$.	$(D7, G\sharp 6), (G, D\sharp m)$,	$(C9, D\sharp 9)$,
		$(F, Fm), (C6-, B\flat maj7)$,	$(D9, C\sharp 9)$,
		$(A9-, C\sharp 4+), (E7, F\sharp 6)$.	$(E9, B9)$.
(2, 12, 6)	$(F\sharp ex2, Fex3)$.	$(F, B\flat m), (C7, G\sharp 6)$,	$(B\flat 9, D\sharp 9)$,
		$(Amaj7, B9-), (E6, E7)$,	$(C9, C\sharp 9)$,
		$(G, C\sharp m), (D7, B6)$.	$(D9, H9)$.

Table 9.10: Inversion of the scale leaving C (and also $F\sharp$) invariant.

C	G	D	A	E	H	F+	C+	G+	D+	B-	F
C	F	$B\flat$	D+	G+	C+	F+	H	E	A	D	G

9.8.4 Appendix

Chord tables for some harmonies and their inverses

The formula for inversion of the harmonic keeping note X as fixed can be represented as a product of translation takin X to C, inversion keeping C fixed, and translation taking C back to X. The inversion maps the chord having C as basic note to its mirror image so that the order of notes can change and basic note can change. For instance, the major chord $CM = CEG$ goes to minor chord $CG\sharp F = Fm$ so that $k = 0$ goes to $k \equiv \Delta k_{inv} = 11$. This delicacy must be taken into account. If X remains fixed inversion is just the transformation

$$k \to k_{inv} = (2 \times k(X) - \Delta k_{inv}) \ \ mod \ \ 12 \ . \tag{9.8.3}$$

Table 9.10 gives the inversion of the scale leaving C (and also $F\sharp$) invariant:
The inversion for the types of the chords does not depend on the basic note as is clear from the distance preserving character of the inversion. **Table 9.11** gives the inversion of for the types of the chords leaving C fixed. The elements of the rows give the type of the chord and the number of quints k corresponding to it. For chords having C as basic note one has $k = 0$. It is easy to deduce the transformation formula in more general case from the table.

The following tables give the chords and corresponding inverse chords for the 11 icosahedral harmonies.

Table 9.11: Table gives the transformation of inversion leaving C invariant on the basic chords having C as basic note.

M, 0	m, 0	sus4, 0	aug, 0	4, 0	9, 0	4+, 0	9-, 0	6-, 0	maj7, 0
m, 11	M, 11	sus, 0	aug, 0	4, 0	9, 10	9-, 11	4+, 11	maj7, 11	6-, 11
6, 0	7, 0	ex1, 0	ex2, 0	ex3, 0	ex4, 0	ex5, 0	ex6, 0	ex7, 0	ex8, 0
7, 11	6, 11	ex1, 10	ex3, 3	ex2, 3	ex4, 8	ex6, 8	ex5, 80	ex8, 6	ex7, 6

Table 9.12: Pairs "X" and "iX" of columns give the chords of the bio-harmonies and their inversions depicted in figures **??**, **??**, **??**, **??**.

ro6	iro6	re41	ire41	re42	ire42	ro21	iro21
F.aug	F.aug	D.7	A.6	C.ex3	A.ex2	E.m	F.M
G.aug	D+.aug	D.6	A.7	E.ex2	F.ex3	B-.m	B.M
C.m	F.M	G+.7	D+.6	F+.ex3	D+.ex2	C.m	A.M
D.m	D+.M	G+.6	D+.7	B-.ex2	B.ex3	F+.m	D+.M
E.m	C+.M	G.4+	E.9-	D.maj7	B.6-	G.6	D.7
F+.m	B.M	A.9-	D.4+	E.9-	A.4+	C+.6	G+.7
G+.m	A.M	C+.4+	B-.9-	A.7	E.6	A.6	C.7
B-.m	G.M	D+.9-	G+.4+	A.6	E.7	D+.6	F+.7
F.6	C.7	E.maj7	G.6-	G+.maj7	F.6-	D.4+	G.9-
G.6	B-.7	G.maj7	E.6-	B-.9-	D+.4+	G+.4+	C+.9-
A.6	G+.7	B-.maj7	C+.6-	D+.7	B-.6	B.4+	B-.9-
B.6	F+.7	C+.maj7	B-.6-	D+.6	B-.7	F.4+	E.9-
C+.6	E.7	C.9-	B.4+	F.9	D+.9	C.maj7	A.6-
D+.6	D.7	A.9-	D.4+	C.9	G+.9	F+.maj7	D+.6-
C.9	C.9	F+.9-	F.4+	G.9	C+.9	G.6-	D.maj7
D.9	B-.9	D+.9-	G+.4+	E.9	E.9	C+.6-	G+.maj7
E.9	G+.9	B.9	G.9	B.9	A.9	D.9	D.9
F+.9	F+.9	E.9	D.9	F+.9	D.9	G+.9	G+.9
G+.9	E.9	F.9	C+.9	C+.9	G.9	E.9	C.9
B-.9	D.9	B-.9	G+.9	B-.9	B-.9	B-.9	F+.9

Table 9.13: Pairs "X" and "iX" of columns give the chords of the bio-harmonies and their inversions depicted in figures **??**, **??**, **??**, **??**.

ro22	iro22	ro23	iro23	re21	ir21	re22	ir22
A.ex4	G.ex4	A.ex2	B-.ex3	F+.ex3	D+.ex2	D.ex4	E.ex4
D+.ex2	C.ex3	H.ex8	B-.ex7	H.ex4	B-.ex4	H.ex4	F+.ex4
A.m	B-.M	D+.ex2	E.ex3	A.m	E.M	F.M	E.m
D+.m	E.M	F.ex8	F.ex7	D+.M	B-.m	F.m	E.M
G.9-	C.4+	D.7	A.6	A.6	E.7	C.6-	A.maj7
C+.9-	F+.4+	G+.7	D+.6	D+.7	B-.6	B-.maj7	B.6-
C.4	C.4	A.maj7	D.6-	D.7	B.6	C.9-	A.4+
F+.4	F+.4	D+.maj7	G+.6-	B-.6	D+.7	D.7	G.6
E.4+	D+.9-	A.4+	D.9-	G.6-	F+.maj7	G+.6	C+.7
B-.4+	A.9-	D+.4+	G+.9-	F.maj7	G+.6-	G.maj7	D.6-
D.maj7	F.6-	E.7	G.6	D.4+	B.9-	D+.6-	F+.maj7
G+.maj7	B.6-	B-.7	C+.6	B-.9-	D+.4+	C+.4	C+.4
B.maj7	G+.6-	B-.9	G+.9	G+.4+	F.9-	A.4+	C.9-
F.maj7	D.6-	G.9	B.9	E.9-	A.4+	E.4+	F.9-
C.9	D.9	C+.9	F.9	C.9	G+.9	F+.6	D+.7
F+.9	G+.9	A.9	A.9	F.9	D+.9	D+.9	C+.9
A.9	F.9	B.9	G.9	B.9	A.9	C+.9	D+.9
D+.9	B.9	F.9	C+.9	F+.9	D.9	E.9	C.9
D.9	C.9	E.9	D.9	E.9	E.9	B.9	F.9
G+.9	F+.9	D+.9	D+.9	C+.9	G.9	D+.9	C+.9

Table 9.14: Pairs"X" and"iX" of columns give the chords of the bio-harmonies and their inversions depicted in figures **??**, **??**, **??**.

re23	ire23	re24	ire24	re25	ire25		
F.ex1	F.ex1	H.ex3	G.ex2	F+.ex2	F.ex3		
D+.ex3	G+.ex2	E.ex7	F+.ex8	F.ex3	F+.ex2		
G+.ex1	D.ex1	D.7	A.6	F.M	B-.m		
A.ex2	D.ex3	G+.6	D+.7	B-.m	F.M		
E.7	B.6	G-.M	B.m	C.7	D+.6		
E.6	B.7	D+.m	G+.M	G+.6	G.7		
A.maj7	F+.6-	F.M	F+.m	A.maj7	F+.6-		
B.9-	E.4+	F.m	F+.M	B.9-	E.4+		
G.M	G+.m	C.6-	B.maj7	E.6	B.7		
C+.m	D.M	B-.maj7	C+.6-	E.7	B.6		
D.7	C+.6	A.9-	D.4+	G.M	G+.m		
F+.6	A.7	C+.4+	B-.9-	C+.m	D.M		
B-.9	C.9	E.7	G.6	D.7	C+.6		
D.9	G+.9	F+.6	F.7	B.6	E.7		
B.9	B.9	C.9	F+.9	D+.9	G.9		
C.9	B-.9	D+.9	D+.9	C.9	B-.9		
F.9	F.9	D.9	E.9	C+.9	A.9		
G+.9	D.9	C+.9	F.9	B-.9	C.9		
D+.9	G.9	E.9	D.9	D.9	G+.9		
C+.9	A.9	B.9	G.9	H.9	B-.9		

Calculation of incidence matrices

The most stringent definition of harmonic chord progression is as a chord sequence in which two subsequent chords have at least one common note: the distance between subsequent chords defined as the minimal distance between triangles representing them vanishes. Some general comments are in order.

1. Incidence matrices can be computed by using expressions of chords as sets of three notes (possible in Python) and just counting the number of common notes defining the value of the element of the incidence matrix. The quint distance between the chords vanishes if they have common notes. More general incidence matrices would correspond to a larger quint distance.

2. In the case of genetic code and amino-acids one Hamilton cycle from each class labelled by Z_n, $n \in \{6, 4, 2\}$ is involved.

   (a) There are $N = 1 \times 3 \times 8 = 24$ cycle combinations if one does not allow the inverse harmonies. Allowing them gives $N = 8 \times 24$ combinations. If transitions between all representations are possible, there are $M = N^2$ 20×20-dimensional incidence matrices to be calculated for the icosahedral restriction of the code. Incidence matrices are symmetric so that only $D(D+1)/2 = 20(20+1)/2 = 210$ independent matrix elements need to be calculated for given 20×20-D incidence matrix.

   (b) Equivalently, one can calculate the incidence matrix for a space with $N \times 20$ points which is Cartesian product of N amino-acid spaces with 20 points. N has values 24 and 8×24. Remarkably, the magic number 24 of also stringy mathematics appears.

   (c) If the transitions can be restricted to single triplet of cycles, one must calculate 6 20×20-dimensional incidence matrices. This situation could be realistic for portions of the genetic code if the transitions between different cycle triplets are analogous to phase transitions. The number of incidence matrices (one can also use single 60×60 incidence matrix) is still reasonably small and can be documented in written form. In a model for random chord sequences one must specify the probabilities for the transitions between chords with different n for Z_n. Simplest starting point assumption is that the probabilities are identical.

3. For the extended genetic code the most natural assumption is that the extension of the code to icosa-tetrahedral code take places place only in Z_2 sector meaning the extension of amino-acid space by 4 amino-acids and the increase of the number of DNA codons from 60 to 64. There are two kinds of transitions between icosahedral and tetrahedral codons. Tetrahedral codon can correspond to a codon, which is outside the icosahedron having at least one common vertex with the icosahedral codon: this allows 3+3 transitions. Tetrahedral codon can correspond also to punct. Unless the codon/amino-acid contains at least one of these notes, it cannot precede stopping codon. These chords extend the harmony by the counterparts of CM and Am and punct corresponds to $C6 = CGA$.

4. Also the situation in which tetrahedral and icosahedral codes are disjoint must be considered. In this case there are no transitions between tetrahedral and icosahedral sectors. In tetrahedral sector the distances between faces always vanish so that the calculation of this part of the incidence matrix is trivial. Icosa-tetrahedral part of the incidence matrix can be readily written. The difficult part of the calculation of incidence matrices reduces to that for the icosahedral case such that the common face corresponds to either punct or Sec/Pyl. This gives selection rules telling which codons/amino-acids can precede stopping codon/punct in given bio-harmony.

Simulation of harmonic DNA sequence

The following sequence represents a random harmonic sequence based on zero quint distance between neighboring chords (at least one common note). The harmony if combination 3 harmonies **??**, **??**, and **??** extended by adding chords $B\flat$, Gm and $G7$ and associated $B\flat 6$ representing stopping codon and punct in tetra- icosahedral codeandSec or Pyl in their unfused variants. These three harmonies correspond to groups of 20, 20, and 24 DNA codons at orbits of Z_6, Z_4, and Z_2 which is now taken to be Z_2^{refl}. To deduce DNA sequence one must assume detailed correspondence between the codons at the orbits and corresponding chords.

It is assumed that all transitions between neighboring DNAs occurs with the same probability and induce the transitions between amino-acids.

```
Faug, A6, Dm, G6, G6, G6, Em, G6, Cm, G6, F6, Faug, F+m, Dm, G6, G6,
Gaug, G+m, Cm, F6, Dm, Dm, F+m, Dm, F6, F6, B-m, C+6, B-m, F6, Dm, G6,
G6, G6, Gaug, G+m, Cm, Gaug, G6, Dm, B-m, F6, Faug, A6, G6, Gaug, G+m,
Cm, F6, Faug, F6, Cm, F6, G6, Gaug, Gaug, B6, Gaug, G6, Gaug, Em, Gaug,
Em, A6, F+m, B-m, F6, Cm, Gaug, Em, A6, Faug, B-m, B-m, Faug, F6, G6,
G6, F6, Faug, F6, Dm, G6, F6, Dm, F+m, Dm, F+m, A6, Faug, F6, Faug, Dm,
Dm, B-m, B-m, C+6, C+6, G+m, B6, A6, F+m, Faug, B-m, Dm, B-m, C+6, B-m,
F+m, B6, Gaug, Cm, G+m, Cm, F6, F6, B-m, Dm, F6, F6, G6, Dm, G6, G6, Em,
A6, G6, Cm, Cm, G+m, B6, G+m, C+6, C+6, C+6, Faug, B-m, Dm, Dm, G6, Cm,
Gaug, Cm, F6, Cm, G6, Gaug, G6, F6, Dm, F6, Faug, Faug, Faug, A6, Em,
Em, G6, Dm, Faug, F6, B-m, F6, Cm, F6, B-m, F+m, Dm, G6, F6, F6, Cm, Cm,
Em, G+m, Em, A6, Em, A6, F+m, B-m, B-m, B-m, F+m, B6, A6, Em, G+m, B6,
B6, Em, G6, Dm, B-m, Dm, Dm, B-m, Dm, Faug, Faug, F6, Cm, G6, Gaug, B6,
G+m, Em, G6, G6, Dm, Faug, Faug, F6, Cm, Gaug, G+m, Gaug, B6, F+m, A6,
G6, Em, Cm, F6, Dm, Dm, Dm, G6, Em, Em, A6, Em, Gaug, Em, Cm, Cm, Gaug,
G6, G6, Cm, F6, Dm, Faug, A6, Faug, A6, Faug, F+m, F+m, B-m, C+6, G+m,
Em, Gaug, G6, Gaug, G6, G6, Dm, G6, Dm, Dm, F6, B-m, F6, G6, Cm, G+m,
Em, G+m, B6, G+m, Cm, Cm, F6, Faug, Faug, Faug, F6, Dm, G6, Dm, F+m,
Faug, Faug, B-m, C+6, G+m, C+6, Faug, F+m, B-m, Faug, Faug, A6, G6, Em,
Cm, F6, G6, Cm.
```

Illustrations of icosahedral Hamiltonian cycles with symmetries

The figures below illustrate the Hamiltonian cycles involved. Quite generally, the Z_n symmetry acts by a shift by $12/n$ quints along the cycle and the orbits of chords consist of at most n chords of same type as the reader is encouraged to verify.

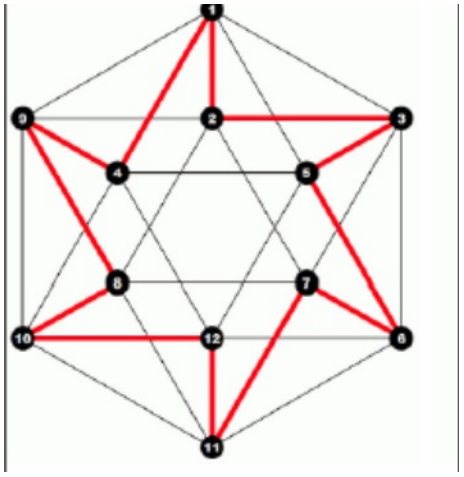

Figure 9.4: $(n_0, n_1, n_2) = (2, 12, 6)$ Hamiltonian cycle with 6-fold rotation symmetry acting shifts generated by a shift of 2 quints.

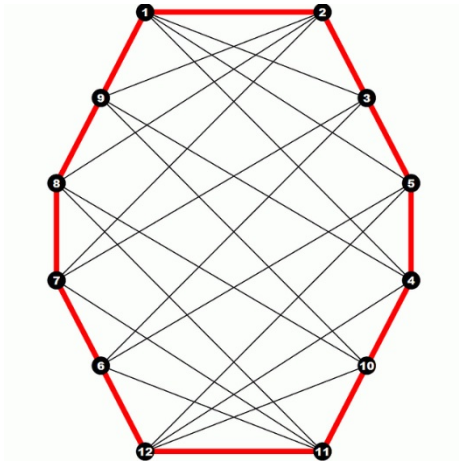

Figure 9.5: $(n_0, n_1, n_2) = (0, 16, 4)$ Hamiltonian cycle with 4 reflection symmetries generated by reflections in vertical and horizontal directions.

9.9 About Physical Representations of Genetic Code in Terms of Dark Nuclear Strings

The view about evolution as a random process suggests that genetic code is pure accident. My own view is that something so fundamental as life cannot be based on pure randomness. TGD has led to several proposals for genetic code, its emergence, and various realizations based on purely mathematical considerations or inspired by physical ideas. One can argue that genetic code is realized in several manners just like bits can be represented in very many manners. Two especially interesting proposals have emerged. The first one is based on geometric model of music harmony involving icosahedral and tetrahedral geometries. Second model has two variants based on dark nuclear strings: the original version maps codons do dark nucleons, the more recent version maps codons to dark 3-nucleon states. Both models predict correctly the numbers of DNA codons coding for a given amino-acid but the model based on dark 3-nucleon triplets is favoured by some recent findings suggesting a pairing between DNA nucleotides and dark nucleons. Also the counterparts

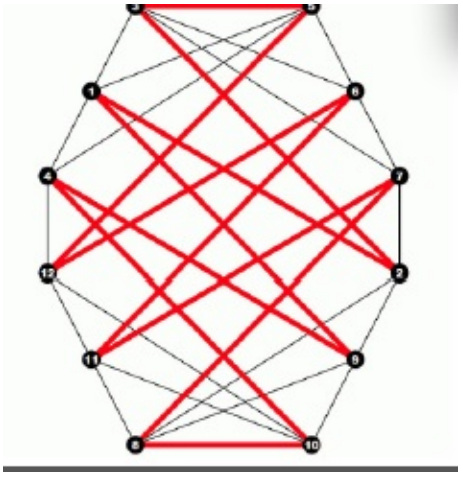

Figure 9.6: $(n_0, n_1, n_2) = (4, 8, 8)$ Hamiltonian cycle with 4 reflection symmetries.

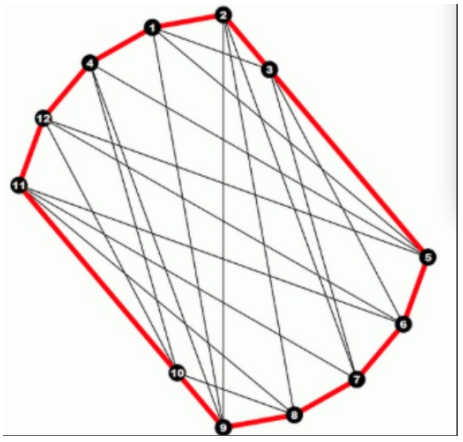

Figure 9.7: $(n_0, n_1, n_2) = (0, 16, 4)$ Hamiltonian cycle with 2-fold rotational symmetry realized as 6-quint shift along the cycle.

of RNA,tRNA, and amino-acids are predicted. In the sequel the updated nuclear string variant is summarized and also its connection with the model of harmony is discussed.

9.9.1 Background

The view about evolution as a random process suggests that genetic code is pure accident. My own view is that something so fundamental as life cannot be based on pure randomness. TGD has led to several proposals for genetic code, its emergence, and various realizations based on purely mathematical considerations or inspired by physical ideas (see chapters of [K22] and [L2, K24]). One can argue that genetic code is realized in several manners just like bits can be represented in very many manners.

Two especially interesting proposals have emerged. The first one is based on geometric model of music harmony [L12] involving icosahedral and tetrahedral geometries. Second one having two variants is based on dark nuclear strings. Both models predict correctly the numbers of DNA codons coding for a given amino-acid. In the sequel the nuclear string variant and also its connection with the model of harmony is discussed in detail.

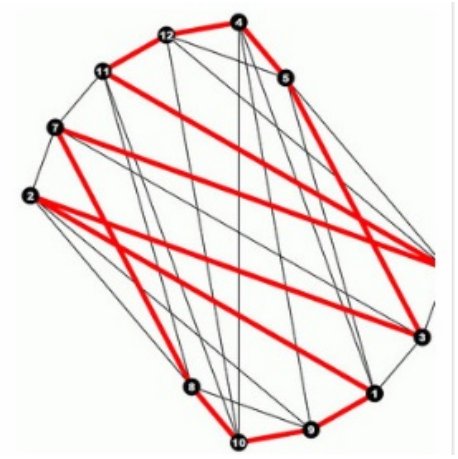

Figure 9.8: $(n_0, n_1, n_2) = (2, 12, 6)$ Hamiltonian cycle with 2-fold rotation symmetry.

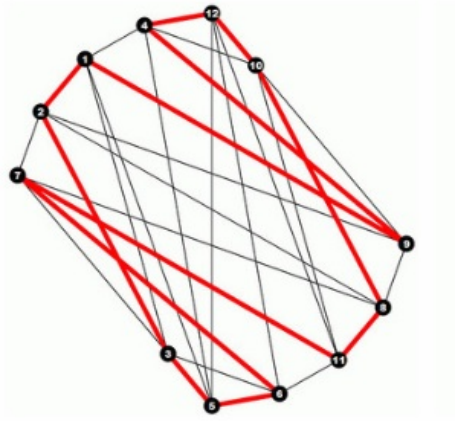

Figure 9.9: $(n_0, n_1, n_2) = (4, 8, 8)$ Hamiltonian cycle with 2-fold rotation symmetry.

It is good to start with an overall view about physical realization of genetic code that I have discussed during last twenty years.

Genetic code and Combinatorial Hierarchy

The first proposal [K23] was purely mathematics inspired and in terms of so called Combinatorial Hierarchy consisting of certain Mersenne primes $M_k = 2^k - 1$ via the formula $M(n+1) = M_{M(n)}$ having interpretation in terms of abstraction. The list beginning from $M(1) = 2$ is $2, M_2 = 3, M_3 = 7, M_7 = 127, M_{127} = 2^{127} - 1$: it is not known whether subsequent integers are Mersenne primes. The idea is that the $2^k - 1$ points define almost full Boolean algebra spanned by k bits- one visualization is as a polygon. The algebra defined $k - 1$ bits is maximal full Boolean sub-algebra having interpretation as maximal number of mutually independent statements, which can hold true simultaneously. For M_7 $(k = 3)$ one would have 2 bits and 4 codons. For M_7 one would have $k = 7$ and 6 bits and genetic code. For M_{127} one would have 126 bits and one would have "memetic" code realizable in terms of sequences of 21 DNA codons.

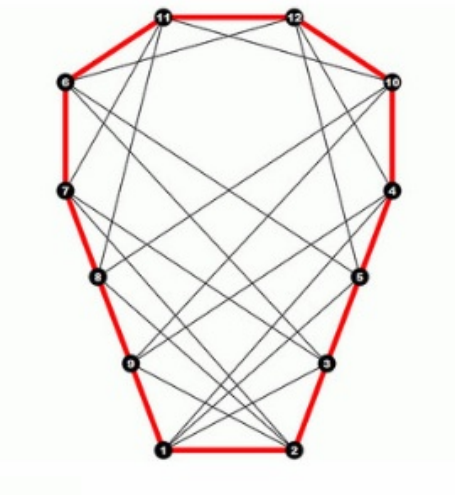

Figure 9.10: $(n_0, n_1, n_2) = (2, 12, 6)$ Hamiltonian cycle with 2-fold reflection symmetry realized as horizontal reflection

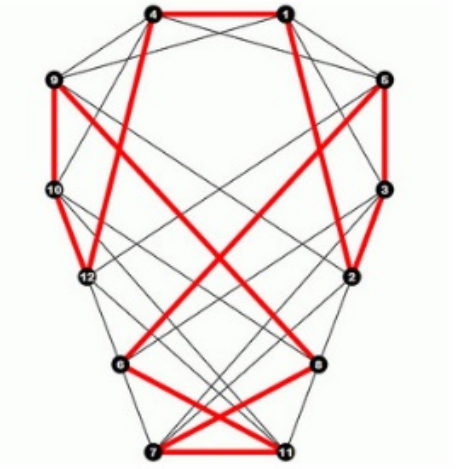

Figure 9.11: $(n_0, n_1, n_2) = (2, 12, 6)$ Hamiltonian cycle with 2-fold reflection symmetry.

Geometric theory of harmony and genetic code

The idea that the 12-note scale could allow mapping to a closed path going through all vertices of icosahedron having 12 vertices and not intersecting itself is attractive. Also the idea that the triangles defining the faces of the icosahedron could have interpretation as 3-chords defining the notion of harmony for a given chord deserves study. The paths in question are known as Hamiltonian cycles and there are 1024 of them [A3]. There paths can be classified topologically by the numbers of triangles containing 0, 1, or 2 edges belonging to the cycle representing the scale. Each topology corresponds to particular notion of harmony and there are several topological equivalence classes.

In the article [L16] I introduced the notion of Hamiltonian cycle as a mathematical model for musical harmony and also proposed a connection with biology: motivations came from two observations. The number of icosahedral vertices is 12 and corresponds to the number of notes in 12-note system and the number of triangular faces of icosahedron is 20, the number of amino-

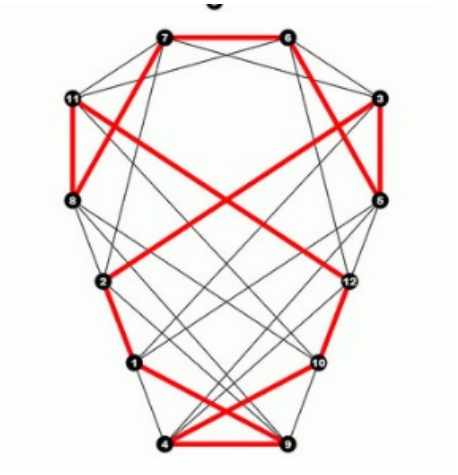

Figure 9.12: $(n_0, n_1, n_2) = (4, 8, 8)$ Hamiltonian cycle with 2-fold reflection symmetry.

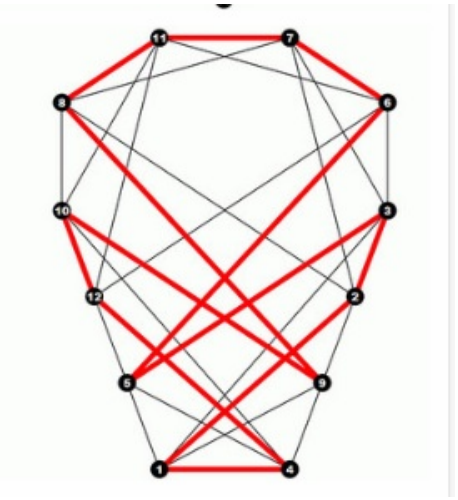

Figure 9.13: $(n_0, n_1, n_2) = (2, 12, 6)$ Hamiltonian cycle with 2-fold reflection symmetry.

acids. This led to a group theoretical model of genetic code and replacement of icosahedron with tetra-icosahedron to explain also the 21st and 22nd amino-acid and solve the problem of simplest model due to the fact that the required Hamilton's cycle does not exist. The outcome was the notion of bioharmony.

All icosahedral Hamilton cycles with symmetries(Z_6,Z_4, Z_2^{rot} and $Z_2 refl$ turned out to define harmonies consistent with the genetic code. In particular, it turned out that the symmetries of the Hamiltonian cycles allow to to predict the basic numbers of the genetic code and its extension to include also 21st and 22nd amino-acids Pyl and Sec: there are actually two alternative codes - maybe DNA and its conjugate are talking different dialects! One also ends up with a proposal for what harmony is leading to non-trivial predictions both at DNA and amino-acid level.

The conjecture is that DNA codons correspond to 3-chords perhaps realized in terms of dark photons or even ordinary sound. There are 256 different bio-harmonies and these harmonies would give additional degrees of freedom not reducing to biochemistry. Music expresses and creates emotions and a natural conjecture is that these bio-harmonies are correlates of emotions/moods at bio-molecular level serving as building bricks of more complex moods. Representations of codons

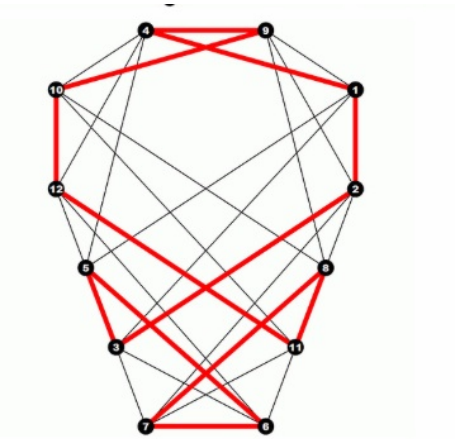

Figure 9.14: $(n_0, n_1, n_2) = (2, 12, 6)$ Hamiltonian cycle with 2-fold reflection symmetry.

as chords with frequencies realized as those of dark photons and also sound is what suggests itself naturally. This together with adelic physics involving hierarchy of algebraic extensions of rationals would explain the mysterious lookin connection between rational numbers defined by ratios of frequencies with emotions.

Letter-wise representations of genetic code in terms of single particle states

The model for DNA-cell membrane system as topological quantum computer with lipids and DNA nucleotide or codons connected by flux tubes led to a proposal for the correspondence of letters of genetic code with particle states.

1. The original proposal was that the 4 letters A,T,C,G correspond to dark u and d quark and their antiparticles $\overline{u}$ and $\overline{d}$. Quarks and their antiparticles would reside at the ends of the flux tube. Spin would not matter in this model. The obvious criticism is that introducing dark antiquarks is too far fetched.

2. One can also consider a variant for which one has u and d quarks and spin matters.

3. TGD based model of bio-superconductivity assumes that flux tubes appear as pairs with members of Cooper pair at parallell flux tubes [K41, K42]. This suggests that electron pairs at in spin 1 and spin 0 states could realize the code. The spin of the electrons would matter and one would obtain 4 states - two qubits in correspondence with A,T,C,G.

Also the model of dark nuclear strings allows to imagine letter-wise representations of the genetic code. The model for cold fusion based on the findings of Prof. Holmlid and his group [C1, L26] leads to the idea that Pollack's EZs [L15] are accompanied by dark nuclear strings consisting of dark protons connected by color flux tubes analogous to mesons [L17, L26]. Color bonds would have quark and antiquark at their ends [L2]. This leads to non-trivial predictions and nuclear anomalies giving support for the notion of nuclear string have emerged, the latest anomaly is so called X boson with mass of 17 MeV [L27, C6] having identification as p-adically scaled analog of pion.

Dark protons could also decay to neutrons by dark weak decays rapidly since dark weak bosons are effectively massless below dark Compton length. Furthermore, proton plus negatively charged color bond could behave like neutron as far as chemistry is considered. The X boson anomaly of nuclear physics [L27] suggests that the flux tubes in the ground state correspond to pion-like states which can be colored: this could bind the nucleons to form a nucleus. The evidence for the occurence of cold fusion in living matter gives support for the role of dark nuclear strings [L19] [L26].nOne can consider several representations of the genetic code in this framework.

Consider first models for which letters are represented separately.

1. Dark protons and neutrons have 4 spin states and could correspond to letter A,T,C,G. In this case dark color bonds would not matter. A rather convincing proposal for a pathway leading to a selection purines as DNA nucleotides has been proposed [I73]. TGD based model [L24] suggests that acidic solutions contain dark protons and purine results when the precursor amine combines with dark proton such that the proton remains dark. Could DNA nucleotide pair with dark protons and neutrons (resulting in dark beta decay from dark proton strings yielded by Pollack's mechanism)?

2. Also the 4 states of dark color bonds between dark nucleons (3 pion-like states and one eta meson like state: spin 1 bonds would be analogous to ρ and ω mesons and have higher mass) correspond to letters A,T,C,G. Now the dark protons and neutrons would not matter. This option would require that the character of the nucleotide correlates with the color flux tube attached to the dark proton. They would have at their ends charge conjugate color bonds. The states would be of form $u\overline{u}, d\overline{d}, u\overline{d}, d\overline{u}$ with the ordering of q and $\overline{q}$ correlating with the direction in which transcription and replication take place being thus same or opposite). For conjugate strand the direction of strand would be opposite in the sense that one would have $\overline{u}u, \overline{d}u, \overline{d}u, \overline{u}u$.

   For this option one could consider the strands of dark DNA double strand being connected by flux tube pairs resulting when U-shaped color flux tube have reconnected. If color flux tubes are colored, color confinement could bind the dark protons to dark nucleus. Similar mechanism could be at work for the ordinary nuclei.

The basic problem of all the proposals based on letter-wise correspondence is that they do not even try to explain the numbers of DNA codons coding for a given amino-acid and are also silent about tRNA.

Codon-wise representations of genetic code realized in terms of dark nuclear strings

For this option entire codons rather than letters would be represented. The difference between two representations is analogous to that between spoken and written languages. In spoken languages words are not analyzed further to letters. These models are able to predict also the numbers of codons coding for a given amino-acid successfully.

1. The geometric theory of harmony represents codons as 3-chords without assigning fixed notes to A,T,C,G and explains also DNA-amino-acid correspondence.

2. The map of codons to the dark nucleon states of dark nucleon consisting of dark u and d type quarks does the same and also predicts the degeneracies successfully.

3. This model can be modified by replacing u and d by dark nucleon states p and n without any change in predictions related to genetic code. The evidence that DNA codons indeed couple to dark nucleon states [L24] supports this option.

In the sequel I consider the models mapping DNA codons to dark nucleons and then generalize the model so that it applies to triplets of dark nucleons.

9.9.2 Models of genetic code based on dark nuclear strings

Water memory is one of the ugly words in the vocabulary of the main stream scientist. The work of pioneers is however now carrying fruit. The group led by Jean-Luc Montagnier, who received Nobel prize for discovering HIV virus, has found strong evidence for water memory and detailed information about the mechanism involved [K24, **?**], [I94]. The work leading to the discovery was motivated by the following mysterious finding. When the water solution containing human cells infected by bacteria was filtered in purpose of sterilizing it, it indeed satisfied the criteria for the absence of infected cells immediately after the procedure. When one however adds human cells to the filtrate, infected cells appear within few weeks. If this is really the case and if the filter does what it is believed to do, this raises the question whether there might be a representation of genetic code based on nano-structures able to leak through the filter with pores size below 200 nm.

The question is whether dark nuclear strings might provide a representation of the genetic code. In fact, I posed this question year before the results of the experiment came with motivation coming from the attempts to understand water memory. The outcome was a totally unexpected finding: the states of dark nucleons formed from three quarks can be grouped to multiplets in one-one correspondence with 64 DNAs, 64 RNAS, and 20 amino-acids and there is natural mapping of DNA and RNA type states to amino-acid type states such that the numbers of DNAs/RNAs mapped to given amino-acid are same as for the vertebrate genetic code.

Mapping DNA and amino-acids to dark nucleon states

The dark model emerged from the attempts to understand water memory [K24]. The outcome was a totally unexpected finding [L2, K24]: the states of dark nucleons formed from three quarks connected by color bonds can be naturally grouped to multiplets in one-one correspondence with 64 DNAs, 64 RNAS, 20 amino-acids, and tRNA and there is natural mapping of DNA and RNA type states to amino-acid type states such that the numbers of DNAs/RNAs mapped to given amino-acid are same as for the vertebrate genetic code.

The basic idea is simple. The basic difference from the model of free nucleon is that the nucleons in question - maybe also nuclear nucleons - consist of 3 linearly ordered quarks - just as DNA codons consist of three nucleotides. One might therefore ask whether codons could correspond to dark nucleons obtained as open strings with 3 quarks connected by two color flux tubes or as closed triangles connected by 3 color flux tubes. Only the first option works without additional assumptions. The codons in turn would be connected by color flux tubes having quantum numbers of pion or η.

This representation of the genetic would be based on entanglement rather than letter sequences. Could dark nucleons constructed as string of 3 quarks using color flux tubes realize 64 DNA codons? Could 20 amino-acids be identified as equivalence classes of some equivalence relation between 64 fundamental codons in a natural manner? The codons would be not be anymore separable to letters but entangled states of 3 quarks.

If this picture is correct, genetic code would be realized already at the level of dark nuclear physics and maybe even in ordinary nuclear physics if the nucleons of ordinary nuclear physics are linear nucleons. Chemical realization of genetic code would be induced from the fundamental realization in terms of dark nucleon sequences and vertebrate code would be the most perfect one. Chemistry would be kind of shadow of the dynamics of positively charged dark nucleon strings accompanying the DNA strands and this could explain the stability of DNA strand having 2 units of negative charge per nucleotide. Biochemistry might be controlled by the dark matter at flux tubes.

The ability of the model to explain genetic code in terms of spin pairing is an impressive achievement, which I still find difficult to take seriously.

1. The original model mapping codons to dark nucleon states assumed the overall charge neutrality of the dark proton strings: the idea was that the charges of color bonds cancel the total charge of dark nucleon so that all states uuu, uud, udd, ddd can be considered. The charge itself would not affect the representation of codons. Neutrality assumption is however not necessary. The interpretation as dark nucleus resulting from dark proton string could quite well lead to the formation the analog of ordinary nucleus via dark beta decays [L26] so that the dark nucleus could have charge. Isospin symmetry breaking is assumed so that neither quarks nor flux tubes are assigned to representations of strong $SU(2)$.

   There is a possible objection. For ordinary baryon the mass of Δ is much larger than that of proton. The mass splitting could be however much smaller for linear baryons if the mass scale of excitations scales as $1/h_{eff}$ as indeed assumed in the model of dark nuclear strings [L17, L26].

2. The model assumes that the states of DNA can be described as tensor products of the four 3-quark states with spin content $2 \otimes 2 \otimes 2 = 4 \oplus 2_1 \oplus 2_2$ with the states formed with the 3 spin triplet states $3 \otimes 3 = 5 \oplus 3 \oplus 1$ with *singlet state dropped*. The means that flux tubes are spin 1 objects and only spin 2 and spin 1 objects are accepted in the tensor product. One could consider interpretation in terms of ρ meson type bonding or gluon type bonding.

With these assumptions the tensor product $(2 \otimes 2 \otimes 2) \otimes (5 \oplus 3)$ contains $8 \times 8 = 64$ states identified as analags of DNA codons.

The rejection of spin 0 pionic bonds looks strange. These would however occur as bonds connecting dark codons and could correspond to different p-adic length scale as suggested by the successful model of X boson [L27].

One can also ask why not identify dark nucleon as as closed triangle so that there would be 3 color bonds. In this case $3 \otimes 3 \otimes 3$ would give 27 states instead of 8 ($\oplus 1$). This option does not look promising.

3. The model assumes that amino-acids correspond to the states 4×5 with $4 \in \{4 \oplus 2 \oplus 2\}$ and $5 \in \{5 \oplus 3\}$. One could tensor product of spin 3/2 quark states and spin 2 flux tube states giving 20 states, the number of amino-acids!

4. Genetic code would be defined by projecting DNA codons with the same total quark and color bond spin projections to the amino-acid with the same (or opposite) spin projections. The attractive force between parallel vortices rotating in opposite directions serves as a metaphor for the idea. This hypothesis allow immediately the calculation of the degeneracies of various spin states. The code projects the states in $(4 \oplus 2 \oplus 2) \otimes (5 \oplus 3)$ to the states of 4×5 with same or opposite spin projection. This would give the degeneracies $D(k)$ as products of numbers $D_B \in \{1, 2, 3, 2\}$ and $D_b \in \{1, 2, 2, 2, 1\}$: $D = D_B \times D_b$. Only the observed degeneracies $D = 1, 2, 3, 4, 6$ are predicted. The numbers $N(k)$ of amino-acids coded by D codons would be

$$[N(1), N(2), N(3), N(4), N(6)] = [2, 7, 2, 6, 3] \ .$$

The correct numbers for vertebrate nuclear code are $(N(1), N(2), N(3), N(4), N(6)) = (2, 9, 1, 5, 3)$. Some kind of symmetry breaking must take place and should relate to the emergence of stopping codons. If one codon in second 3-plet becomes stopping codon, the 3-plet becomes doublet. If 2 codons in 4-plet become stopping codons it also becomes doublet and one obtains the correct result $(2, 9, 1, 5, 3)$!

It is difficult to exaggerate the importance of this simple observation suggesting that genetic code is realized already at the level of dark or even ordinary nuclear physics and bio-chemistry is only a kind of shadow of dark matter physics.

Objections based on group theory and statistics

The model and its generalization replacing u, d with nucleon states p, n works amazingly nicely but is better to try to invent objections against the proposal and try to find inconsistencies. Fermi and Bose statisticsare the most obvious providers of killer arguments.

1. The basic objection is that if the quarks are organized in linear structures, one cannot talk about representation of 3-D rotation group since symmetry breaking to SO(2) acting along common axis which could be either the local axis along dark DNA helix of the axis of the entire helix. The linear ordering of the quarks is not consistent with the full harmonics. Rather, harmonics restricted to half space $0 \leq \theta \leq \pi/2$ ($\pi \geq \theta \geq \pi/2$) should characterize the "upper" ("lower") flux tube direction at the position of quark in the middle.

   If reflection along quantization axis and SO(2) generate the symmetries one still has labelling of the states by angular momentum projection and states form doublets $(m, -m)$. The representations of SO(3) split into these representation and the numbers of states with given spin projection remain the same. Therefore the predictions for the numbers of DNA codons coding given aminoacid are not changed. It is quite possible that braid statistics made possible by 1-dimensionality is needed to realize the idea about ordering and this would allow to have full DNA multiplets.

2. In quark model one forms tensor product of tensor products of 3 quark spin states and 3 quark isospin states and by color singletness requires that the state is completely antisymmetric in quark degrees of freedom. The state is completely symmetric in the non-colored degrees

of freedom. One obtains only two representations $\Delta \leftrightarrow (3/2, 3/2)$ and $N = (1/2, 1/2)$ with positive parity. In quark model context the presence of other tensor products in $(4 \oplus 2_1 \oplus 2_2)_S \otimes (4 \oplus 2_1 \oplus 2_2)_I$ is forbidden. One reason is that spatial wave function is assumed to be symmetric in ground state. This forbids 2_2 in spin degrees of freedom. Symmetrization leaves only the Δ and N (Note that the total number of these state is 20!). Now strong isospin is broken and it is natural to not include it to the tensor product.

3. The presence of 2_2 would be forbidden in quark model since it would require antisymmetric spatial wave function to compensate for the antisymmetry of 2_2. In the recent case the situation is 1-dimensional and the ordering along nuclear string forces localization of quarks and one cannot have identical wave functions for quarks.

   1-D situation also suggests strongly braid statistics. Perhaps the situation could be understood in terms of fermionic oscillator operators along nuclear string having anti-commutation relations corresponding to non-trivial braid statistics - maybe making the statistics commutative. This could naturally allow anti-symmetrization along nuclear string for 2_2 states.

4. If one assumes ordinary statistics, one could one take care of the statistics of the 16 states in $2_2 \otimes (5 \oplus 3)$ by assuming that for 2_2 the color state is symmetric and thus 10-D representation of $SU(3)$. The state associated with color flux tubes cannot compensate this color (triality is 1) since it must correspond to triality zero representation. If the colors of DNA strand and conjugate correspond to 10 and $\overline{10}$ and color entanglement cold guarantee color singletness for the codon pairs. This would however require anti-quarks for the conjugate strand.

   3 10:s associated with 3 codons contains in their tensor product a singlet (see `http://tinyurl.com/zjxxqhj`). Minimal color singlet dark DNA sequence would requite 3 color codons. One can of course wonder whether the presence of 3 decouplet codons - 2 at the beginning and 2 at end and one in the middle could define genes as basic units.

5. The statistics problem is encountered also for the flux tubes. 5 (and 1) as symmetric representation is allowed by statistics but triplet is antisymmetric and thus not allowed. Again braid statistics might help. If one assumes that the flux tubes are colored - say color octets - and color wave function for flux tube pairs is antisymmetric, one can achieve Bose statistics for 3. Flux tube pair would correspond to $8 \in \{8 \times 8\}$ and minimum of two flux codons would be needed for color singletness in flux tube degrees of freedom.

6. For the counterparts of amino-acids one has only $4 \otimes 5$ allowed also by statistics considerations assuming color singlets. Could distinction between DNA/RNA and amino-acids related to statistics, perhaps braid statistics. The suggested role of braid strands possibly connecting DNA double strands and DNA double strands and lipid layers of cell membrane encourages the question whether the DNA strand and its conjugate entangle via via the reconnection of the color flux tubes defining U-shaped "tentacles" to a flux tube pair connecting the strands. For amino-acids they would not be needed. Same could happen in the transcription process of DNA to mRNA and in the translation process for mRNA tentacles and those associated with tRNA.

It is also possible to map DNA and amino-acids to dark 3-nucleon states

The assumption that entire codon rather than letter corresponds to a state of dark proton does not conform with the model for the origin of purines as DNA nucleotides [L24] assuming that purines and in fact all nucleotides are combined with dark proton unless one assumes that 3 nucleotides combine with the same dark proton. This looks somewhat artificial but cannot be excluded.

Amazingly, the arguments of the model involve only the representations of rotation group and since p and n have same spin as u and d, the arguments generalize to 3- nucleon states (ppp, ppn, pnn, nnn) connected by two color bounds and organized to linear structures. Concerning genetic code, exactly the same predictions follow in the recent formulation of the model. In this case quark color is not present. One could however use the 1-dimensionality and the ordering of dark nucleons as already described.

This variant has several nice features. The model is consistent with the model for dark nucleon strings consisting of nucleons and color bonds between them. There is no need to introduce

Δ type nucleon states and colored states are not needed in fermionic sector. Color bonds must be colored if one wants ordinary bosonic statistics for flux tubes but here braid statistics might help. Colored bonds could of course have some important function.

Ordinary or braid statistics?

There are four options to consider: ordinary/braid statistics (1/2) and dark nucleon/dark nucleon triplet as representation of DNA codon (a/b). One has options 1a,1b,2a,2b.

1. Option 1a. For the ordinary statistics amino-acid like dark nucleons are color singlets. Part of DNA codons represented as dark nucleons and would be colored and 10-D representation of SU(3). Dark amino-acids need not have color bonds with dark parts of other colored biomolecules like DNA,RNA, with exception possible formed by dark tRNA. DNA double strand could realize color confinement via the reconnection of color flux tubes.

2. Option 1b. Option 1b requires in ordinary statitics for antisymmetric doublet an antisymmetric wave function for the 3 nucleons not allowing constant valued wave function also disfavored by the linear ordering. This condition might have the same implications as braid statistics.

3. Options 1a and 1b. DNA is the only molecule that appears as double strands. A possible explanation is that codons and anticodons are paired by U-shaped flux tubes associated with the color bonds of dark DNA to form color singlets. Nucleonic colors would sum up to zero along the strand.

4. Option 2a. For braid statistics it could be possible to avoid colored states of nucleon and flux tubes altogether.

5. Option 2b. The codons would have no color and amino-acids could obey braid statistics reducing to ordinary statistics. This would not be the case for DNA/RNA.

Objections Against the Identification of Codons as Dark Nucleon States

Consider next some particle physicist's objections against the option mapping codons to dark nucleon states.

1. The realization of the model requires the dark scaled variants of spin 3/2 baryons known as Δ resonance and the analogs (and only the analogs) of spin 1 mesons known as ρ mesons. The lifetime of these states is very short in ordinary hadron physics. Now one has a scaled up variant of hadron physics: possibly in both dark and p-adic senses with latter allowing arbitrarily small overall mass scales. Hence the lifetimes of states could be scaled up.

2. Both the absolute and relative mass differences between Δ and N *resp.* ρ and π are large in ordinary hadron physics and this makes the decays of Δ and ρ possible kinematically. This is due to color magnetic spin-spin splitting proportional to the color coupling strength $\alpha_s \sim .1$, which is large. In the recent case α_s could be considerably smaller - say of the same order of magnitude as fine structure constant 1/137 - so that the mass splittings could be so small as to make decays impossible.

   The color magnetic spin interaction energy give rise to hyperfine splitting of quark in perturbative QCD is of form $E_c \propto \hbar g B/m$, where m is mass parameter which is of the order of baryon mass. Magnetic flux scales as $\hbar$ by flux quantization and if flux tube thickness scales as $\hbar^2$, one has $B \propto 1/\hbar$. Mass splittings would not depend on $\hbar$, which does not make sense. Mass splitting becomes small for large $\hbar$ if the area of flux quantum scales as $\hbar^{2+n}$, $n > 0$ so that color magnetic hyper-fine splitting scales as $1/\hbar^n$ from flux conservation. The magnetic energy for a flux tube of length L scaling as $\hbar$ and thickness $S \propto \hbar^{2+n}$ has order of magnitude $g^2 B^2 LS$ and does not depend on $\hbar$ for $n = 1$. Maybe this could provide first principle explanation for the desired scaling.

   The size scale of DNA would suggest that single DNA triplet corresponds to 3 Angstrom length scale. Suppose this corresponds to the size of dark nucleon. If this size scales as $\sqrt{\hbar}$ as

p-adic mass calculations suggest, one obtains a rough estimate $\hbar/hbar_0 = 2^{38}$. The proton-Δ mass difference due to hyper-fine splitting would be scaled down to about $2^{-38} \times 300$ MeV $\sim 10^{-9}$ eV, which is completely negligible in the metabolic energy scale .5 eV. If the size of dark nucleon scales as $\hbar$ the mass difference is about 12 eV which corresponds to the energy scale for the ionization energy of hydrogen. Even this might be acceptable.

For these reasons the option mapping codons to dark nucleon triplets is clearly favored and will be discussed in the following.

9.9.3 The model mapping codons to dark 3-nucleon states

The model based on dark 3-nucleon states is discussed seems more realistic and will be discussed in more detail in the sequel.

Could dark DNA, RNA, tRNA and amino-acids correspond to different charge states of codons?

If dark codons correspond to dark nucleon triplets as assumed in the following considerations there are 4 basic types of dark nucleon triplets: ppp, ppn, pnn, nnn. Also dark nucleons could represent codons as uuu, uud, udd, ddd: the following discussion generalizes as such also to this case. If strong isospin/em charge decouples from spin the spin content is same independently of the nucleon content. One can consider the possibility of charge neuralization by the charges assignable to color flux tubes but this is not necessarily. In any case, one would have 4 types of nucleon triplets depending on the values of total charges.

Could different dark nucleon total charges correspond to DNA,RNA, tRNA and amino-acids? Already the group representation content - perhaps correlating with quark charges - could allow to distinguish between DNA, RNA, tRNA, and amino-acids. For amino-acids one would have only 4×5 and ordinary statistics and color singlets. For DNA and RNA one would have full multiplet also color non-singlets and for tRNA one could consider $(4 \oplus 2_1 \oplus 2_2) \times 5$ containing 40 states. 31 is the minimum number of tRNAs for the realization of the genetic code. The number of tRNA molecules is known to be between 30-40 in bacterial cells. The number is larger in animal cells but this could be due to different chemical representations of dark tRNA codons.

If the net charge of dark codon distinguishes between DNA,RNA, tRNA, and amino-acid sequences, the natural hypothesis to be tested is that dark ppp, ppn, pnn, and nnn sequences are accompanied by DNA,RNA, tRNA, and amino-acid sequences. The dark beta decays of dark protons proposed to play essential role in the model of cold fusion [**?**]ould transform dark protons to dark neurons. Peptide backbones are neutral so that dark nnn sequence could be also absent but the dark nnn option is more natural if the general vision is accepted. There is also the chemically equivalent possibility that only dark protons are involved: dark proton + neutral color bond would represent proton and dark proton + negatively charged color bond would represent neutron. At this moment it is not possible to distinguish between these two options.

Is this picture consistent with what is known about charges of amino-acids DNA,RNA, tRNA, and amino-acids? Consider first the charges of these molecules.

1. DNA strand has one negative charge per nucleotide. Also RNA molecule has high negative charge. This conforms with the idea that dark nucleons accompany both DNA and RNA. DNA codons could be accompanied by dark ppp implying charge neutralization in some scale and RNA codons by dark ppn. The density of negative charge for RNA would be 2/3 for that for DNA.

2. Arg, His, and Lys have positively charged side chains and Asp,Glu negative side chains (see `http://tinyurl.com/jsphvgt`). The charge state of amino-acid is sensitive to the pH value of solution and its conformation is sensitive to the counter ions present. Total charge for amino-acid in peptide however vanishes unless it is associated with the side chain: as in the case of DNA and RNA it is the backbone whose charge is expected to matter.

3. Amino-acid has central C atom to which side chain, NH_2, H and COOH are attached. For free amino-acids in solution water solution $NH_2 \rightarrow NH_3^+$ tends to occur pH=2.2 by receiving

possibly dark proton whereas COOH tends to become negatively charged above pH= 9.4 by donating proton, which could become dark. In peptide OH attach to C and one H attached to N are replaced with peptide bond. In the pH range 2.2-9.4 amino-acid is zwitterion for which both COOH is negatively charged and NH_2 is replaced with NH_3^+ so that the net charge vanishes. The simplest interpretation is that the ordinary proton from negatively ionized COOH attaches to NH_2 - maybe via intermediate dark proton state.

4. The backbones of peptide chains are neutral. This conforms with the idea that dark amino-acid sequence consists of dark neutron triplets. Also free amino-acids would be accompanied by dark neutron triplets. If the statistics is ordinary only 4 dark nnn states are possible as also 5 dark color flux tube states.

5. tRNA could involve dark pnn triplet associated with the codon. An attractive idea is secondary genetic code assigning RNA codons to tRNA-amino-acid complex and projecting $8 \otimes (5 \oplus 3)$ containing 64 dark RNA spin states to $8 \otimes 5$ containing 40 dark tRNA spin states with same total nucleon and flux tube spins. Dark tRNA codons would in turn be attached to dark amino-acids by a tertiary genetic code projecting spin states $8 \otimes 5$ to $4 \otimes 5$ by spin projection. In the transcription dark tRNA would attach to dark mRNA inducing attachment of dark amino-acid to the growing amino-acid sequence and tRNA having only dark tRNA codon would be left. The free amino-acids in the water solution would be mostly charged zwitterions in the pH range 2.2-9.4 and the negative charge of COO^- would be help in the attachement of the free amino-acid to the dark proton of tRNA codon. Therefore also the chemistry of free amino-acids would be important.

   An interesting question is why pnn triplets for tRNA would only 5 in flux tube degrees of freedom entire 8 in nucleon degrees of freedom. For RNA consisting of ppn triplets also 3 would be possible. What distinguishes between ppn and pnn?

The model should explain the widely different properties of DNA,RNA , tRNA, and amino-acids. There are two options.

1. DNA/RNA/amino-acid codons could correspond to ppp/ppn/nnn and tRNA would correspond to pnn (order is not necessarily this). Different charge or dark codons explain why DNA (RNA) has H (OH) in $2'$ position. The repulsive Coulomb energy between dark codons would be stronger for DNA and the compensation of this forces by the magnetic tension associated with the flux tube pair connecting codon and anticodon this might have something to do with the stability of DNA double strand.

   (a) The instability of RNA as compared to DNA would result from the instability of the ribose in RNA (deoxiribose in DNA) as indeed believed. The absence of RNA double strands could be due to the instability of the flux tube pair assignable to n-n. This trivially implies absence of replication and transcription if it is based on same mechanism as in the case of DNA.

   (b) pnn structure could explain why tRNA does not form sequences and allow to understand wobble pairing, which states that the third mRNA codon does not correspond to unique tRNA anticodon but one has C,A,U $\rightarrow$ I and U$\rightarrow$ I. Due to the symmetries of the third letter of the codon, this is consistent with the genetic code. The physical explanation for wobble base pairing could relate to pnn structure of tRNA. If the charge ordering is random one would have nnp,npn,pnn and C,A,U $\rightarrow$ I could correspond to these 3 situations whereas for U$\rightarrow$ I the correspondence would not depend on the ordering. Also for RNA one would have ppn,pnp, npp degeneracy but in this case one would have charge independence.

   A possible charge pairing between RNA and tRNA would be p$\leftrightarrow$n. The charge pairing between DNA and RNA could be p $\rightarrow$ n for the third least significant letter of DNA. This would minimize the coding errors possibly induced this pairing.

   (c) One can criticize the charge assignment ppn (possibly allowing permutations) for RNA codons. Could dark weak beta decays give rise to 1-D lattice like structure? Could the repetitive structure be due to energy minimization.

2. Could the correspondence be letterwise? For DNA A,T,C,G would correspond to p, and for RNA A,C,G to p and U to n. Codons not containing U wold be ppp type codons and one can wonder why the oxiribose for them is not replaced with de-oxiribose. The possible presence of n in dark codons could explain why RNA sequences are highly unstable and why they do not replicate and transcribe.

Replication, transcription, translation

The formation of flux tube pairs between molecules would be central in replication and transcription and in all bio-catalysis. Dark DNA would replicate first to dark DNA or mRNA. This requires that the building bricks of dark DNA and mRNA emerge from environment perhaps by mechanism involving reconnection for the magnetic tentacles and reduction of h_{eff} bringing the molecules near each other. Flux tube pairs between dark DNA codonsandtheir conjugates (individual dark RNA codons) would be formed during replication (transcription). The formation of flux tube pair between mRNA and dark tRNA part of tRNA would bring tRNA to mRNA, where amino-acid would associate with the growing amino-acid sequence.

For options 1a and 1b based on ordinary statistics color singletness condition could play an important role in the replication and transcription.

1. If the value of h_{eff} before reconnection and contraction of flux tube dictating the scale of color confinement is large enough, colored dark nucleons could float as free - possibly colored states - in the environment for option 1a). For option 1b dark nucleons could be present in environment - this could relate directly to the ionization in electrolyte. For options 1a and 1b dark codons representing dark tRNA molecules would accompany them.

2. For options 1a) and 1b) color confinement in flux tube degrees of freedom by forming dark color flux tube pairs between dark DNA and its conjugate in codon-wise manner could give rise to DNA double strands as chemical shadows of dark double strands. The coupling between codon and anticodon would be defined by the condition that the total color bond spins of paired codons are opposite. Quark color could be compensated for option 1a along DNA strand: 3 10:s give singlet. One can of course ask whether dark DNA RNA sequences exist rather than being built during replication and transcription.

Are sound-like bubbles whizzing around in DNA essential to life?

I got a link to a very interesting article [I86] about sound waves in DNA (see `http://tinyurl.com/z7hod9b`). The article tells about THz de-localized modes claimed to propagate forth and back along DNA double strand somewhat like bullets. These modes involve collective motion of many atoms. These modes are interpreted as a change in the stiffness of the DNA double strand leading to the splitting of hydrogen bonds in turn leading to a splitting into single strands. The resulting gap is known as transcriptional bubble propagating along double strand is the outcome. I do not how sound the interpretation as sound wave is.

It has been proposed that sound waves along DNA give rise to the bubble. The local physical properties of DNA double strand such as helical structure and elasticity affect the propagation of the waves. Specific local sequences are proposed to favor a resonance with low frequency vibrational modes, promoting the temperary splitting of the DNA double strand. Inside the bubble the bases are exposed to the surrounding solvent, which has two effects.

Bubbles expose the nucleic acid to reactions of the bases with mutagens in the environment whereas so called molecular intercalators may insert themselves between the strands of DNA. On the other hand, bubbles allow proteins known as helicases to attach to DNA to stabilize the bubble, followed by the splitting the strands to start the transcription and replication process. The splitting would occur at certain portions of DNA double strand. For this reason, it is believed that DNA directs its own transcription.

The problem is that the strong interactions with the surrounding water are expected to damp the sound wave very rapidly. Authors study experimentally the situation and report that propagating bubbles indeed exist for frequencies in few THz region. Therefore the damping deo not seem to be effective. How this is possible? As an innocent layman I also wonder how this kind of mechanism can be selective: it would seem that the bullet like sound wave initiates transcription

at many positions along DNA. The transcription should be localized to a region assignable to single gene. What could guarantee this?

Can TGD say anything interesting about the mechanism behind transcription and replication?

1. In TGD magnetic body controls and coordinates the dynamics. The strongest hypothesis is that basic biochemical process are induced by those for dark variants of basic bio-molecules (dark variants of DNA, enzymes,...). The belief that DNA directs its own transcription translates to the statement that the dark DNA consisting most plausibly from sequences of dark proton triplets ppp at dark magnetic flux tubes controls the transcription: the transcription/replication at the level of dark DNA induces that at the level of ordinary DNA.

2. If the dark DNA codons represented as dark proton triplets (ppp) are connected by 3 flux tube pairs, the reverse of the reconnection should occur and transform flux tube pairs to two U-shaped flux tubes assignable to the two dark DNA strands. Dark proton sequences have positive charge +3e per dark codon giving rise to a repulsive Coulomb force between them. There would be also an attractive force due to magnetic tension of the flux tubes. These two forces would compensate each other in equilibrium (there also the classical forces due to the negatively charged phosphates associated with nucleotides but these would not be so important).

   If the flux tube pairs are split, the stabilizing magnetic force however vanishes and the dark flux tubes repel each other and force the negatively charged DNA strands to follow so that also ordinary DNA strand splits and bubble is formed. The primary wave could therefore be the splitting of the flux tube pairs: whether one can call it as a sound wave is not clear to me. Perhaps the induced propagating splitting of ordinary DNA double strand could be regarded as an analog of sound wave.

   The splitting of flux tube pairs for a segment of DNA would induces a further splitting of flux tubes since repulsive Coulomb force tends to drive the flux tubes further away. The process could be restricted to DNA if the "upper" end of the split DNA region has some dark DNA codons which are not connected by flux tubes pairs. This model reason why for dark proton sequences.

3. This model does not yet explain how the propagating splitting wave is initiated. Could a quantum phase transition increasing the value of h_{eff} associated with the flux tube pairs occur for some minimal portion of dark DNA "below" the region associated with gene and lead to the propagating wave induced by the above classical mechanism? That the wave propagates in one direction only could be due to chirality of DNA double helix.

An interesting question is how the RNA world vision (see `http://tinyurl.com/gpmxcmk`) relates to this general picture.

1. There are strong conditions on the predecessor of DNA and RNA satisfies many of them: reverse transcription to DNA making possible transition to DNA dominated era is possible. Double stranded RNA exists `http://tinyurl.com/y9mex4v7` in cells and makes possible RNA genome: this would however suggest that cell membrane came first. RNA is a catalyst. RNA has ability to conjugate an amino-acid to the $3'$ end of RNA and RNA catalyzes peptide bond formation essential for translation. RNA can self-replicate but only relatively short sequences are produced.

2. TGD picture allows to understand why only short sequences of RNA are obtained in replication. If the replication occurs at the level of dark ppn sequences as it would occur for DNA in TGD framework, long RNA sequences might be difficult to produce because of the stopping of the propagation of the primary wave splitting the flux tube pairs. This could be due to the neuron pairs to which there is associated no Coulomb repulsion essential for splitting.

3. In TGD framework RNA need not be the predecessor of DNA since the evolution would occur at the level of dark nucleon strings and DNA as the dark proton string is the simpest dark nucleon string and might have emerged first. Dark nuclear strings would have served as templates and biomolecules would have emerged naturally via the transcription of their dark counterparts to corresponding bio-polymers.

Is bio-catalysis a shadow of dark bio-catalysis based on generalization of genetic code?

Protein catalysis and reaction pathways look extremely complex (see `http://tinyurl.com/kp3sdlm`) as compared to replication, transcription, translation, and DNA repair. Could simplicity emerge if biomolecules are identified as chemical shadows of objects formed from dark nuclear strings consisting of dark nucleon triplets and their dynamics is shadow of dark stringy dynamics very much analogous to text processing?

What if bio-catalysis is induced by dark catalysis based on reconnection as recognition mechanism? What if contractions and expansions of U-shaped flux tubes by h_{eff} increasing phase transitions take that reactants find each other and change conformations as in the case of opening of DNA double strand? What if codes allowing only the dark nucleons with same dark nuclear spin and flux tubes spin to be connected by a pair of flux tubes?

This speculation might make sense! The recognition of reactants is one part of catalytic action. It has been found in vitro RNA selection experiments that RNA sequences are produced having high frequency for the codons which code for the amino-acid that these RNA molecules recognize (`http://tinyurl.com/kp3sdlm`. This is just what the proposal predicts!

Genetic codes DNA to RNA as $64 \to 64$ map, RNA to tRNA as $64 \to 40$, tRNA to amino-acids with $40 \to 20$ map are certainly not enough. One can however consider also additional codes allowed by projections of $(4 \oplus 2_1 \oplus 2_2) \otimes (5 \oplus 3(\oplus 1))$ to lower-dimensional sub-spaces defined by projections preserving spins. One could also visualize bio-molecules as collections of pieces of text attaching to each other along conjugate texts. The properties of catalysts and reactants would also depend by what texts are "visible" to the catalysts. Could the most important biomolecules participating biochemical reactions (proteins, nucleic acids, carbohydrates, lipids, primary and secondary metabolites, and natural products, see `http://tinyurl.com/jlfxags`) have dark counterparts in these sub-spaces.

The selection of bio-active molecules is one of the big mysteries of biology. The model for the chemical pathway leading to the selection of purines as nucleotides [L24] assumes that the predecessor of purine molecule can bind to dark proton without transforming it to ordinary proton. A possible explanation is that the binding energy of the resulting bound state is higher for dark proton than the ordinary one. Minimization of the bound state energy could be a completely general criterion dictating which bio-active molecules can pair with dark protons. The selection of bio-active molecules would not be random after all although it looks so. The proposal for DNA-nuclear/cell membrane as topological quantum computer with quantum computations coded by the braiding of magnetic flux tubes connecting nucleotides to the lipids wlead to the idea that flux tubes being at O=-bonds [K17].

Comparing TGD view about quantum biology with McFadden's views

McFadden [I114] has very original view about quantum biology: I have written about his work for the first time for years ago, much before the emergence of ZEO, of the recent view about self as generalized Zeno effect, and of the understanding the role of magnetic body containing dark matter [K19]. The pleasant surprise was that I now understand McFadden's views much better from TGD viewpoint.

1. McFadden sees decoherence as crucial in biological evolution: here TGD view is diametric opposite although decoherence is a basic phenomenon also in TGD.

2. McFadden assumes quantum superpositions of different DNAs. To me this looks an unrealistic assumption in the framework of PEO. In ZEO it is quite possible option.

3. McFadden emphasizes the importance of Zeno effect (in PEO). In TGD the ZEO variant of Zeno effect is central for TGD inspired theory of consciousness and quantum biology. Mc Fadden suggests that quantum effects and Zeno effect are central in bio-catalysis: the repeated measurement keeping reactants in the same position can lead to an increase of reaction rate by factors of order billion. McFadden describe enzymes as quantum mousetraps catching the reactants and forcing them to stay in same position. The above description for how catalysis catches the reactants using U-shaped flux tube conforms with mousetrap picture.

McFadden discusses the action of enzymes in a nice manner and his view conforms with TGD view. In ZEO the system formed by catalyst plus reactants could be described as a negentropically entangled sub-self, and self indeed corresponds to a generalized Zeno effect. The reactions can proceed in shorter scales although the situation is fixed in longer scales (hierarchy of CDs): this would increase the length of the period of time during which reactions can proceed and lead to catalytic effect. Zeno effect in ZEO plus hierarchies of selves and CDs would be essentially for the local aspects of enzyme action.

4. Protons associated with hydrogen bonds and electronic Cooper pairs play a universal role in McFadden's view and the localization of proton in quantum measurement of its position to hydrogen bond is the key step of enzyme catalysis. Also TGD dark protons at magnetic flux tubes giving rise to dark nuclear strings play a key role. For instance, McFadden models enzyme catalysis as injection of proton to a very special hydrogen bond of substrate. In TGD one has dark protons at magnetic flux tubes and their injection to a properly chosen hydrogen bond and transformation to ordinary proton is crucial for the catalysis. Typical places for reactions to occur are C=O type bonds, where the transition to C-OH can occur and would involve transformation of dark proton to ordinary proton. The transformation of dark proton to ordinary one or vice versa in hydrogen bonds would serve as a biological quantum switch allowing magnetic body to control biochemistry very effectively.

   What about electronic Cooper pairs assumed also by McFadden. They would flow along the flux tube pairs. Can Cooper pairs of electrons and dark protons reside at same flux tubes? In principle this is possible although I have considered the possibility that particles with different masses (cyclotron frequencies) reside at different flux tubes.

McFadden [I114] has proposed quantum superposition for ordinary codons: This does not seem to make sense in PEO since the chemistries of codons are different) but could make sense in ZEO. In TGD one could indeed imagine quantum entanglement (necessary negentropic in p-adic degrees of freedom) between dark codons. This NE could be either between additional degrees of freedom or between spin degrees of freedom determining the dark codons. In the latter case complete correlation between dark and ordinary DNA codons would imply also the superposition of their tensor products with ordinary codons.

The NE between dark codons could also have a useful function: it could determine physically gene as a union of disjoint mutually entangled portions of DNA. Genes are known to be highly dynamical units, and after pre-transcription splicing selects the portions of the transcript translated to protein. The codons in the complement of the real transcript are called introns and are spliced out from mRNA after the pre-transcription (see `http://tinyurl.com/gmphzzy`).

What could be the physical criterion telling whether a given codon belongs to exonic or intronic portion of DNA? A possible criterion distinguish between exons and introns is that exons have NE between themselves and introns have no entanglement with exons (also exons could have NE between themselves). Introns would not be useless trash since the division into exonic and exonic region would be dynamical. The interpretation in terms of TGD inspired theory of consciousness is that exons correspond to single self.

Is there a connection between geometric model of harmony and nuclear string model of genetic code?

There should exists a connection between the geometric model of harmony and genetic code and the model of genetic code discussed.

1. Dark DNA strands could be connected by color flux tubes to form a double strand by reconnections of U-shaped color flux tubes. What would induce a codon-wise or letter-wise pairing of DNA codons and their conjugates represented as dark quark triplets to form double DNA strand? Cyclotron resonance could accompany reconnection (magnetic field strength would be identical and reconnection could occur).

2. One has the correspondence codon $\leftrightarrow$ state of dark nucleon or codon $\leftrightarrow$ state of dark nucleon triplet. The geometric model of harmony and genetic code [L12] represents the codons as 3-chords. The 3-chord would be represented in terms of cyclotron frequencies of dark photons

assignable to the 3 dark quarks (nucleons) in the state. Each quark-color bond pair (including the pion-like bond) could be in 12 states with corresponding cyclotron frequency mappable to the basic octave. The cyclotron frequency triplets would be same for codons and conjugates. The only manner to understand the scale is in terms of spectrum of magnetic field strengths for U-shaped flux tube pairs.

This would require 3 pairs of flux tubes between the dark codons of DNA strands. If the quarks inside linear dark proton are connected by color flux tubes (like protons in the model of dark nucleus). Reconnection for U-shaped flux tube connecting quarks would give rise to the double strand formed by dark proton strings. The magnetic field strength of the 3-flux tubes would be determined by the state of dark proton and would be same for DNA and RNA codons and also for RNA codons and corresponding tRNA-amino-acid complexes. The cyclotron frequencies would define a scaled up variant of Pythagorean scale projected to the basic octave [L12]. This option does not favor the idea about separater 4-letter code.

3. The geometric model for harmony is formulated in terms of orbits of the subgroups of the isometry groups of tetrahedral and icosahedral geometries. The DNAs coding particular amino-acid correspond correspond to the orbit of the triangle of icosahedron corresponding to the amino-acid. The decomposition $60 \to 20+20+20$ suggests strongly decomposition of I to 20 Z_3 cosets containing 3 elements each other and in correspondences with the triangular faces of icosahedron.

4. The model of the genetic code just discussed relies on the model of dark nucleon based on group theory. The symmetric groups of Platonic solids are in turn associated with inclusion of hyper-finite factors and appear in Mc Kay correspondence, whose proof involves decompositions of SU(2) representations to the representations of the discrete subgroups of Platonic solids. A further observation is that the numbers of elements for isometries of icosahedron and tetrahedron are 60 and 4 respectively: the sum is 64. Could the action of Z_3 leaving face invariant could be posed as an additional condition on amino-acids and reduce the amino-acid representation to $4 \otimes 5$.

5. In the geometric model of harmony genetic icosahedral 20+20+20 part of the code involves a combination of three different Hamilton's cycles mapping 60 DNAs to 20 amino-acids: in terms of icosahedral group I and its coset space I/Z_3 these maps correspond to coset projections. Could the decomposition $(4 \oplus 2_1 \oplus 2_2) \otimes (5 \otimes 3)$ be understood in terms of a reduction to icosahedral and tetrahedral subgroups of rotation group or of their spin coverings.

   In this process finite-dimensional representation of $SO(3)$ decomposes to a direct sum of representations of the discrete subgroup if its dimension is larger than any of the dimensions of representations of the finite sub-group (for basic facts about these see `http://tinyurl.com/ho4onbs`). One might hope that the decomposition of the representations of SO(3) appearing in the above formula under icosahedral group and or tetrahedral group could allow to understand the emergence of DNA, RNA, tRNA, and amino-acids as kind of symmetry breaking.

6. In the geometric model of harmony 64-codon code [L12] is obtained as a fusion 60-codon code assignable to icosahedron + 4 codon code assignable to tetrahedron. There are actually two codes corresponding to tetrahedron and icosahedron as disjoint entities and tetrahedron glued to icosahedron along one face. The model explains the two additional amino-acids Pyl and Sec coded for a variant of the genetic code.

How could these two successful models relate to each other? In p-adic physics of cognition Platonic solids and polygons can be seen as discrete approximation for sphere [L25] and biomolecules could be understood as cognitive representation in the intersection of real and p-adic space-time surface consisting of algebraic points. Could one assign icosahedron and tetrahedron to a codon in some concrete manner? Could the attachment of tetrahedron to icosahedron along one face have concrete meaning? The answer seems to be negative.

1. One can about the interpretation of the 12 vertices of the icosahedron - how number 12 could be assigned with the genetic code? The vertices correspond to notes perhaps represented as

magnetic field strength at the flux tubes assignable to color bonds. This field strength should be determined by the spin state of dark 3-nucleon. No concrete nuclear string counterpart seems to exist for the closed Hamiltonian cycle consisting of 12 notes and in case of tetrahedral extension of 13 notes. 12 vertices of icosahedron correspond to 12 notes and 20 faces to 3-chords so that there is not need for more concrete correspondence.

2. The attachment of tetrahedron to icosahedron would bring in further note very near to one of the notes of Pythagorean scale and corresponding 3-chords. This has concrete interpretation and there is no need to make this more concrete at the level of geometry of DNA. If icosahedron and tetrahedron are disjoint one obtains four additional codons. It seems that all these 4 3-chords be assigned with the 3 color bonds, one note for each of them. What distinguishes at the level of dark nucleon string the situations in which tetrahedron is attached and non-attached to the color bond? In presence of attachment there would be 1 shared 3-chord corresponding to stop codon assignable with the shared face. The 13:th note appearing in 4 3-chords differs very little from one of the notes of the icosahedral scale: this corresponds to the fact that 12 perfect quints do not quite give 7 octaves as already Pythagoras realized. Crazy question: Could this small difference relate to the small relative mass difference $(m_p - m_n)/m_p \simeq .0014$ making itself possible visible in cyclotron frequency scale? The idea does not seem plausible: $[(3/2)^{12} - 2^7]/2^7 \simeq .014$ is 10 times larger than $(m_p - m_n)/m_p \simeq .0014$.

The conclusion is that genetic code can be understand as a map of stringy nucleon states induced by the projection of all states with same spin projections to a representative state with the same spin projections (total quark spin and total flux tube spin). Genetic code would be realized at the level of dark nuclear physics and biochemical representation would be only one particular higher level representation of the code. A hierarchy of dark baryon realizations corresponding to p-adic and dark matter hierarchies can be considered. Translation and transcription machinery would be realized by flux tubes connecting only states with same quark spin and flux tube spin.

9.10 Flux Tube Realization Of The Divisor Code

Divisor code discovered by Khrennikov and Nilsson [K56] allows a flux tube realization and a close connection with dark baryon code seems to be possible.

9.10.1 Divisor Code

The idea of divisor code discussed in [A30] is inspired by the following observations.

1. Consider the number $N(n)$ of integer divisors for integers n in the range $[1, 21]$ corresponding to amino-acids with stopping sign counted as amino-acid.

2. Denote the number of integers $n \leq 21$ for which the number of divisors is k by $B(k)$. Also stopping sign is counted as an amino-acid and $n = 0$ corresponds to amino-acid also. This number $N(k)$ varies in the range $[1, 6]$. $B(k)$ has the values $(1, 8, 2, 5, 1, 3)$ where k runs from 1 to 6.

3. Denote by $A(k)$ the number of amino-acids coded by k DNA codons. $A(k)$ has the values $2, 9, 2, 5, 0, 3$.

The spectrum of $A(k)$ is very similar to that of $B(k)$ and this raises the question whether one could understand genetic code as a divisor code in the sense that the degeneracy of amino-acid would be dictated by the number of the integers $1 \leq n \leq 21$ coding it. One might also ask whether the amino-acids which are abundant and thus important are coded by integers with a large number of divisors. Also one can ask whether the divisor structure possibly correlates with the structure of the amino-acid.

Divisor code in this form would be only approximate and one can wonder could try to imagine some simple symmetry breaking mechanism. In this respect the crucial observations might be following.

1. The number of DNAs needed to realize divisor code would be 70 instead of 64. One must drop 6 codons and by choosing them suitably one might hope of getting correct degeneracies.

2. The most natural manner to break the symmetry is to drop the 4 codons from the codons coding for 5-plet which would thus become 1-plet. 5-plet corresponds to integer $n = 16$ and its product compositions $(16, 1), (1, 16), (2, 8), (8, 2), (4, 4)$ correspond to the DNAs coding for it. $(4, 4)$ would naturally correspond to singlet.

3. By dropping 2 codons from some 4-plet one obtains 2-plet and correct degeneracies. One candidate for 4-plet corresponds to $n = 8$ and its product decompositions $(1, 8), (8, 1), (2, 4), (4, 2)$. By dropping two of these one obtains correct degeneracies. It might that power of 2 property of $n = 8$ and $n = 16$ somehow relates to 2-adicity and to the special role of these amino-acids.

4. A possible interpretation is in terms of symmetry based on cyclic group $Z(n)$ serving as a symmetry of DNA codons coding for amino-acid labeled n. Z_n allows decompositions $Z_n = Z_{n_1} \times Z_{n_2}$, $n = n_1 \times n_2$ and if the representations are invariant under Z_{n_2} and thus reduce to those of Z_{n_1} codons coding for a given amino-acid correspond to the product decompositions. Symmetry breaking would be due to the lacking 6 codons and would mean that only Z_4 invariant states would be realized for Z_{16} and Z_1 and Z_8 of Z_2 and Z_4 invariant states are realized for $n = 8$. $n = 4$ could correspond to triplet of stopping codons so that powers of 2 would be in special role for vertebrate code suggesting 4-adicity. 4-adicity is also suggests by the almost exact A-G and T-C symmetries of the last nucleotide.

9.10.2 Topological Interpretation Of The Divisor Code In TGD Framework

The most concrete physical interpretation of the divisor code found in TGD framework is topological and based on TGD inspired vision about the role of dark matter in biology [K56].

1. The generalized 8-D imbedding space has a book like structure with pages glued together along back which is 4-D surface of $H = M^4 \times CP_2$ [K18, K39]. Particles at different pages are dark relative to each other since they cannot have local interactions (appear in the same vertex of Feynman diagram). The pages are partially characterized by the value of Planck constant which can be arbitrary large. This explains the macroscopic quantum coherence of living matter. Matter can leak between different pages meaning a phase transition changing Planck constant.

2. The notion of magnetic body with flux tubes carrying dark matter and connecting different bio-molecules central for the TGD inspired model of living matter [K17]. Magnetic bodies of bio-molecules can be also connected by magnetic flux tubes, even those in different pages of the book. For instance, the phase transition reducing $\hbar$ reduces the distance between two bio-molecules connected in this manner and forces them near to each other. This explains the extreme selectivity of bio-catalysis and the miraculous ability of two bio-molecules to find each other in the dense soup of bio-molecules. In particular, DNA and its conjugate codons, mRNA codons, and tRNA would be connected by this kind of flux tubes. Also amino-acids would be connected to tRNA codons in this manner since tRNA molecules catch the amino-acids and bring them to the mRNA-amino-acid translation site. Genetic code could reduce to the selection rules for the flux tube connections connecting in general situation magnetic bodies belonging to different pages of the book.

3. The pages of book are almost copies of $M^4 \times CP_2$. This means that M^4 is replaced with n_a-fold singular covering and CP_2 with n_b-fold singular covering. The coverings have cyclic groups Z_{n_a} and Z_{n_b} act as discrete symmetries for the wave functions of particles in the covering. A given page is thus labeled by two pager numbers (n_a, n_b). Two pages contain common points and thus a direct tunnelling of 3-surfaces between these pages is possible only if the number n_{a_1} of the sheets of covering divides n_{a_2} or vice versa. Same holds true for n_{b_1} and n_{b_2}. This rule is just the basic rule about how symmetries of system can change in phase transition. This number theoretic rule could be behind genetic code and the extreme selectivity of bio-catalysis.

4. Suppose that both bio-molecules correspond to ordinary matter with $n_a = n_b = 1$ but that the magnetic body of a given amino-acid corresponds to $(n_a(A), n_b(A))$ and DNA, RNA, and tRNA codon to $(r_a(DNA), r_b(DNA))$. Since the flux tube from tRNA codon to the amino-acid page is essential for the process in which amino-acid is attached to tRNA, only tRNA for with $r_a(tRNA)$ divides $n_a(A)$ can catch an amino-acid labeled by n_a. Same applies to r_b and n_b.

5. Without the presence of the integer n_b the code would fail since DNA codon labeled by r_a would code for all amino-acids for which n_a has r_a as a factor. n_b can indeed save the situation. Suppose that one has $r_b(tRNA) = n_b(A)$ if DNA codes for an amino-acid. Assume also that $n_b(a)$ is prime: $n_b(A) = p_b(A)$, and different for each amino-acid. This prime does not correspond to p-adic prime, which is expected to be very large in the length scales of atomic physics (electron corresponds to $M_{127} = 2^{127} - 1$). Note that the assumption that amino-acids are labeled by small primes was made in both TGD inspired number theoretical models of the genetic code.

6. The assumptions mean that tRNA and amino-acid can be connected by a magnetic flux tube only if one has

$$p_b(tRNA) = p_b(A)$$

and $r_a(tRNA)$ divides $n_a(A)$. If the pages numbers n_a vary in the range $[1, 21]$ the divisor code follows from the argument of the previous section. Taking the previous argument seriously, one should also understand why there is no amino-acid labeled by $n_a = 4$ and why corresponding DNAs correspond to prime characterizing $n_a = 4$, why the number of DNA codons labeled by the factors of $n_a = 8$ is two, and why the number of codons associated with $n_a = 16$ only one.

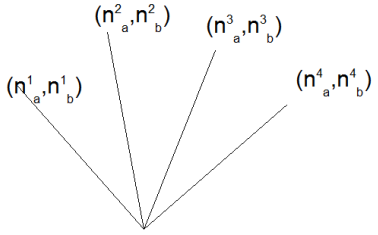

Figure 9.15: Illustration of the book-like structure of the generalized imbedding space.

Some further comments are in order.

1. The realization of the genetic code is not unique since the integers r_a and n_a could be replaced with Nn_a, where N is a product of primes larger than $p = 19$. It is also enough that the integers characterizing amino-acids are relative primes (have not common factors). The simplest assumption would be that the primes $p(A)$ satisfy $p(A) > 19$ so that $p(A)$ does not divide $n(A)$ for any A. If $p(A)$ is as small as possible the value spectrum of $p(A)$ is

$$\{23, 29, 31, 37, 41, 43, 47, 53, 59, 61, 67, 71, 73, 79, 83, 89, 97, 101, 103, 107, 109\} \ .$$

If one assumes that the two additional amino-acids coded in some cases by non-vertebrate genetic code correspond to primes also the primes $113, 127$ are included.

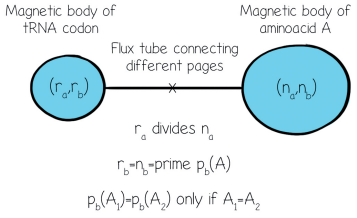

Figure 9.16: Illustration of the selection rules for magnetic flux tubes connecting magnetic bodies of tRNA and amino-acid.

What is interesting is that Mersenne prime $M_7 = 2^7 - 1 = 127$ appears in the model of genetic code based on the notion of Combinatorial Hierarchy [K23]. This model assumes that DNA codons correspond to 64 integers in the range $1, ..., 127$. This realization of the genetic code cannot however be consistent with the divisor code realized in the proposed manner since it would require that the integers $n(A)p(A)$ belong to the range $1, .., 127$. The prime factors of these integers can however belong to this range.

2. The quantum states of dark baryons realize vertebrate genetic code with very general assumptions group theoretically [L2, K24, **?**], [L2]. Since dark matter is involved in both cases, one might wonder whether these codes could be related somehow. A one-one correspondence between the quantum states of dark nucleons representing codon and the integers r_a, p_b is required in order to have this connection. The simplest possibility is that that energy minimization implies that given dark nucleon resides with high probability at aflux tube labeled by unique value of r_a. Same applies to amino-acids.

3. The model in principle allows an infinite number of analogous codes and an interesting question is whether the bio-catalysis involves this kind of codes. The quantum antenna model for remote replication discussed in [K24] allows a dynamical interpretation for the flux tube realization of the genetic code as a divisor code in terms of quantum antenna hypothesis [K36], and predicts that sequences of DNA codons serve as names for polar molecules quite generally so that genetic code would define a universal language in living matter. This leads to an identification of the basic mechanism responsible for the functioning and evolution of the immune system.

9.10.3 About Detailed Correspondence Between DNA Codons, Dark Baryon Codons, And Their Divisor Code Counterparts

One can make some conclusions also about the detailed correspondence between DNA codons and dark baryon codons as well as their divisor code counterparts. $L_z = -1$ requires that there is a rotating kink in flux tube representing nuclear string. One can ask whether also the corresponding DNA codons could be somehow special.

1. Maximal spin projections for both quarks ($J_z^q = 3/2$) and flux tube $J_z^f = \pm 2$ correspond to amino-acids met and trp coded by single codon. For the proposed interpretation of the divisor code these codons would correspond to $n = 1$ and $n = 16$.

2. Amino-acids coded by two codons correspond to $(J_z^q = 3/2, J_z^f \in \{1, 0, -1\})$ and $(J_z^q \in \{1/2, -1/2\}, J_z^f \in \{2, -2\})$. For the divisor code these amino-acids correspond to 8 primes plus lacking 9: th doublet results when one drops two codons from one 4-plet ($n = 8$ 4-plet is a good candidate).

3. For the baryonic realization 2 3-plets $J_z^q = -3/2, J_z^f \in \{2, -2\}$) contain one member corresponding to rotating kink. The first corresponds to ile and the DNA codon coding for met if T-C symmetry of the third nucleotide were exact. Second corresponds to stop codon coding

for trp if T-C symmetry were exact. In divisor code triplets corresponds to $n = 4$ (stop codon?) and $n = 9$.

4. Three 6-plets correspond to ($J_z^q = -3/2, J_z \in \{1, 0, -1\}$ contain one anomalous member each and the corresponding codon would naturally belong to the doublet part of 6-plet in the code table. In divisor code 6-plets correspond to $n \in \{12, 18, 20\}$.

5. Three of the six 4-plets ($J_z^q = 1/2, -3/2, J_z \in \{1, 0, -1\}$ contain 2 anomalous members. From one 4-plet 2 codes for nothing or formally stop codon so that it becomes 2-plet: naturally these codons correspond to $L_z = -1$ and a rotating kink in the helix model of the nuclear string. From second 3-plet one $L_1 = -1$ codon would codes for nothing becoming formally stop codon and one obtains second 2-plet.

6. The only regularity which comes in mind is that the 3 anomalous 4-plets and 2 anomalous doublets could populate the lowest row of the code table. The 16 oddballs would reside at the boundaries of the code table. In divisor code these would correspond to $n \in \{6, 8, 10, 14, 15, 21\}$. Dropping from $n = 8$ 4-plet 2 codons one would obtain 5 4-plets and 9 2-plets as required. Besides this one must drop 4 codons from $n = 16$ 5-plet to get singlet. As already noticed, 2-adicity suggests that $n = 2^k$ represents something special.

9.11 A Model For Protein Folding And Catalytic Action

It would be fascinating if the vision about the role of flux tube connections would generalize to interactions of all molecules in living matter. The mere selection rules would mean hidden simplicity behind extremely complex looking interactions in living matter. The model for protein folding and catalytic action discussed in [K2] is the first attempt in this direction. In the following this model is briefly summarized and the improvement of the model inspired by recent considerations is suggested.

9.11.1 Earlier Model For The Folding Code

The model for the evolution of the genetic code led [K19] to the idea that the folding of proteins obeys a code inherited from the genetic code. One can imagine several variants of this code. One of the is that amino-acid behaves like the conjugate Y_c of the middle nucleotide of the codon XYZ coding for it. Conjugation for amino-acids would correspond to the hydrophilic-hydrophobic dichotomy. Also catalyst action could reduce to effective base pairing in this picture chemically and at the level of quarks associated with the flux tube to matter antimatter conjugation. The guess that amino-acid and its conjugate form pairs turned out to be wrong however and after various twists and turns I ended up with the hypothesis that the amino-acid in protein behaves like $Y_c Z_c$ where Z corresponds to third nucleotide for some codon coding for the amino-acid.

It however turned that the model as such is probably too restrictive and not fully consistent in the particular cases studied. In the following this model is discussed briefly and later an improved model for protein folding is proposed.

Flux tubes as correlates of directed attention at molecular level

After some trials one ends up with a general conceptualization of the situation with the identification of ("wormhole") magnetic flux tubes as correlates for attention at molecular level so that a direct connection with TGD inspired theory of consciousness emerges at quantitative level. Whether wormhole flux tubes or ordinary flux tubes are needed is not a completely settled question yet and the attribute "wormhole" will not be used in the sequel. This allows a far reaching generalization of the DNA as topological quantum computer paradigm and makes it much more detailed. The final outcome is very simple quantitative model for both protein folding and catalyst action based on minimization of energy, which seems to be consistent with basic experimental facts as well as general ideas.

What kind of atoms can be connected by flux tubes?

1. Hydrogen bonds play a key role in bio-catalysis but are not understood completely satisfactorily in the standard chemistry. Hence the basic question is whether hydrogen bonds can be regarded as or are accompanied by short (wormhole) magnetic flux tubes: note that the subject-object asymmetry of directed attention would correspond to donor-acceptor asymmetry of they hydrogen bond. If this is the case, the identification of the magnetic flux tube connection as a prerequisite for a hydrogen bond or as hydrogen bond becomes natural. At least the atoms able to form hydrogen bonds could form flux tube contacts so that the model would be very predictive and would conform with the known important role of hydrogen bonds in bio-catalysis.

2. The fact that hydrogen bonds connect base pairs suggests a generalization of the notion of base pairing stating that under some conditions amino-acids coded by XYZ and UY_cV can behave like base pairs. These amino-acic pairs correspond to pairs of amino-acid residues which are hydrophilic *resp*. hydrophobic and hydrophobic residue do not form hydrogen bonds in general. These flux tubes would thus be more general and in general long. The model for DNA as topological quantum computer requires this kind of flux tubes and they would in general connect atoms or molecules which act as acceptors in hydrogen bonding: $O =$ atom in amino-acid and aromatic ring are basic examples.

3. If one assumes that both $N-H$ and $O =$ associated with the constant part of the amino-acid can act as flux tube terminals and represent Z and Y nucleotides of the codon XYZ coding for the amino-acid, one obtains $Y = Z$ pairing of $O = -O =$ flux tubes are allowed and $Y = Z_c$ pairing if only hydrogen bond like pairings are allowed.

Color inheritance by a reconnection of flux tubes

1. There should exist some mechanism allowing amino-acids to inherit the base pairing property from the tRNAs associated with them so that one can identify amino-acid with the middle nucleotide of the codon coding it. If tRNA middle nucleotide is connected to $O =$ of the amino-acid, this becomes possible since the reconnection of flux tubes preserves the "color" of the flux tubes coded by (A, T, G, C) that is by the quark or anti-quark coding for the nucleotide. The temporary formation of a hydrogen bond between $N - H$ and $O =$ of two amino-acids as in the case of alpha helix would allow $N - H$ to inherit the conjugate of the color associated with $O =$. Alternative interpretation is that this hydrogen bond is possible only if the predetermined color of $N-H$ is consistent with the inherited one. The inheritance of flux tube color would be a completely general mechanism and even the donor atoms in the residues of amino-acids could inherit the color of $O =$ in this manner.

2. A possible interpretation for the fixing of the flux tube color is in terms of quantum measurement selecting one color from quantum superposition in the reconnection process. This would mean that the unitary process can bring superposition back and reconnection process can change the inherited color. The hydrogen bonds between water molecules could correspond to quantum superpositions of different colors. This superposition property might relate to the wobble base pairing phenomenon for the third nucleotide in tRNA.

Folding code

The identification of $N - H$ as a representation for the conjugate of the third nucleotide Z means that amino-acids would remember which codon coded them. If only hydrogen bond like flux tubes are allowed, flux tubes can connect only amino-acids satisfying $Y = Z_c$. If $= O - O =$ flux tubes are allowed $Y = Z$ rule favored by the model of DNA as topological quantum computer follows. The isospin symmetry of the third nucleotide implies that both rules are quite flexible. If one identifies hydrogen bond with flux tube ($Y(n) = Z(n + k)$) the model works badly for both options. If one assumes only that the presence of a flux tube connecting amino-acids in either direction ($Y(n) = Z(n + k)$ or $Z(n) = Y(n + k)$) is a prerequisite for the formation of hydrogen bond, the model works. $Y = Z$ rule is favored by the study of five enzymes: the possible average length of alpha helix is considerably longer than the average length of alpha helix if gene is the

unique gene allowing to satisfy $Y = Z$ rule. The explicit study of alpha helices and beta sheets for these enzymes demonstrates that the failure to satisfy the condition for the existence of hydrogen bond fails rarely and at most for two amino-acids (for 2 amino-acids in single case only).

$Y = Z$ rule could mean a solution of the basic problem of proteonics: Do genes determine the folding of proteins and how this would take place? The interpretation would be that the information loss suggested by the many-to-one character of the genetic code is only apparent. The apparently lost information which corresponds to the $A - G$ and $T - C$ symmetries of the third nucleotide codes for the hydrogen bonding and hence for the folding of the protein. The model in its most stringent form is easy to kill since in the case of alpha helices and beta sheets the hydrogen bonding fixes completely the DNA sequence coding for the protein. A weaker variant of the model based on quantum variant of wobble base pairing: in this case there are no conditions on DNA sequence. It turns out that only this variant works. Hence hydrogen bonded amino-acid behave as if they were coded by the unique codon consistent with $Y = Z$ rule.

Quantitative model

The quantitative model relies on the assumption that the contribution of a flux tube connecting two amino-acids to the potential energy depends only on the distance between the molecules in question. The extremals of the total interaction energy are same for any choice of the potential and only the absolute minimum of the interaction energy depends on the choice of the potential. The simplest potential corresponds to harmonic oscillator potential and would explain formation of alpha helices and beta sheets and with the fact that hydrophilic and hydrophobic residues tend to have a large distance and only few flux tube contacts. For large Planck constant also long flux tubes could correspond to attractive harmonic oscillator potential. Also the contribution of other interactions between neighboring amino-acids are expected to be present but are neglected in the simplest model. The model predicts alpha helices and beta sheets, and more generally, periodic structures, as solutions to energy minimization equations.

The model fails to catch completely the basic rules of protein folding, and the predictions are not fully consistent with empirical facts in the cases studied. A model in which the hydrophilic and hydrophobic interactions are mediated by flux tubes between magnetic bodies of the molecule and water molecule and in this manner induce long range interactions between amino-acids - somewhat like the attractive interactions of electrons with ions induce attractive interaction between the members of a Cooper pair - looks more attractive. This model is however computationally much heavier and is not discussed in [K2]. In the sequel a formulation of this model is discussed.

9.11.2 Hydrophily And Hydrophoby Number Theoretically

Amino-acids can be classified to hydrophilic and hydrophobic ones whereas all DNA codons are hydrophilic. Hydrophily and hydrophoby are believed to relate to the standard chemistry alone and this might be the case. One can however just for fun ask whether hydrophily and hydrophoby could have a connection with divisor code, formation of flux tubes connecting the molecule to water molecules, and phase transitions changing the value of Planck constant and changing the length of flux tube. I have discussed this idea already in the model of protein folding [K2].

To simplify the model assume that only single dark page is associated with water molecule and labeled by (n_a^W, n_b^W). Of course, several levels characterized by different integers are also possible and this would bring in additional flexibility. Both hydrophoby and hydrophily would mean interaction mediated by the flux tubes to the magnetic body of water with the sign of the force differing for hydrophilic and hydrophobic amino-acids. There is no need to assume that quarks and anti-quarks generate the interaction. Gly for which the residue is just hydrogen atom does not allow classification as a hydrophilic or hydrophobic which would suggest that it does not have any flux tube connections with the magnetic body of the water. The interaction mediated by flux tubes between amino-acids and water molecules would be analogous to the interaction induced by the interaction between electrons and ions inducing attractive interaction between the members of Cooper pair. It would induce attractive interaction between hydrophilic amino-acids and repulsive interaction between hydrophilic and hydrophobic amino-acids favoring the formation of hydrophilic outer surfaces and hydrophobic inner surfaces.

One could understand hydrophily/hydrophoby dichotomy number theoretically for both options. The discussion of the first option makes clear that also second option is possible to realize.

1. Assume that n_a^W is divisible by all integers n_a^{DNA} associated with DNA codons and thus involves suitable powers of primes $p \leq 19$. It could contain also an integer factor which is product of primes larger than $p = 19$. This is necessary for achieving hydrophily of DNA codons.

2. Hydrophily of DNA codons also requires n_b^W must be proportional to the product of coprime integers n_b^W (primes for the simplest option) assignable to DNA codons. n_b^W could involve also a factor proportional to second integer expressible as product of primes $p > 19$. The simplest option is that this integer equals to 1.

3. For hydrophobic amino-acids integers n_b^A must be of form $mn_b^A = n_b^{DNA} m_b$ such that m_a does not divide n_b^W and n_b^W. This is enough to guarantee that magnetic flux tubes in either direction are impossible so that hydrophoby is guaranteed in the proposed sense. This definition extends also to other molecules and can be expressed in terms of the integers (n_a, n_b) labeling the magnetic body of the molecule.

4. Second option is obtained by assigning the integer m_b only to Gly which is neither hydrophilic nor hydrophobic.

9.11.3 Could There Be New Physics Behind Hydrophily AndHydrophoby

One could accept just as a fact that magnetic flux tubes to the magnetic body of water mediate an interaction which is attractive or repulsive between water molecules and amino-acids and attractive between DNA molecules and water. Accepting that this induces interaction between amino-acids one could proceed to model building without any mention about TGD.

One could also try to dig deeper and ask what might be the origin of this interaction.

1. **Option I**: Could one understand the interaction in terms of phase transitions changing the Planck constant of the magnetic flux tube. The interaction would be repulsive (attractive) would result if the interaction energy increases (decreases) when Planck constant is reduced. Magnetic interaction energy is certainly the best candidate and could also imply the equivalence of the divisor code and dark baryon code.

2. **Option II**: Could hydrophily and hydrophoby be described in terms of em interactions of quarks representing nucleotides in the model of DNA as TQC. For instance, could amino-acids and water molecules be characterized by charges which are of opposite sign for water molecules and hydrophilic molecules and of same sign for water molecules and hydrophobic molecules.

For **Option I**, which represents completely new physics (using the standards of TGD!), the situation looks promising. The magnetic interaction energy assignable to the flux tube is a function of the integers (n_a, n_b) -in particular of the Planck constant of the flux tube- and the minimization is performed by keeping the charges of the quarks possibly at its ends fixed. This new physics fits also nicely with the idea that magnetic body controls the living matter by utilizing phase transitions changing Planck constant.

What comes in mind in the case of **Option II** is that the ends of the flux tube carry opposite charges correlating with the codon coding for the amino-acid and giving rise to ordinary gauge interactions. Unfortunately this scenario does not seem to work.

1. In [K2] it was found that (denoting codons by XYZ) only $Y = A, G$ type amino-acid residue can form hydrogen bonds and is hydrophilic and thus interacts strongly with water and DNA and RNA. If water end of flux tube corresponds to anti-quarks the attractive interaction between quark and anti-quark at the ends of flux tube could relate to hydrophily. For hydrophobic amino-acids one would have interaction between identical quarks and already Fermi statistics would cause repulsion. In DNA as TQC model based on the coding of A, G

and T, C in terms of quarks u, d and their anti-quarks hydrophily-hydrophoby dichotomy corresponds to matter-antimatter dichotomy for quark assigned to the ends of the flux tube. Quarks and anti-quark have opposite charges. Hence the flux tube ends of hydrophilic amino-acids could correspond to quarks and water and hydrophobic ends of flux tubes to anti-quarks. Therefore the DNA as TQC model would predict the needed behavior of the forces. In the case of Gly containing only hydrogen as residue the flux tube might be simply absent.

2. DNA codons A, T, C, G are bases and thus polar and hydrophilic. In the case of DNA charge conjugation for quarks corresponds to the puridine-pyrimidine complementarity corresponding to conjugation of nucleotides. The rule applying in the case of amino-acids would predict T, C to be hydrophobic nucleotides which does not make sense. Therefore it seems that hydrophily and hydrophoby cannot reduce to the interactions of dark quarks and that they only represent conjugation of nucleotides symbolically.

9.11.4 An Improved Model For Protein Folding

To begin with let us summarize some basic facts about protein folding.

1. Hydrophily and hydrophoby play a key role in protein folding and dictate to a high degree the resulting folding patterns. This suggests that one cannot neglect the role of water in the process.

2. Protein folding proceeds from short to long length scales starting with the formation of secondary structures such as alpha helices, beta sheets, and random coil portions and is followed by the formation of tertiary and higher structures.

3. The formation of hydrogen bonds is in a decisive role in the formation of secondary structures. The mechanism leading to their formation might be contraction of magnetic flux tube by a phase transition changing Planck constant.

4. The folding patterns do not depend strongly on the precise primary structure, that is precise amino-acid decomposition which suggests that instead of the detailed chemistry the forces between quarks and anti-quarks mediated by flux tubes is what matter so that hydrophily and hydrophoby would become the basic characterizers of the interaction. The phase transitions changing Planck constant would indeed represent this kind of universal interactions independent of the chemistry.

5. In the first approximation amino-acids could be labeled by a variable telling whether it is hydrophobic, hydrophilic, or neither or these (Gly). This approximation would be broken by special amino-acids which appear in edges if beta sheets (Pro) and Cys which often appear as S-S boded pair in junctions. By bringing in forces depending on the angles between tangent vectors of successive amino-acids and on amino-adics themselves this tendency could be modeled.

The earlier approach to protein folding inspired by DNA as TQC idea did not start from this picture but assumed that direct flux tube connections between amino-acids rather than the interactions induced by flux tube connections with the magnetic bodies of water molecules were responsible for the folding. The model did not lead to any spectacular results and the proposed rules were not fully consistent in the cases studied.

9.11.5 The Model For Which The Magnetic Body Of Water Is Involved

The improved approach to protein folding starts from the general vision about magnetic body containing dark matter as a controller of visible matter in living system. The protein and its magnetic body would be regarded as a living system in itself.

1. Magnetic body must have large number of flux tube contacts to the visible matter. An excellent candidate for the magnetic body is that assignable with water and having flux tube connections to DNA and both hydrophilic and hydrophobic amino-acids. The magnetic body

could control and at least fasten the self-organization process leading to the folding pattern which - by applying standard argument - would otherwise take astronomical time otherwise. The two-step attractive connections between all hydrophilic amino-acids would be possible via the magnetic body of water. The non-hydrophilic amino-acids not in direct contact with water are known to be more like passive structural stuff responsible for a fixed structure but not so relevant for the functioning of the bio-molecule. Hydrophily and hydrophoby would reflect the dependence of interaction energy on the value of Planck constant associated with the flux tube mediating the interaction.

2. This picture implies a straightforward modification of the earlier model. The simplest model would minimize a potential function V expressible as a sum $V = V_1 + V_2 + V_3$ of three terms. V_1 would be sum of the values of a universal two-particle potential function $V_{phi,phi}(r)$ for arguments $r_{ij} = |r_i - r_j|$ varying over all hydrophilic amino-acid pairs and giving rise to an attractive force. V_2 would be a sum of a universal two-particle potential function $V_{pho,pho}(r)$ for arguments $r_{ij} = |r_i - r_j|$ varying over all hydrophobic amino-acid pairs. V_3 would be would be sum of the values of a universal potential function $V_{phi,pho}(r)$ for arguments $r_{ij} = |r_i - r_j|$ varying over all pairs of hydrophilic and hydrophobic amino-acids. This potential function would induce a repulsive force. Besides this a constraint force due to the fact that amino-acids form a sequence would be present.

3. The resultant of the forces along lines connecting amino-acids would be parallel to the amino-acid sequence in the mechanical equilibrium. Hydrogen bonds and other bonds are indeed formed between neighboring hydrophilic amino-acids and the contraction of the flux tubes connecting the amino-acids in question to the magnetic body of water could be the mechanism. The model seems to be consistent with the basic qualitative facts about folding. The quantitative testing of the model would require determination of the conformations minimizing the potential function subject to the constraint provided by amino-acid sequence. Here of course the freedom to choose the three functions provides a considerable flexibility and symmetry arguments might allow to pose conditions on the form of these functions.

4. One could also include to the potential function describing a direct interaction with water molecules depending on parameters like pH affecting the folding pattern. The resultant for a given amino-acid would be sum of forces directed from a hydrophilic amino-acids to neighboring water molecules. It is not clear whether the normal component of this force could be compensated by the induced forces between amino-acids in a typical equilibrium configuration and the formation of hydrogen bonds involving the contraction of the flux tube could be the manner to achieve this.

Could one regard amino-acids and DNAs of given type as analog of species?

An interesting idea raised by the work with the model for protein folding is that the magnetic bodies amino-acids or DNA codon of a given type could behave like single phase on their respective page of the book so that the mutual interactions of their magnetic bodies could affect considerably the behavior of this phase to first order although amino-acids themselves are at different positions and one might expect only small correlations between their motions. Whether the dynamics of amino-acids of given type in protein folding are strongly correlated could be tested.

In certain sense one could speak of single species formed by amino-acids of given type and folding as long range interaction could be seen as an outcome of self-organizing interaction between members of various species and between species themselves plus short range constraints due to the fact that amino-acids form a sequence. The question applies to DNA and RNA codons and also to larger units such as genes formed to which one could assign their own page of the book. Water would represent the page to which all DNAs can send flux tubes. Even the notion of biological species could involve common dark space-time sheet(s) where the magnetic bodies of the members of species are and interact making the members of species to behave like single coherent unit.

9.12 Appendix: Generalization Of The Notion Of Imbedding Space

This section summarizes the the attempt to understand how the hierarchy of Planck constants is realized at the level of imbedding space and what quantum criticality for phase transitions changing Planck constant means.

9.12.1 Hierarchy Of Planck Constants And The Generalization Of The Notion Of Imbedding Space

In the following the recent view about structure of imbedding space forced by the quantization of Planck constant is summarized. The question is whether it might be possible in some sense to replace H or its Cartesian factors by their necessarily singular multiple coverings and factor spaces. One can consider two options: either M^4 or the causal diamond CD. The latter one is the more plausible option from the point of view of WCW geometry.

The evolution of physical ideas about hierarchy of Planck constants

The evolution of the physical ideas related to the hierarchy of Planck constants and dark matter as a hierarchy of phases of matter with non-standard value of Planck constants was much faster than the evolution of mathematical ideas and quite a number of applications have been developed during last five years.

1. The starting point was the proposal of Nottale [E5] that the orbits of inner planets correspond to Bohr orbits with Planck constant $\hbar_{gr} = GMm/v_0$ and outer planets with Planck constant $\hbar_{gr} = 5GMm/v_0$, $v_0/c \simeq 2^{-11}$. The basic proposal [K45] was that ordinary matter condenses around dark matter which is a phase of matter characterized by a non-standard value of Planck constant whose value is gigantic for the space-time sheets mediating gravitational interaction. The interpretation of these space-time sheets could be as magnetic flux quanta or as massless extremals assignable to gravitons.

2. Ordinary particles possibly residing at these space-time sheet have enormous value of Compton length meaning that the density of matter at these space-time sheets must be very slowly varying. The string tension of string like objects implies effective negative pressure characterizing dark energy so that the interpretation in terms of dark energy might make sense [K46]. TGD predicted a one-parameter family of Robertson-Walker cosmologies with critical or over-critical mass density and the "pressure" associated with these cosmologies is negative.

3. The quantization of Planck constant does not make sense unless one modifies the view about standard space-time is. Particles with different Planck constant must belong to different worlds in the sense local interactions of particles with different values of $\hbar$ are not possible. This inspires the idea about the book like structure of the imbedding space obtained by gluing almost copies of H together along common "back" and partially labeled by different values of Planck constant.

4. Darkness is a relative notion in this framework and due to the fact that particles at different pages of the book like structure cannot appear in the same vertex of the generalized Feynman diagram. The phase transitions in which partonic 2-surface X^2 during its travel along X^3_l leaks to another page of book are however possible and change Planck constant. Particle (say photon -) exchanges of this kind allow particles at different pages to interact. The interactions are strongly constrained by charge fractionization and are essentially phase transitions involving many particles. Classical interactions are also possible. It might be that we are actually observing dark matter via classical fields all the time and perhaps have even photographed it [**?**].

5. The realization that non-standard values of Planck constant give rise to charge and spin fractionization and anyonization led to the precise identification of the prerequisites of anyonic phase [K39]. If the partonic 2-surface, which can have even astrophysical size, surrounds the

tip of CD, the matter at the surface is anyonic and particles are confined at this surface. Dark matter could be confined inside this kind of light-like 3-surfaces around which ordinary matter condenses. If the radii of the basic pieces of these nearly spherical anyonic surfaces - glued to a connected structure by flux tubes mediating gravitational interaction - are given by Bohr rules, the findings of Nottale [E5] can be understood. Dark matter would resemble to a high degree matter in black holes replaced in TGD framework by light-like partonic 2-surfaces with a minimum size of order Schwartschild radius r_S of order scaled up Planck length $l_{Pl} = \sqrt{\hbar_{gr} G} = GM$. Black hole entropy is inversely proportional to $\hbar$ and predicted to be of order unity so that dramatic modification of the picture about black holes is implied.

6. Perhaps the most fascinating applications are in biology. The anomalous behavior ionic currents through cell membrane (low dissipation, quantal character, no change when the membrane is replaced with artificial one) has a natural explanation in terms of dark supra currents. This leads to a vision about how dark matter and phase transitions changing the value of Planck constant could relate to the basic functions of cell, functioning of DNA and amino-acids, and to the mysteries of bio-catalysis. This leads also a model for EEG interpreted as a communication and control tool of magnetic body containing dark matter and using biological body as motor instrument and sensory receptor. One especially amazing outcome is the emergence of genetic code of vertebrates from the model of dark nuclei as nuclear strings [L2, **?**], [L2].

The most general option for the generalized imbedding space

Simple physical arguments pose constraints on the choice of the most general form of the imbedding space.

1. The fundamental group of the space for which one constructs a non-singular covering space or factor space should be non-trivial. This is certainly not possible for M^4, CD, CP_2, or H. One can however construct singular covering spaces. The fixing of the quantization axes implies a selection of the sub-space $H_4 = M^2 \times S^2 \subset M^4 \times CP_2$, where S^2 is geodesic sphere of CP_2. $\hat{M}^4 = M^4 \backslash M^2$ and $\hat{CP}_2 = CP_2 \backslash S^2$ have fundamental group Z since the codimension of the excluded sub-manifold is equal to two and homotopically the situation is like that for a punctured plane. The exclusion of these sub-manifolds defined by the choice of quantization axes could naturally give rise to the desired situation.

2. CP_2 allows two geodesic spheres which left invariant by $U(2$ *resp.* $SO(3)$. The first one is homologically non-trivial. For homologically non-trivial geodesic sphere $H_4 = M^2 \times S^2$ represents a straight cosmic string which is non-vacuum extremal of Kähler action (not necessarily preferred extremal). One can argue that the many-valuedness of $\hbar$ is un-acceptable for non-vacuum extremals so that only homologically trivial geodesic sphere S^2 would be acceptable. One could go even further. If the extremals in $M^2 \times CP_2$ can be preferred non-vacuum extremals, the singular coverings of M^4 are not possible. Therefore only the singular coverings and factor spaces of CP_2 over the homologically trivial geodesic sphere S^2 would be possible. This however looks a non-physical outcome.

   (a) The situation changes if the extremals of type $M^2 \times Y^2$, Y^2 a holomorphic surface of CP_3, fail to be hyperquaternionic. The tangent space M^2 represents hypercomplex sub-space and the product of the Kähler-Dirac gamma matrices associated with the tangent spaces of Y^2 should belong to M^2 algebra. This need not be the case in general.

   (b) The situation changes also if one reinterprets the gluing procedure by introducing scaled up coordinates for M^4 so that metric is continuous at $M^2 \times CP_2$ but CDs with different size have different sizes differing by the ratio of Planck constants and would thus have only piece of lower or upper boundary in common.

3. For the more general option one would have four different options corresponding to the Cartesian products of singular coverings and factor spaces. These options can be denoted by $C-C$, $C-F$, $F-C$, and $F-F$, where C (F) signifies for covering (factor space) and first (second) letter signifies for CD (CP_2) and correspond to the spaces $(\hat{CD}\hat{\times}G_a) \times (\hat{CP_2}\hat{\times}G_b)$, $(\hat{CD}\hat{\times}G_a) \times \hat{CP_2}/G_b$, $\hat{CD}/G_a \times (\hat{CP_2}\hat{\times}G_b)$, and $\hat{CD}/G_a \times \hat{CP_2}/G_b$.

4. The groups G_i could correspond to cyclic groups Z_n. One can also consider an extension by replacing M^2 and S^2 with its orbit under more general group G (say tetrahedral, octahedral, or icosahedral group). One expects that the discrete subgroups of $SU(2)$ emerge naturally in this framework if one allows the action of these groups on the singular sub-manifolds M^2 or S^2. This would replace the singular manifold with a set of its rotated copies in the case that the subgroups have genuinely 3-dimensional action (the subgroups which corresponds to exceptional groups in the ADE correspondence). For instance, in the case of M^2 the quantization axes for angular momentum would be replaced by the set of quantization axes going through the vertices of tetrahedron, octahedron, or icosahedron. This would bring non-commutative homotopy groups into the picture in a natural manner.

About the phase transitions changing Planck constant

There are several non-trivial questions related to the details of the gluing procedure and phase transition as motion of partonic 2-surface from one sector of the imbedding space to another one.

1. How the gluing of copies of imbedding space at $M^2 \times CP_2$ takes place? It would seem that the covariant metric of CD factor proportional to $\hbar^2$ must be discontinuous at the singular manifold since only in this manner the idea about different scaling factor of CD metric can make sense. On the other hand, one can always scale the M^4 coordinates so that the metric is continuous but the sizes of CDs with different Planck constants differ by the ratio of the Planck constants.

2. One might worry whether the phase transition changing Planck constant means an instantaneous change of the size of partonic 2-surface in M^4 degrees of freedom. This is not the case. Light-likeness in $M^2 \times S^2$ makes sense only for surfaces $X^1 \times D^2 \subset M^2 \times S^2$, where X^1 is light-like geodesic. The requirement that the partonic 2-surface X^2 moving from one sector of H to another one is light-like at $M^2 \times S^2$ irrespective of the value of Planck constant requires that X^2 has single point of M^2 as M^2 projection. Hence no sudden change of the size X^2 occurs.

3. A natural question is whether the phase transition changing the value of Planck constant can occur purely classically or whether it is analogous to quantum tunnelling. Classical non-vacuum extremals of Chern-Simons action have two-dimensional CP_2 projection to homologically non-trivial geodesic sphere S^2_I. The deformation of the entire S^2_I to homologically trivial geodesic sphere S^2_{II} is not possible so that only combinations of partonic 2-surfaces with vanishing total homology charge (Kähler magnetic charge) can in principle move from sector to another one, and this process involves fusion of these 2-surfaces such that CP_2 projection becomes single homologically trivial 2-surface. A piece of a non-trivial geodesic sphere S^2_I of CP_2 can be deformed to that of S^2_{II} using 2-dimensional homotopy flattening the piece of S^2 to curve. If this homotopy cannot be chosen to be light-like, the phase transitions changing Planck constant take place only via quantum tunnelling. Obviously the notions of light-like homotopies (cobordisms) are very relevant for the understanding of phase transitions changing Planck constant.

How one could fix the spectrum of Planck constants?

The question how the observed Planck constant relates to the integers n_a and n_b defining the covering and factors spaces, is far from trivial and I have considered several options. The basic physical inputs are the condition that scaling of Planck constant must correspond to the scaling of the metric of CD (that is Compton lengths) on one hand and the scaling of the gauge coupling strength $g^2/4\pi\hbar$ on the other hand.

1. One can assign to Planck constant to both CD and CP_2 by assuming that it appears in the commutation relations of corresponding symmetry algebras. Algebraist would argue that Planck constants $\hbar(CD)$ and $\hbar(CP_2)$ must define a homomorphism respecting multiplication and division (when possible) by G_i. This requires $r(X) = \hbar(X)\hbar_0 = n$ for covering and $r(X) = 1/n$ for factor space or vice versa.

2. If one assumes that $\hbar^2(X)$, $X = M^4$, CP_2 corresponds to the scaling of the covariant metric tensor g_{ij} and performs an over-all scaling of H-metric allowed by the Weyl invariance of Kähler action by dividing metric with $\hbar^2(CP_2)$, one obtains the scaling of M^4 covariant metric by $r^2 \equiv \hbar^2/\hbar_0^2 = \hbar^2(M^4)/\hbar^2(CP_2)$ whereas CP_2 metric is not scaled at all.

3. The condition that $\hbar$ scales as n_a is guaranteed if one has $\hbar(CD) = n_a\hbar_0$. This does not fix the dependence of $\hbar(CP_2)$ on n_b and one could have $\hbar(CP_2) = n_b\hbar_0$ or $\hbar(CP_2) = \hbar_0/n_b$. The intuitive picture is that n_b- fold covering gives in good approximation rise to n_an_b sheets and multiplies YM action action by n_an_b which is equivalent with the $\hbar = n_an_b\hbar_0$ if one effectively compresses the covering to $CD \times CP_2$. One would have $\hbar(CP_2) = \hbar_0/n_b$ and $\hbar = n_an_b\hbar_0$. Note that the descriptions using ordinary Planck constant and coverings and scaled Planck constant but contracting the covering would be alternative descriptions.

   This gives the following formulas $r \equiv \hbar/\hbar_0 = r(M^4)/r(CP_2)$ in various cases.

	$C-C$	$F-C$	$C-F$	$F-F$
r	n_an_b	$\frac{n_a}{n_b}$	$\frac{n_b}{n_a}$	$\frac{1}{n_an_b}$

Preferred values of Planck constants

Number theoretic considerations favor the hypothesis that the integers corresponding to Fermat polygons constructible using only ruler and compass and given as products $n_F = 2^k \prod_s F_s$, where $F_s = 2^{2^s} + 1$ are distinct Fermat primes, are favored. The reason would be that quantum phase $q = exp(i\pi/n)$ is in this case expressible using only iterated square root operation by starting from rationals. The known Fermat primes correspond to $s = 0, 1, 2, 3, 4$ so that the hypothesis is very strong and predicts that p-adic length scales have satellite length scales given as multiples of n_F of fundamental p-adic length scale. $n_F = 2^{11}$ corresponds in TGD framework to a fundamental constant expressible as a combination of Kähler coupling strength, CP_2 radius and Planck length appearing in the expression for the tension of cosmic strings, and the powers of 2^{11} was proposed to define favored as values of n_a in living matter [K15].

The hypothesis that Mersenne primes $M_k = 2^k - 1$, $k \in \{89, 107, 127\}$, and Gaussian Mersennes $M_{G,k} = (1+i)k - 1$, $k \in \{113, 151, 157, 163, 167, 239, 241..\}$ (the number theoretical miracle is that all the four scaled up electron Compton lengths $L_e(k) = \sqrt{5}L(k)$ with $k \in \{151, 157, 163, 167\}$ are in the biologically highly interesting range 10 nm-2.5 μm) define scaled up copies of electro-weak and QCD type physics with ordinary value of $\hbar$ and that these physics are induced by dark variants of corresponding lower level physics leads to a prediction for the preferred values of $r = 2^{k_d}$, $k_d = k_i - k_j$, and the resulting picture finds support from the ensuing models for biological evolution and for EEG [K15]. This hypothesis - to be referred to as Mersenne hypothesis - replaces the rather ad hoc proposal $r = \hbar/\hbar_0 = 2^{11k}$ for the preferred values of Planck constant.

How Planck constants are visible in Kähler action?

$\hbar(M^4)$ and $\hbar(CP_2)$ appear in the commutation and anti-commutation relations of various super-conformal algebras. Only the ratio of M^4 and CP_2 Planck constants appears in Kähler action and is due to the fact that the M^4 and CP_2 metrics of the imbedding space sector with given values of Planck constants are proportional to the corresponding Planck. This implies that Kähler function codes for radiative corrections to the classical action, which makes possible to consider the possibility that higher order radiative corrections to functional integral vanish as one might expect at quantum criticality. For a given p-adic length scale space-time sheets with all allowed values of Planck constants are possible. Hence the spectrum of quantum critical fluctuations could in the ideal case correspond to the spectrum of $\hbar$ coding for the scaled up values of Compton lengths and other quantal lengths and times. If so, large $\hbar$ phases could be crucial for understanding of quantum critical superconductors, in particular high T_c superconductors.

9.12.2 Updated View About The Hierarchy Of Planck Constants

The original hypothesis was that the hierarchy of Planck constants is real. In this formulation the imbedding space was replaced with its covering space assumed to decompose to a Cartesian

product of singular finite-sheeted coverings of M^4 and CP_2.

Few years ago came the realization that it could be only effective but have same practical implications. The basic observation was that the effective hierarchy need not be postulated separately but follows as a prediction from the vacuum degeneracy of Kähler action. In this formulation Planck constant at fundamental level has its standard value and its effective values come as its integer multiples so that one should write $\hbar_{eff} = n\hbar$ rather than $\hbar = n\hbar_0$ as I have done. For most practical purposes the states in question would behave as if Planck constant were an integer multiple of the ordinary one. In this formulation the singular covering of the imbedding space became only a convenient auxiliary tool. It is no more necessary to assume that the covering reduces to a Cartesian product of singular coverings of M^4 and CP_2 but for some reason I kept this assumption.

The formulation based on multi-furcations of space-time surfaces to N branches. For some reason I assumed that they are simultaneously present. This is too restrictive an assumption. The N branches are very much analogous to single particle states and second quantization allowing all $0 < n \leq N$-particle states for given N rather than only N-particle states looks very natural. As a matter fact, this interpretation was the original one, and led to the very speculative and fuzzy notion of N-atom, which I later more or less gave up. Quantum multi-furcation could be the root concept implying the effective hierarchy of Planck constants, anyons and fractional charges, and related notions- even the notions of N-nuclei, N-atoms, and N-molecules.

Basic physical ideas

The basic phenomenological rules are simple and there is no need to modify them.

1. The phases with non-standard values of effective Planck constant are identified as dark matter. The motivation comes from the natural assumption that only the particles with the same value of effective Planck can appear in the same vertex. One can illustrate the situation in terms of the book metaphor. Imbedding spaces with different values of Planck constant form a book like structure and matter can be transferred between different pages only through the back of the book where the pages are glued together. One important implication is that light exotic charged particles lighter than weak bosons are possible if they have non-standard value of Planck constant. The standard argument excluding them is based on decay widths of weak bosons and has led to a neglect of large number of particle physics anomalies [K52].

2. Large effective or real value of Planck constant scales up Compton length - or at least de Broglie wave length - and its geometric correlate at space-time level identified as size scale of the space-time sheet assignable to the particle. This could correspond to the Kähler magnetic flux tube for the particle forming consisting of two flux tubes at parallel space-time sheets and short flux tubes at ends with length of order CP_2 size.

   This rule has far reaching implications in quantum biology and neuroscience since macroscopic quantum phases become possible as the basic criterion stating that macroscopic quantum phase becomes possible if the density of particles is so high that particles as Compton length sized objects overlap. Dark matter therefore forms macroscopic quantum phases. One implication is the explanation of mysterious looking quantal effects of ELF radiation in EEG frequency range on vertebrate brain: $E = hf$ implies that the energies for the ordinary value of Planck constant are much below the thermal threshold but large value of Planck constant changes the situation. Also the phase transitions modifying the value of Planck constant and changing the lengths of flux tubes (by quantum classical correspondence) are crucial as also reconnections of the flux tubes.

   The hierarchy of Planck constants suggests also a new interpretation for FQHE (see `http://tinyurl.com/y89xp4bu`) (fractional quantum Hall effect) [K39] in terms of anyonic phases with non-standard value of effective Planck constant realized in terms of the effective multi-sheeted covering of imbedding space: multi-sheeted space-time is to be distinguished from many-sheeted space-time.

3. In astrophysics and cosmology the implications are even more dramatic if one believes that also $\hbar_{gr}$ corresponds to effective Planck constant interpreted as number of sheets of multi-furcation. It was Nottale (see `http://tinyurl.com/ya6f3s4l` [E5] who first introduced

the notion of gravitational Planck constant as $\hbar_{gr} = GMm/v_0$, $v_0 < 1$ has interpretation as velocity light parameter in units $c = 1$. This would be true for $GMm/v_0 \geq 1$. The interpretation of $\hbar_{gr}$ in TGD framework is as an effective Planck constant associated with space-time sheets mediating gravitational interaction between masses M and m. The huge value of $\hbar_{gr}$ means that the integer $\hbar_{gr}/\hbar_0$ interpreted as the number of sheets of covering is gigantic and that Universe possesses gravitational quantum coherence in super-astronomical scales for masses which are large. This would suggest that gravitational radiation is emitted as dark gravitons which decay to pulses of ordinary gravitons replacing continuous flow of gravitational radiation.

It must be however emphasized that the interpretation of $\hbar_{gr}$ could be different, and it will be found that one can develop an argument demonstrating how $\hbar_{gr}$ with a correct order of magnitude emerges from the effective space-time metric defined by the anti-commutators appearing in the Kähler-Dirac equation. Why Nature would like to have large effective value of Planck constant? A possible answer relies on the observation that in perturbation theory the expansion takes in powers of gauge couplings strengths $\alpha = g^2/4\pi\hbar$. If the effective value of $\hbar$ replaces its real value as one might expect to happen for multi-sheeted particles behaving like single particle, α is scaled down and perturbative expansion converges for the new particles. One could say that Mother Nature loves theoreticians and comes in rescue in their attempts to calculate. In quantum gravitation the problem is especially acute since the dimensionless parameter $GMm/\hbar$ has gigantic value. Replacing $\hbar$ with $\hbar_{gr} = GMm/v_0$ the coupling strength becomes $v_0 < 1$.

Space-time correlates for the hierarchy of Planck constants

The hierarchy of Planck constants was introduced to TGD originally as an additional postulate and formulated as the existence of a hierarchy of imbedding spaces defined as Cartesian products of singular coverings of M^4 and CP_2 with numbers of sheets given by integers n_a and n_b and $\hbar = n\hbar_0$. $n = n_a n_b$.

With the advent of zero energy ontology, it became clear that the notion of singular covering space of the imbedding space could be only a convenient auxiliary notion. Singular means that the sheets fuse together at the boundary of multi-sheeted region. The effective covering space emerges naturally from the vacuum degeneracy of Kähler action meaning that all deformations of canonically imbedded M^4 in $M^4 \times CP_2$ have vanishing action up to fourth order in small perturbation. This is clear from the fact that the induced Kähler form is quadratic in the gradients of CP_2 coordinates and Kähler action is essentially Maxwell action for the induced Kähler form. The vacuum degeneracy implies that the correspondence between canonical momentum currents $\partial L_K/\partial(\partial_\alpha h^k)$ defining the Kähler-Dirac gamma matrices [K58] and gradients $\partial_\alpha h^k$ is not one-to-one. Same canonical momentum current corresponds to several values of gradients of imbedding space coordinates. At the partonic 2-surfaces at the light-like boundaries of CD carrying the elementary particle quantum numbers this implies that the two normal derivatives of h^k are many-valued functions of canonical momentum currents in normal directions.

Multi-furcation is in question and multi-furcations are indeed generic in highly non-linear systems and Kähler action is an extreme example about non-linear system. What multi-furcation means in quantum theory? The branches of multi-furcation are obviously analogous to single particle states. In quantum theory second quantization means that one constructs not only single particle states but also the many particle states formed from them. At space-time level single particle states would correspond to N branches b_i of multi-furcation carrying fermion number. Two-particle states would correspond to 2-fold covering consisting of 2 branches b_i and b_j of multi-furcation. $N-$particle state would correspond to N-sheeted covering with all branches present and carrying elementary particle quantum numbers. The branches co-incide at the partonic 2-surface but since their normal space data are different they correspond to different tensor product factors of state space. Also now the factorization $N = n_a n_b$ occurs but now n_a and n_b would relate to branching in the direction of space-like 3-surface and light-like 3-surface rather than M^4 and CP_2 as in the original hypothesis.

In light of this the working hypothesis adopted during last years has been too limited: for some reason I ended up to propose that only N-sheeted covering corresponding to a situation in which all N branches are present is possible. Before that I quite correctly considered more general

option based on intuition that one has many-particle states in the multi-sheeted space. The erratic form of the working hypothesis has not been used in applications.

Multi-furcations relate closely to the quantum criticality of Kähler action. Feigenbaum bifurcations (see http://tinyurl.com/2swb2p) represent a toy example of a system which via successive bifurcations approaches chaos. Now more general multi-furcations in which each branch of given multi-furcation can multi-furcate further, are possible unless on poses any additional conditions. This allows to identify additional aspect of the geometric arrow of time. Either the positive or negative energy part of the zero energy state is "prepared" meaning that single n-sub-furcations of N-furcation is selected. The most general state of this kind involves superposition of various n-sub-furcations.

Basic phenomenological rules of thumb in the new framework

It is important to check whether or not the refreshed view about dark matter is consistent with existent rules of thumb.

1. The interpretation of quantized multi-furcations as WCW anyons explains also why the effective hierarchy of Planck constants defines a hierarchy of phases which are dark relative to each other. This is trivially true since the phases with different number of branches in multi-furcation correspond to disjoint regions of WCW so that the particles with different effective value of Planck constant cannot appear in the same vertex.

2. The phase transitions changing the value of Planck constant are just the multi-furcations and can be induced by changing the values of the external parameters controlling the properties of preferred extremals. Situation is very much the same as in any non-linear system.

3. In the case of massless particles the scaling of wavelength in the effective scaling of $\hbar$ can be understood if dark n-photons consist of n photons with energy E/n and wavelength $n\lambda$.

4. For massive particle it has been assumed that masses for particles and they dark counterparts are same and Compton wavelength is scaled up. In the new picture this need not be true. Rather, it would seem that wave length are same as for ordinary electron.

   On the other hand, p-adic thermodynamics predicts that massive elemenetary particles are massless most of the time. ZEO predicts that even virtual wormhole throats are massless. Could this mean that the picture applying on massless particle should apply to them at least at relativistic limit at which mass is negligible. This might be the case for bosons but for fermions also fermion number should be fractionalized and this is not possible in the recent picture. If one assumes that the n-electron has same mass as electron, the mass for dark single electron state would be scaled down by $1/n$. This does not look sensible unless the p-adic length defined by prime is scaled down by this fact in good approximation.

   This suggests that for fermions the basic scaling rule does not hold true for Compton length $\lambda_c = \hbar_m$. Could it however hold for de-Broglie lengths $\lambda = \hbar/p$ defined in terms of 3-momentum? The basic overlap rule for the formation of macroscopic quantum states is indeed formulated for de Broglie wave length. One could argue that an $1/N$-fold reduction of density that takes place in the de-localization of the single particle states to the N branches of the cover, implies that the volume per particle increases by a factor N and single particle wave function is de-localized in a larger region of 3-space. If the particles reside at effectively one-dimensional 3-surfaces - say magnetic flux tubes - this would increase their de Broglie wave length in the direction of the flux tube and also the length of the flux tube. This seems to be enough for various applications.

One important notion in TGD inspired quantum biology is dark cyclotron state.

1. The scaling $\hbar \to k\hbar$ in the formula $E_n = (n+1/2)\hbar eB/m$ implies that cyclotron energies are scaled up for dark cyclotron states. What this means microscopically has not been obvious but the recent picture gives a rather clearcut answer. One would have k-particle state formed from cyclotron states in N-fold branched cover of space-time surface. Each branch would carry magnetic field B and ion or electron. This would give a total cyclotron energy equal

to kE_n. These cyclotron states would be excited by k-photons with total energy $E = khf$ and for large enough value of k the energies involved would be above thermal threshold. In the case of Ca^{++} one has $f = 15$ Hz in the field $B_{end} = .2$ Gauss. This means that the value of $\hbar$ is at least the ratio of thermal energy at room temperature to $E = hf$. The thermal frequency is of order 10^{12} Hz so that one would have $k \simeq 10^{11}$. The number branches would be therefore rather high.

2. It seems that this kinds of states which I have called cyclotron Bose-Einstein condensates could make sense also for fermions. The dark photons involved would be Bose-Einstein condensates of k photons and wall of them would be simultaneously absorbed. The biological meaning of this would be that a simultaneous excitation of large number of atoms or molecules can take place if they are localized at the branches of N-furcation. This would make possible coherent macroscopic changes. Note that also Cooper pairs of electrons could be $n = 2$-particle states associated with N-furcation.

There are experimental findings suggesting that photosynthesis involves de-localized excitations of electrons and it is interesting so see whether this could be understood in this framework.

1. The TGD based model relies on the assumption that cyclotron states are involved and that dark photons with the energy of visible photons but with much longer wavelength are involved. Single electron excitations (or single particle excitations of Cooper pairs) would generate negentropic entanglement automatically.

2. If cyclotron excitations are the primary ones, it would seem that they could be induced by dark n-photons exciting all n electrons simultaneously. n-photon should have energy of a visible photon. The number of cyclotron excited electrons should be rather large if the total excitation energy is to be above thermal threshold. In this case one could not speak about cyclotron excitation however. This would require that solar photons are transformed to n-photons in N-furcation in biosphere.

3. Second - more realistic looking - possibility is that the incoming photons have energy of visible photon and are therefore $n = 1$ dark photons de-localized to the branches of the N-furcation. They would induce de-localized single electron excitation in WCW rather than 3-space.

Charge fractionalization and anyons

It is easy to see how the effective value of Planck constant as an integer multiple of its standard value emerges for multi-sheeted states in second quantization. At the level of Kähler action one can assume that in the first approximation the value of Kähler action for each branch is same so that the total Kähler action is multiplied by n. This corresponds effectively to the scaling $\alpha_K \to \alpha_K/n$ induced by the scaling $\hbar_0 \to n\hbar_0$.

Also effective charge fractionalization and anyons emerge naturally in this framework.

1. In the ordinary charge fractionalization (see `http://tinyurl.com/26tmhoe`) the wave function decomposes into sharply localized pieces around different points of 3-space carrying fractional charges summing up to integer charge. Now the same happens at at the level of WCW ("world of classical worlds") rather than 3-space meaning that wave functions in E^3 are replaced with wave functions in the space-time of 3-surfaces (4-surfaces by holography implied by General Coordinate Invariance) replacing point-like particles. Single particle wave function in WCW is a sum of N sharply localized contributions: localization takes place around one particular branch of the multi-sheeted space time surface. Each branch carries a fractional charge q/N for teh analogs of plane waves.

   Therefore all quantum numbers are additive and fractionalization is only effective and observable in a localization of wave function to single branch occurring with probability $p = 1/N$ from which one can deduce that charge is q/N.

2. The is consistent with the proposed interpretation of dark photons/gravitons since they could carry large spin and this kind of situation could decay to bunches of ordinary photons/gravitons. It is also consistent with electromagnetic charge fractionalization and fractionalization of spin.

3. The original - and it seems wrong - argument suggested what might be interpreted as a genuine fractionalization for orbital angular momentum and also of color quantum numbers, which are analogous to orbital angular momentum in TGD framework. The observation was that a rotation through 2π at space-time level moving the point along space-time surface leads to a new branch of multi-furcation and $N+1$: th branch corresponds to the original one. This suggests that angular momentum fractionalization should take place for M^4 angle coordinate ϕ because for it 2π rotation could lead to a different sheet of the effective covering.

   The orbital angular momentum eigenstates would correspond to waves $exp(i\phi m/N)$, $m = 0, 2, ..., N-1$ and the maximum orbital angular momentum would correspond the sum $\sum_{m=0}^{N-1} m/N = (N-1)/2$. The sum of spin and orbital angular momentum be therefore fractional.

   The different prediction is due to the fact that rotations are now interpreted as flows rotating the points of 3-surface along 3-surface rather than rotations of the entire partonic surface in imbedding space. In the latter interpretation the rotation by 2π does nothing for the 3-surface. Hence fractionalization for the total charge of the single particle states does not take place unless one adopts the flow interpretation. This view about fractionalization however leads to problems with fractionalization of electromagnetic charge and spin for which there is evidence from fractional quantum Hall effect.

What about the relationship of gravitational Planck constant to ordinary Planck constant?

Gravitational Planck constant is given by the expression $\hbar_{gr} = GMm/v_0$, where $v_0 < 1$ has interpretation as velocity parameter in the units $c = 1$. Can one interpret also $\hbar_{gr}$ as effective value of Planck constant so that its values would correspond to multi-furcation with a gigantic number of sheets. This does not look reasonable.

Could one imagine any other interpretation for $\hbar_{gr}$? Could the two Planck constants correspond to inertial and gravitational dichotomy for four-momenta making sense also for angular momentum identified as a four-vector? Could gravitational angular momentum and the momentum associated with the flux tubes mediating gravitational interaction be quantized in units of $\hbar_{gr}$ naturally?

1. Gravitational four-momentum can be defined as a projection of the M^4-four-momentum to space-time surface. It's length can be naturally defined by the effective metric $g_{eff}^{\alpha\beta}$ defined by the anti-commutators of the modified gamma matrices. Gravitational four-momentum appears as a measurement interaction term in the Kähler-Dirac action and can be restricted to the space-like boundaries of the space-time surface at the ends of CD and to the light-like orbits of the wormhole throats and which induced 4- metric is effectively 3-dimensional.

2. At the string world sheets and partonic 2-surfaces the effective metric degenerates to 2-D one. At the ends of braid strands representing their intersection, the metric is effectively 4-D. Just for definiteness assume that the effective metric is proportional to the M^4 metric or rather - to its M^2 projection: $g_{eff}^{kl} = K^2 m^{kl}$.

   One can express the length squared for momentum at the flux tubes mediating the gravitational interaction between massive objects with masses M and m as

$$g_{eff}^{\alpha\beta} p_\alpha p_\beta = g_{eff}^{\alpha\beta} \partial_\alpha h^k \partial_\beta h^l p_k p_l \equiv g_{eff}^{kl} p_k p_l = n^2 \frac{\hbar^2}{L^2} \quad . \tag{9.12.1}$$

   Here L would correspond to the length of the flux tube mediating gravitational interaction and p_k would be the momentum flowing in that flux tube. $g_{eff}^{kl} = K^2 m^{kl}$ would give

$$p^2 = \frac{n^2\hbar^2}{K^2L^2} \quad .$$

$\hbar_{gr}$ could be identifed in this simplified situation as $\hbar_{gr} = \hbar/K$.

3. Nottale's proposal requires $K = GMm/v_0$ for the space-time sheets mediating gravitational interacting between massive objects with masses M and m. This gives the estimate

$$p_{gr} = \frac{GMm}{v_0}\frac{1}{L} \quad . \tag{9.12.2}$$

For $v_0 = 1$ this is of the same order of magnitude as the exchanged momentum if gravitational potential gives estimate for its magnitude. v_0 is of same order of magnitude as the rotation velocity of planet around Sun so that the reduction of v_0 to $v_0 \simeq 2^{-11}$ in the case of inner planets does not mean that the propagation velocity of gravitons is reduced.

4. Nottale's formula requires that the order of magnitude for the components of the energy momentum tensor at the ends of braid strands at partonic 2-surface should have value GMm/v_0. Einstein's equations $T = \kappa G + \Lambda g$ give a further constraint. For the vacuum solutions of Einstein's equations with a vanishing cosmological constant the value of h_{gr} approaches infinity. At the flux tubes mediating gravitational interaction one expects T to be proportional to the factor GMm simply because they mediate the gravitational interaction.

5. One can consider similar equation for gravitational angular momentum:

$$g^{\alpha\beta}_{eff}L_\alpha L_\beta = g^{kl}_{eff}L_kL_l = l(l+1)\hbar^2 \quad . \tag{9.12.3}$$

This would give under the same simplifying assumptions

$$L^2 = l(l+1)\frac{\hbar^2}{K^2} \quad . \tag{9.12.4}$$

This would justify the Bohr quantization rule for the angular momentum used in the Bohr quantization of planetary orbits.

Maybe the proposed connection might make sense in some more refined formulation. In particular the proportionality between $m^{kl}_{eff} = Km^{kl}$ could make sense as a quantum average. Also the fact, that the constant v_0 varies, could be understood from the dynamical character of m^{kl}_{eff}.

Could $h_{gr} = h_{eff}$ hold true?

The obvious question is whether the gravitational Planck constant deduced from the Nottale's considerations and the effective Planck constant $h_{eff} = nh$ deduced from ELF effects on vertebrate brain and explained in terms of non-determinism of Kähler action could be identical. At first this seems to be non-sensical idea since $\hbar_{gr} = GMm/v_0$ has gigantic value.

It is however essential to realize that by Equivalence Principle one describe gravitational interaction by reducing it to elementary particle level. For instance, gravitational Compton lengths do not depend at all on the masses of particles. Also the radii of the planetary orbits are independent of the mass of particle mass in accordance with Equivalence Principle. For elementary particles the values of h_{gr} are in the same range as in quantum biological applications. Typically 10 Hz ELF radiation should correspond to energy $E = h_{eff}f$ of UV photon if one assumes that

dark ELF photons have energies of biophotons and transform to them. The order of magnitude for n would be therefore $n \simeq 10^{14}$.

The experiments of M. Tajmar et al [E7, E11] discussed in [K72] provide a support for this picture. The value of gravimagnetic field needed to explain the findings is 28 orders of magnitude higher than theoretical value if one extrapolates the model of Meissner effect to gravimagnetic context. The amazing finding is that if one replaces Planck constant in the formula of gravimagnetic field with h_{gr} associated with Earth-Cooper pair system and assumes that the velocity parameter v_0 appearing in it corresponds to the Earth's rotation velocity around its axis, one obtains correct order of magnitude for the effect requiring $r \simeq 3.6 \times 10^{14}$.

The most important implications are in quantum biology and Penrose's vision about importance of quantum gravitation in biology might be correct.

1. This result allows by Equivalence Principle the identification $h_{gr} = h_{eff}$ at elementary particle level at least so that the two views about hierarchy of Planck constants would be equivalent. If the identification holds true for larger units it requires that space-time sheet identifiable as quantum correlates for physical systems are macroscopically quantum coherent and gravitation causes this. If the values of Planck constant are really additive, the number of parallel space-time sheets corresponding to non-determinism evolution for the flux tube connecting systems with masses M and m is proportional to the masses M and m using Planck mass as unit. Information theoretic interpretation is suggestive since hierarchy of Planck constants is assumed to relate to negentropic entanglement very closely in turn providing physical correlate for the notions of rule and concept.

2. That gravity would be fundamental for macroscopic quantum coherence would not be surprising since by EP all particles experience same acceleration in constant gravitational field, which therefore has tendency to create coherence unlike other basic interactions. This in principle allows to consider hierarchy in which the integers $h_{gr,i}$ are additive but give rise to the same universal dark Compton length.

3. The model for quantum biology relying on the notions of magnetic body and dark matter as hierarchy of phases with $h_{eff} = n \times h$, and biophotons [K66, K65] identified as decay produces of dark photons. The assumption $h_{gr} \propto m$ becomes highly predictable since cyclotron frequencies would be independent of the mass of the ion.

   (a) If dark photons with cyclotron frequencies decay to biophotons, one can conclude that biophoton spectrum reflects the spectrum of endogenous magnetic field strengths. In the model of EEG [K15] it has been indeed assumed that this kind spectrum is there: the inspiration came from music metaphors suggesting that musical scales are realized in terms of values of magnetic field strength. The new quantum physics associated with gravitation would also become key part of quantum biophysics in TGD Universe.

   (b) For the proposed value of h_{gr} 1 Hz cyclotron frequency associated to DNA sequences would correspond to ordinary photon frequency $f = 3.6 \times 10^{14}$ Hz and energy 1.2 eV just at the lower limit of visible frequencies. For 10 Hz alpha band the energy would be 12 eV in UV. This plus the fact that molecular energies are in eV range suggests very simple realization of biochemical control by magnetic body. Each ion has its own cyclotron frequency but same energy for the corresponding biophoton.

   (c) Biophoton with a given energy would activate transitions in specific bio-molecules or atoms: ionization energies for atoms except hydrogen have lower bound about 5 eV (`http://tinyurl.com/233vcad`). The energies of molecular bonds are in the range 2-10 eV (`http://tinyurl.com/bfsy4ft`). If one replaces v_0 with $2v_0$ in the estimate, DNA corresponds to.62 eV photon with energy of order metabolic energy currency and alpha band corresponds to 6 eV energy in the molecular region and also in the region of ionization energies.

   Each ion at its specific magnetic flux tubes with characteristic palette of magnetic field strengths would resonantly excite some set of biomolecules.This conforms with the earlier vision about dark photon frequencies as passwords.

   It could be also that biologically important ions take care of their ionization self. This would be achieved if the magnetic field strength associated with their flux tubes is such

that dark cyclotron energy equals to ionization energy. EEG bands labelled by magnetic field strengths could reflect ionization energies for these ions.

(d) The hypothesis means that the scale of energy spectrum of biophotons depends on the ratio M/v_0 of the planet and on the strength of the endogenous magnetic field, which is.2 Gauss for Earth (2/5 of the nominal value of the Earth's magnetic field). Therefore the astrophysical characteristics of planets should be tuned for molecular life. Taking v_0 to be rotational velocity one obtains for the ratio $M(planet)/v_0(planet)$ using the ratio for Earth as unit the following numbers for the planets (Mercury, Venus, Earth, Mars, Jupiter, Saturnus, Uranus, Neptune): $M/v_0 = (8.5, 209, 1, .214223, 1613, 6149, 9359)$. If the energy scale of biophotons is required to be the same, the scale of endogenous magnetic field should be divided by this ratio in order to obtain the same situation as in Earth. For instance, in Mars the magnetic field should be roughly 5 times stronger: in reality the magnetic field of Mars is much weaker. Just for fun one can notice that for Sun the ratio is 1.4×10^6 so that magnetic field should be by the inverse of this factor weaker.

4. An interesting question is how large systems can behave as coherent units with $\hbar_{gr} = GMm/v_0$. In living matter one might consider the possibility that entire organism might be this kind of system. Interestingly, for larger masses the gravitational quantum coherence would be easier. For particle with mass m $h_{gr}/h > 1$ requires larger mass to satisfy $M > M_P^2/m_e$. The first guess that life has evolved from long to shorter scales and reached elementary particle last. Planck mass is the critical mass corresponds to the mass of water blog with volume of size scale of 10^{-4} m (big neuron) is the limit.

5. The Universal gravitational Compton wave length of $GM/v_0 \simeq 864$ meters gives an idea about largest possible living matter system if Earth is the second body. Of course, also other large bodies are possible.In the case of solar system this length is 3×10^3 km. The radius of Earth is 6.37×10^3 km - roughly twice the Compton length. The radii of Mercury, Venus, Earth, Mars, Jupiter, Saturnus, Uranus, Neptunus are (.38, .99, .533, 1, 10.6, 8.6, 4.0, 3.9) using Earth radius as unit the value of h_{gr} is by factor 5 larger than for three inner planets so that the values are reasonably near to gravitational Compton length or twice it. Does this mean that dark matter associated with Earth and maybe also other planets is in macroscopic quantum state at some level of the hierarchy of space-time sheets? Does this mean that Mother Gaia as conscious entity might make sense. One can of course make same question in the case of Sun. The universal gravitational Compton length in Sun would be 18 per cent of the radius of Sun if v_0 is taken to be the rotational velocity at the surface of Sun. The radius of solar core, where fusion takes place, is 20-25 per cent of solar radius.

6. There are further interesting numerical co-incidences. One can for a moment forget the standard hostility of scientist towards horoscopes and ask whether Sun and Moon could have somehow affect our life via astrocopic quantum coherence. The gravitational Compton length for particle-Moon or particle-Sun system multiplied by the natural value of magnetic field is the relevant parameter. For Sun the parameters in question are mass of Sun, and rotational velocity of Earth with respect to Sun, plus magnetic fields of Sun at flux tubes associated with solar magnetic field measured to be about 5 nT at the position of Earth and 100 times stronger than expected from dipole field behavior. This gives that the range of biophoton energies is scaled down with factor of 1/4 in good approximation so that Father Sun might affect terrestrial biology! If one uses for the rotational velocity of particle at surface of Moon as parameter v_0 (particle would be at Moon), biophoton energy scaled scaled up by factor 1.2.

The general proposal discussed above is testable. In particular, a detailed study of molecular energies with those associated with resonances of EEG could be highly rewarding and reveal the speculated spectroscopy of consciousness.

Summary

The hierarchy of Planck constants reduces to second quantization of multi-furcations in TGD framework and the hierarchy is only effective. Anyonic physics and effective charge fractionalization

are consequences of second quantized multi-furcations. This framework also provides quantum version for the transition to chaos via quantum multi-furcations and living matter represents the basic application. The key element of dynamics of TGD is vacuum degeneracy of Kähler action making possible quantum criticality having the hierarchy of multi-furcations as basic aspect. The potential problems relate to the question whether the effective scaling of Planck constant involves scaling of ordinary wavelength or not. For particles confined inside linear structures such as magnetic flux tubes this seems to be the case.

There is also an intriguing connection with the vision about physics as generalized number theory. The conjecture that the preferred extremals of Kähler action consist of quaternionic or co-quaternionic regions led to a construction of them using iteration and also led to the hierarchy of multi-furcations [K58]. Therefore it seems that the dynamics of preferred extremals might indeed reduce to associativity/co-associativity condition at space-time level, to commutativity/co-commutativity condition at the level of string world sheets and partonic 2-surfaces, and to reality at the level of stringy curves (conformal invariance makes [**?**] so that conformal dynamics represents conformal evolution) [**?**].

Chapter 10

Homonymy of the genetic code from TGD point of view

10.1 Introduction

This article was motivated by the article of Peter Gariaev [**?**] about the linguistic notions of synonymy and homonymy applied to genetic code (for other works of Gariaev and collaborators on the linguistic aspects of DNA see [**?**, I102]). In another article by Peter Gariaev and Ekaterina Leonova-Gariaeva to be published in Open Journal of Genetics the notion of syhomy fusing these concepts is introduced. Homonymy is visible in mRNa-tRNA pairing and induced by the 1-to-many pairing of the third mRNA nucleotide with tRNA nucleotide. The homonymy in mRNA-AA (AA for amino-acid) pairing is also present albeit rare and might be explainable in terms of context dependence of this pairing.

The article summarizes much what is known about the theoretically poorly understood role of the third nucleotide of mRNA in the translation of mRNA to AAs. That many tRNAs correspond to same mRNA - synonymy - is not surprising since the number of tRNAs is smaller than that of mRNAs. There is however also homonymy present - the third nucleotide of mRNA can correspond to several tRNAs. If the AAs associated with homonymous tRNAs are same, the is no homonymy in mRNA-AA pairing. This is not quite always the case but the deviations are surprisingly small.

The article emphasizes the fact that the codons for the standard code can be divided to two classes. For 32 codons the first two letters fix AA completely. For the remaining 32 codons there is almost unbroken symmetry in that U and C *resp.* A and G code for the same AA. This symmetry is broken only for the the three 4-columns of the code table containing Stop codon or Start codon coding also for met: this symmetry breaking is unavoidable given that the number of both start and Stop codons is odd. This symmetry breaking is minimal and applies only to A-G whereas T-C symmetry is exact. For the deviations of the code from the standard code the deviation as a rule breaks A-G or T-C symmetry or re-establishes it.

The notion of homonymy is extremely interesting from TGD point of view. TGD leads to two basic proposals predicting the numbers of DNA codons coding for given AA rather successfully.

1. The first proposal [L21] relies on TGD view about dark matter as $h_{eff}/h = n$ phases of ordinary matter [K18, K75, K76] [L34, L35] motivated by adelic physics extending physics to include also the correlates of cognition [L34] [L35]. The empirical motivation comes from several sources, in particular from the findings of Pollack [L15] discussed in [L15]. One can understand the formation of negatively charged regions - exclusion zones (EZs) - as being due to the transformation of part of protons to dark protons residing at magnetic flux tubes.

   Dark genetic code would be realized in ters of dark proton sequences - to be denoted by DDNA, DmRNA, DtRNA, and DAA - would provide dark analogs of DNA, mRNA, tRNA, and AA. Biochemistry would emerge as a shadow of the much simpler dynamics of dark matter at flux tubes and genetic code would be induced by dark code code. The dark code would be sequence DDNA $\rightarrow$ DmRNA $\rightarrow$ DtRNA$\rightarrow$ DAA of many-to-1 maps free of

homonymies.

2. Second model of genetic code emerged accidentally from a geometric model of music harmony [L12] (see `http://tinyurl.com/yad4tqwl`) involving icosahedral (12 vertices-12-note scale and 20 faces-number of AAs) and tetrahedral geometries leading to the proposal that DNA codons and possibly also AAs correspond to 3-chords defining the harmony and obtained as unions of 20+20+20 3-chords associated with icosahedral 20-chord harmonies with symmetries Z_6, Z_4, Z_2 plus tetrahedral 4-chord harmony. There is large number of these harmonies bringing in additional degrees of freedom.

   Remark: This model has obviously analogies with the notion of wave genome introduced by Peter Gariaev [I82, I83, I105].

   Since music both expresses and creates emotions the proposal is that these harmonies assigning additional hidden degrees of freedom to the magnetic bodies of DDNA, DRNA, etc... serve as correlates of emotions also at the molecular level. This emotional context could also give rise to context dependence of the code if several harmonies are realizable chemically. Taking seriously TGD inspired theory of consciousness [L36] and model of emotions [L43] (see `http://tinyurl.com/ydhxen4g`), one might say that the details of the code might depend slightly on the "emotional" state of DNA, RNA, and possibly other molecules.

In the sequel I will consider the following proposal for the various pairings of dark DNA and ordinary DNA visualizable as a 2×4-matrix with two rows representing DDNA, DmRNA, DtRNA, DAA *resp.* DNA, mRNA, tRNA, AA.

1. The proposal is that genetic code at dark level extends to a sequence DDNA $\rightarrow$ DmRNA $\rightarrow$ DtRNA $\rightarrow$ DAA of horizontal pairings analogous to projections is the fundamental one, and realized via dark photon triplet resonance expect for the coupling to DAA for which coupling is based on the sum $f_{XYZ} = f_1 + f_2 + f_3$ of 3-chord frequencies. One might perhaps say that AA sequence defines melody and mRNA sequence the accompaniment. The frequencies f_{XYZ} for codons coding same AA would be same modulo octave multiple. There is context dependence and homonymies already in DmRNA-DtRNA pairing and due the fact that DtRNA corresponds to a 2-harmony as sub-harmony of 3-harmony and can be chosen in 3 different manners. Also this choice - perhaps by state function reduction - could correlate with emotional state.

2. There are also vertical mappings DDNA $\rightarrow$ DNA, DmRNA $\rightarrow$ mRNA, DtRNA $\rightarrow$ tRNA and DAA $\rightarrow$ AA. These pairings would induce the horizontal pairings DNA $\rightarrow$ mRNA $\rightarrow$ tRNA $\rightarrow$ AA at the chemical level. The homonymy at mRNA-tRNA level would have no effects on DNA-AA pairing.

3. Apart from mRNA-AA pairing all these pairings would be realized dynamically in terms of 3-chords (f_1, f_2, f_3) and giving rise to a resonant coupling between members of the pair connected by magnetic flux tubes to single dynamical unit carrying the dark photon triplets at the frequencies characterized by the 3-chord. The model for musical harmony [L12] leading also to a realization of genetic code suggests the existence of a large number of harmonies.

   It is not however obvious whether these harmonies can be realized bio-chemically since the 3-chords must be resonance 3-chords for bio-molecules. For DNA-AA and mRNA-AA correspondence the constraints are the slightest ones since they couple to $f_{XYZ} = f_1 + f_2 + f_3$: AAs could have emerged in rather early stages of the prebiotic evolution. One cannot even exclude the possibility f_{XYZ} are same for different harmonies. Slight chemical modifications of DNA and mRNA and AA analogous to wobbling for tRNA might allow to realize the slightly different collections of 3-chords defining the harmonies.

4. The model leads to an explanation for the homonymy of mRNA $\rightarrow$ tRNA pairing as being induced by the mRNA-tRNA homonymy realized already at dark level. The rather rare homonymies in DNA-AA pairing can be understood as accidental degeneracies. AA couples resonantly to the sum $f_{XYZ} = f_1 + f_2 + f_3$ of frequencies associated with codon XYZ, and one can have $f_{X_1Y_1Z_1} = f_{X_2Y_2Z_2}$ modulo octave multiple for two codons. DAA coded by DDNA codes for AA and tRNA serves only in the role of transferring DAA-AA pairs and attaching

them to DmRNA-mRNA pairs: the mRNA-AA pairing would be determined completely by dark molecules. It is actually advantageous to have tRNA homonymy since it can happen that the concentration of particular certain kind of tRNA is low.

5. What distinguishes between DNA and RNA and between codons and anti-codons is not obvious in the harmonic model. The most plausible identification for the map mapping codons to anti-codons is reflection symmetry of the icosahedron permuting opposite faces. An internal reflection changing the orientation of the scale could map DNA to RNA: this makes sense if the chords can be regarded as arpeggios.

6. The vision of biological evolution as chemical evolution in which dark variants of genetic code gradually find biological representations suggests a concrete model for RNA era. At that era AAs would have catalyzed mRNA replication possibly as non-faithful process. This era might have preceded tRNA era with mRNA replaced with tRNA analog corresponding to to the fusion of two 20-chord representations. The era before this could have been era with single 20-chord representation and corresponding tRNAs and amino-acids.

10.2 Some background

In the following I will discuss briefly the basic facts about genetic code at Wikipedia level with emphasis on the poorly understood aspects of the code.

10.2.1 Variations of the genetic code

There exists also as many as 31 genetic codes (see `http://tinyurl.com/ydeeyhjl`) and an interesting question is whether this relates to the context dependence. Mitochondrial codes differs from the nuclear code and there are several of them. The codes for viruses, prokaryotes, mitochondria and chloroplasts deviate from the standard code. As a rule, the non-standard codes break U-C or A-G symmetries for the third code letter. Some examples are in order (see `http://tinyurl.com/puw82x8`).

1. UUU can code Leu instead of Phe and CUG can code Ser rather than Leu. In bacteria the GUG and UUG coding for Val and Leu normally can serve as Start codons.

2. UGA can code to Trp rather than Stop: in this case the broken symmetry is restored since also UGG codes for Trp.

3. There is variation even in human mitochondrial code (see `http://tinyurl.com/puw82x8`). In 2016, researchers studying the translation of malate dehydrogenase found that in about 4 per cent of the mRNAs encoding this enzyme the UAG Stop codon is naturally used to encode the AAs Trp and Arg. This phenomenon is known as Stop codon readthrough (see `https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5133446/`).

4. There is also a variant of genetic code in which there are 21st and 22nd AAs Sec and Pyl coded by Stop codons. UGA can code for Sec and Stop in the same organism. UAG can code for Pyl instead of Stop and introduces additional breaking of A-G symmetry for the third letter (UAA to Stop and UAG to Pyl).

10.2.2 Wobble base pairing

Wobble base pairing (see `http://tinyurl.com/y73se8vs`) emerges from the observation that the number of tRNAs pairing with mRNAs is smaller than 45 and considerably smaller than that of mRNAs. The needed minimum number of tRNAs is 32. Therefore the RNA-tRNA pairing cannot be 1-1 and some mRNA codons must correspond to several tRNA codons.

Remark: One could ask whether mRNAs code for tRNAs just like DNAs code for AAs. Homonymy for mRNA-tRNA pairing implies that the pairing can be many-to-1 only in given context.

1. According to the standard code, the first two bases of mRNA codon corresponds to two last bases of tRNA anti-codon and obey standard code. Wobble base pairing hypothesis applies to the pairing of the 3rd mRNA base to the 1st base in tRNA anticodon. At the level of chemistry the hypothesis is that the position of the first tRNA anticodon base pairing with the third mRNA base is variable and allows it to pair with several bases appearing as 3rd base in mRNA. This homonymy would be due to "wobbling" of the position of the first tRNA anticodon.

2. In the original model for wobble base pairing tRNA bases contain besides standard A, C, G, U also inosine I as a modification of G obtained by dropping NH_2 from the 6-cycle of G. It has turned out that there are actually variants of C and 5 variants of U (see `http://tinyurl.com/y73se8vs`). The large amount of homonymy for tRNAs forces to ask whether chemistry alone really dictates the genetic code.

3. The first tRNA letter is assumed to be spatially wobbling so that the association of tRNA with RNA is not unique and mRNA-tRNA pairing involves both synonymy and homonymy as the two tables for the pairing of the 1st 5' anticodon base of tRNA and 3rd 3' codon base of mRNA show. In the second column bold letters for mRN bases allow to read the standard pairing with tRNA codons in the first column and non-bold letters allow to deduce the non-standard behavior.

4. The first table (see `http://tinyurl.com/y73se8vs`) represents the original Watson-Crick proposal.

   (a) The pairings of the 3rd letter of mRNA codon to the 1st letter of tRNA anti-codon are following.

   - U $\rightarrow$ G.
   - G $\rightarrow$ U
   - {A, C or U} $\rightarrow$ I.

   The 2nd and 3rd tRNA letters A and C are paired with the 1st and 2nd mRNA letters in the canonical manner. There are only 3 tRNA letters, which implies that the number of tRNAs is smaller than maximal.

   (b) There is single 1-to-many pairing: U$\rightarrow$ {G, I} giving rise to 2-fold homonymy.

5. Revised pairing rules (see `http://tinyurl.com/y73se8vs`) are more complex since the number of tRNA bases is larger (U has 5 variants and C has 2 variants). All mRNA letters have 1-to-many pairing. Even if one counts the variants of U as single U there is 4-fold homonymy for U and homonymies for other codons. For A one has 9-fold homonymy.

These variations do not induce variation in DNA $\rightarrow$ AA pairing if the AA associated with the homonyms of tRNA are identical. This seems to be the case almost always since the variation of the genetic code is surprisingly small. This raises the question whether there is some mechanism eliminating to high degree the expected effects of homonymy in mRNA$\rightarrow$ tRNA pairing.

10.3 Two TGD based realizations of genetic code

During years I have considered several visions about genetic code. Two of them have allowed to build concrete contacts with the empirical reality. They are realized in terms of dark protons sequences [L21] and in terms of 3-chords of bio-harmony [L12].

10.3.1 Dark realization of genetic code

The first TGD view about this is based on the dark realization of the genetic code [L21] (see `http://tinyurl.com/jgfjlbe`). This relies on general vision that dark matter and magnetic flux tubes - magnetic body (MB) - controls the biochemistry and that biochemical realization need not be complete.

1. TGD proposal is that dark proton sequences - dark nuclei - at magnetic flux tubes parallel to DNA strands provide the fundamental realization of the genetic code. Dark proton triplets would represent the analogs of DNA, mRNA, tRNA, and AAs. There would be 64 DDNAs, 64 DmRNAs, 40 DtRNAs and 20 DAAs. Dark codon cannot be separated to a product of letters but is an entangled state of 3 dark protons. There is a linguistic analogy: in primitive languages entire words are holistic basic units having no decomposition to letters.

2. DDNA, dmRNA, dtRNA, and DAA would control their biochemical variants and would be associated flux tubes carrying dark proton sequences. Dark code would dictate what happens at the chemical level. Chemistry would be a shadow of dark dynamics. Transcription and translation would take place at dark level.

   One can argue that this assumption is too strong. It requires that also the Stop codon codes for DAA and this in turn requires at the level of chemistry to an analog of tRNA attaching to the Stop codon. For standard realization of the genetic code there are indeed 2 release factors RF1, RF2 which are proteins not involving RNA (see `http://tinyurl.com/ydcgnlb3`) attaching to Stop codons and stopping the translation. RF1 recognizes UAA and UAG. RF2 recognizes UAA and UGA.

   There is also release factor RF3 binding to GTP (not appearing in RNA) and leading to a dissociation of RF1/RF2 after peptide release. Therefore RF3 does not play a role of tRNA. Note that both release factors recognize UAA so that the map from RNA codon to release factor is 1-to-2.

   The 1-to-many character of mRNA-AA association requires hidden degrees of freedom for DDNA affecting the genetic code by changing DAA $\rightarrow$ ordinary AA pairingat the level of chemistry.

3. If there is **no** homonymy at the dark level, one would have the following picture to start with.

   Remark: One could of course ask whether the dark variants of the 3 codes unique - are there several dialects possible already at this level. The degeneracies of dark codons coding for dark codon at lower levels down the ladder DNA-mRNA-tRNAA-As are unique but how many codes satisfying this condition are possible? In the sequence dark code is however assumed to be universal.

   (a) Dark genetic code decomposes to a sequence of three many-to-one codes without context dependence/homonymy: DDNA $\rightarrow$ DmRNA, which is 1-to-1, DmRNA $\rightarrow$ DtRNA, which is 64-to-40 and DtRNA $\rightarrow$ AA, which is 40$\rightarrow$ 20.

   (b) Chemical representation of dark variants of biomolecules is induced by the dark-chemical pairing, which can be context dependent to some degree. This in turn would induce context dependence of mRNA-tRNA pairing and possibly tRNAA-A pairing and as a consequence also that of mRNAA-A pairing. It is important to notice that the DX-X pairing involves transformation of dark photons to ordinary photons. The proposal is that the ordinary photons are bio-photons with much higher frequencies. The transition reducing the value of $h_{eff}/h = n$ would allow energy preserving transformation of extremely low frequency photons with large n and to bio-photons inducing molecular transitions.

   Remark: mRNA-AA correspondence is basically induced by DAA $\rightarrow$ AA correspondence.

   (c) One could say that there are several dialects each free of homonymies in their own context. Even the genes or the two strands of DNA might speak different dialects. What could be the quantum physics behind these dialects? At which level one can find the contexts causing the dialects? In TGD framework magnetic body (MB) carrying dark matter suggest itself.

   One can ask whether DDNA and DRNA, and maybe DtRNA and DAA could have a context defined by internal degrees of freedom, which varies in the situation when same DNA/RNA codes for 2 different AAs or AA and stopping sign. Magnetic body (MB) would naturally give rise to these new integral degrees of freedom.

10.3.2 The notion of magnetic body carrying dark matter and resonance as a mechanism of pairing

Pairing is the basic mechanism of molecular biology appearing in DNA replication, translation, and transcription. Pairing could be based on resonance coupling by dark photons propagating along magnetic flux tubes connecting the pairing systems.

The pairing between DDNA and DmRNA and DDNA and ordinary DNA would rely on resonance. More generally both dark and ordinary variants of the basic biomolecules would be characterized by collections of frequencies and if the frequencies are same the objects pair with each other. The 3-letter structure of the genetic codon suggests that resonance coupling occurs simultaneously for 3 frequencies defining the 3-chord. The pairing objects able to pair must be characterized by same the 3-chord.

1. DDNA, mRNA, tRNA, and AAs would pair horizontally. These horizontal pairings together with vertical pairings of dark molecules to their ordinary counterparts (DDNA →DNA, DmRNA → mRNA- DtRNA → tRNA, DAA → AA would induce the horizontal pairings of DNA, mRNA, tRNA, and AAs.

2. All these pairings would rely on resonant coupling and the structure of codons suggests that 3-chords of frequencies are involved.

3. The first idea was that there is no context dependence at the level of horizontal pairings. It turned out that there are naturally 3 different DmRNA-DtRNA pairings for a given harmony for mRNA. This induces context dependence at the level of chemistry and would due to variation of the collection of 3-chords characterizing DtRNA.

10.3.3 The geometric model for music harmony and genetic code

For some years ago I developed a model of music harmony [L12] (see `http://tinyurl.com/yad4tqwl`), which should define map of dark codons to 3-chords represented as dark photon triplets and defining allowed 3-chords of music harmony (music of light and perhaps also of sound). The Appendix provides the tables describing the details of the harmonies.

1. The model of music harmony is separate from the model of genetic code based on dark proton triplets and one of the challenges has been to demonstrate that they are equivalent. The model relies on the geometries of icosahedron and tetrahedron and representation of 12-note scale as so called Hamiltonian cycle at icosahedron going through all 12 vertices of icosahedron. The 20 faces correspond to allowed 3-chords for harmony defined by given Hamiltonian cycle. This brings in mind 20 AAs.

   Single step of Hamiltonian cycle connecting vertices of a face of icosahedron (triangle) is assume to correspond to a scaling of the frequency by factor 3/2. This leads to a problem since 12 scalings of this kind does not quite given 7 octaves which reduced octave equivalence to the basic octave would give 12-note scale. The solution is to add single notice slightly differing from 7 octaves and represented as vertex P of a tetrahedron glued to icosahedron along face. The Hamilton cycles are deformed so that they begin and end from this vertex. This also gives the missing 4 DNA codons realized as 3-chords and also defines unique ground note for the scales.

2. It turns out that has three basic types of harmonies depending on whether the symmetries of icosahedron leaving the shape of the Hamiltonian cycle is Z_6, Z_4 or Z_2. For Z_2 there are two options: $Z_{2,rot}$ is generated by rotation of π and $Z_{2,refl}$ by reflection with respect to a median of equilateral triangle.

   Combining together one harmony from each type one obtains union of 3 harmonies and if there are no common chords between the harmonies, one has 20+20+20 3-chords and a strong resemblance with the code table. To given AA one assigns the orbit of given face under icosahedral isometries so that codons correspond to the points of the orbit and orbit to the corresponding AA.

4 chords are however missing from 64. These one obtains by adding tetrahedron. One can glue it to icosahedron along chosen face or keep is disjoint. The model predicts a highly unique and realistic model for numbers of DNA codons coding for a given AA. The model in its original form predicts two codes and also explains the fact that there are two additional AAs Pyl and Sec that appear as end-products.

3. The model in its original form predicts 256 different harmonies with 64 3-chords defining the harmony. DNA codon sequences would be analogous to sequences of chords, pieces of music. Same applies to mRNA. Since music expresses emotions and produces them, the proposal is that these harmonies correspond to different molecular emotional states. The fundamental realization could be in terms of dark photon triplets replacing phonon triplets for ordinary music. Geometrically the two codes can be described as attachment of tetrahedron to icosahedron along face or as union of the two. Icosahedron corresponds to 60 DNAs and tetrahedron to 4 DNAs.

   During writing of this article I learned that the number of harmonies could be different, probably larger. There is however the question of the chemical realizability of the harmony: it is not at all clear whether there exist biomolecules to which the 3-chords of several harmonies could couple resonantly.

4. As I developed the model of bio-harmony [L12] (see `http://tinyurl.com/yad4tqwl`) it did not occur to me that also the tRNA part of the dark code should have counterpart in the icosahedral model. AAs correspond to single 20-codon code, DNA and RNA to union of 3 20-codon codes with symmetries Z_6, Z_4 or Z_2: here Z_2 would correspond to $Z_{2,rot}$ or $Z_{2,refl}$ and this would give to two two different codes.

   Could tRNA correspond to a union of 2 20-codon codes? Combining only 2 20-codon codes with 40 codons and tetrahedral code with 4 codons would give maximally 44-letter code and the upper bound for tRNAs is according to Wikipedia 45! Dark proton model predicts 40 DtRNAs suggesting that only the 40 isosahedral codons contribute to DtRNA code. The additional tRNAs could result from homonymy. The code sequences could be seen as a hierarchical sequence $3 \to 2 \to 1$ in this framework.

   An important implication is that there are many realizations of DtRNA and tRNA harmony: (Z_6, Z_4), (Z_6, Z_2), (Z_4, Z_2) and Z_2 could be either $Z_{2,rot}$ or $Z_{2,refl}$. This could explain the homonymy of mRNA-tRNA pairing via difference in the chords in turn affecting biochemical counterparts. Note however that the chords for tRNA must be a subset of chords for mRNA so that RNA harmony determines tRNA harmony apart from the three choices (Z_6, Z_4), (Z_6, Z_2) or (Z_4, Z_2) giving rise to 3 different contexts. If DAAs code by 3-chords the AAs then this choice does not affect AAs.

What conditions pairings pose on the frequency triplets?

The realization of DDNA-DtRNA and DDNA-DAA pairings in terms of frequencies must involve a loss of information since the correspondence is many-to-one.

1. For DNA-mRNA pairing information is not lost and the pairing must be of form $(f_1, f_2, f_3) \to (f_1, f_2, f_3)$. Note that the frequencies cannot be associated with the letters. It is however possible to consider the assignment of (f_1, f_2) to the first letter pair XY as a whole and f_3 to the third letter Z.

2. For DDNA-DAA and DmRNA-DAA pairing the natural hypothesis is $(f_1, f_2, f_3) \to f_1 + f_2 + f_3$. AA couples to the sum of the frequencies of the triplet. The simplest possibility is that the $f_1 + f_2 + f_3$ is same for all codons codin for given AA. One might say that AA sequence defines melody and mRNA sequence the accompaniment.If the sums for codons coding given AA are different they must couple resonantly to it. If there are several harmonies the sum must same for all realizable 3-harmonies or all chords of 3-chord harmonies coding for same AA couple to it resonantly. Since one has linear 1-D structures one might ask whether frequency differences coming as multiples of lattice frequencies are allowed. Second natural possibility is octave equivalence. mRNA-AA pairing would take place directly rather than with the mediation of of tRNA.

3. In the case of DmRNA-DtRNA pairing one one does not lose so much information since the number of dark DNAs is 40 (as also the 3-chords if tetrahedron does not contribute). One must remember that tRNAs are pairs of RNA like codons - call them RNA_t, and AAs. Therefore there pairing involves also the pairing mRNA-AA give by $(f_1, f_2, f_3) \to f_1 + f_2 + f_3$ and guaranteeing that the code is realized by this pairing alone irrespective of mRNA-RNA_t pairing. At chemical level the first to mRNA codons pair with tRNA anticodons according to the standard rules. Could RNA_t have completely passive role in carrying the AA? This cannot be the case since the last two letters of RNA_t couple in standard manner to the first two letters of mRNA.

   Remark: tRNA is analogous to melody + accompaniment using one of the 3 possible 2-harmonies for a given 3-harmony.

   Suppose that mRNA-RNA_t pairing corresponds to 3 possible choices of 2-harmonies as sub-harmonies of 3-harmony. This would suggest these different sub-harmonies define maps $(f_1, f_2, f_3) \to (f_1, f_2, f_3)$ such that RNA_t pairs only with two sub-harmonies. For each choice RNA_t would correspond effectively to 40 sub-codons of the entire code (forgetting the tetrahedral part giving 4 additional codons). The three different realizations of the projection would give rise to the homonymy. Also the AA-trNA coupling would come out correctly.

DAAs would be different in the sense that they couple only to the sum of the frequencies. This is in accordance with bio-harmony in which AAs correspond to orbits of 3-chords for DNA under isometries rather than single 20-chord harmony. The coupling to the sum of frequencies is in accordance with the quantal interpretation as 3-dark-photon state whose energy is $E = h_{eff}(f_1 + f_2 + f_3)$ and couples to AA chemically via the transition to ordinary photons with the same energy.

This leaves some questions.

1. Could one consider the possibility that the chords of one of the 20-chord harmonies corresponds to AAs? There would be 3 basic types of AAs. This does not look plausible and the association of AAs with the orbits of 20-note chords is more natural and fits nicely with $f = f_{XYZ}$ picture.

2. It would be nice to assign notes to the individual letters of codons. This is not possible since codons with 2 or 3 identical letters would reduce to 2-chords or 1-chords. It is also impossible to assign frequencies with letters at dark level since letter decomposition does not exist. Thus the 3-chord has resonant interaction with the entire codon.

3. The symmetries of the genetic code however suggest that it might make sense to treat the first two letters XY of the codon as a single unit and the third letter as separate single unit. Could one assign to XY a 2-chord not reducible to frequencies for the letters X and Y, and to letter Z its own frequency. The frequencies of A, G, T, C as third letter must be different. Four 32 codons of standard code the AA would not be sensitive to the frequency of Z: this is possible if these frequencies are resonance frequencies of the same AA. For the remaining 32 codons the AA would not distinguish between frequencies of T and C *resp.* A and G so that the two frequencies would be both resonance frequencies of the corresponding AA.

Probabilistic estimates for single 20-chord harmony

One can make first some naive probabilistic estimates about single 20-chord harmony.

1. Given 20-chord harmony makes $20/220 = 1/11 \simeq 9$ per cent about al possible 3-chords. Three 20 chord harmonies would make $3 \times 9 = 27$ per cent about all possible 3-chords if there are no common chords so that the optimistic expectation might make sense. Of course, one cannot exclude the possibility that there are also triplets of 20-codon codes which gives smaller number of codons.

2. The total number of chords with different notes is $12 \times 11 \times /3! = 220$. Bio-harmony has 64 chords corresponding to faces of icosahedron: this is about 64/220 making 29 per cent of all possible 3-chords with different notes. Given bio-harmony thus throws out roughly 2/3 of

all possible codons. This should be easy to test. For instance, does given gene correspond to a fixed bioharmony? Or does even entire genome do so. If bio-harmony is realized for non-nuclear genomes, it must satisfy rather strong constraints.

3. Given 20-chord harmony corresponds to 12 edges. Each edge is shared by two adjacent triangles. If all 20 triangles would contain just single face, there would be 24 triangles altogether. Therefore there must be triangles containing two subsequent edges of the cycle. Each triangle of this kind reduces the number of 24 neighbours by 2 units. Hence it seems that one must have at least 2 triangles with 2 edges at the cycle (two quints in the 3-chord).

   If there are more than 2 triangles of this kind, there must be triangles having no edges along the path. Each vertex of icosahedron is shared by 5 triangles and there are 5 edges starting from it.

4. The notion of Hamilton cycle generalizes to any graph and magnetic flux tube networks define such graphs as tensor networks. Why only icosahedron? Could one consider the possibility that any tensor network is characterized by harmonies characterize by Hamiltonian cycles and that one could assign some kind of codes with the combinations of these cycles? In the general case symmetries would be absent so that the notion of code in the proposed sense would fail: one could not identified codons as points at orbits of symmetry group. Rather, one can imagine that the notion of code could be defined quite generally in terms of orbits as AAs and points at them as DNAs coding them. For regular polygons in any dimension the symmetries are present and one could define the notion of code and also fuse the codes.

   For arbitrary tensor network the faces need not be symmetry related and one can also have faces that can be interpreted as higher-dimensional polytopes.

   One can also ask whether the icosahedron is realized physically. Icosahedral geometry is indeed very common in biology. Could the fusion of icosahedral and tetrahedral geometries have some concrete realization at molecular level?

Is the maximal number of codons for the fusion of 3 20-codon codes possible?

It has not earlier occurred to me to wonder whether the chords associated with the 3-different icosahedral harmonies giving 20 codons each correspond to 20+20+20=60 different chords as assumed. Could there be common 3-chords? This question could be answered by studying the Hamiltonian cycles at icosahedron.

Remark: Perhaps more important constraint than absence of common chords is the chemical realizability of the codes. If same mRNAs and DNAs realized different bio-harmonies then they must be able to respond resonantly to several 3-chords.

One can make naive probability estimates for a pair of codes to allow the maximal number of 60 codons. It seems natural to assume that the isometries of icosahedron (or their subgroup) can be applied separately and only the isometries acting on both in similar manner are symmetries. The situation would be the same as in the case of many-particle system: only the translations acting on all particles simultaneously remain symmetries and relative translations cease to be symmetries.

With this assumption the icosahedral group gives a large number of code pairs. For the fusion of 3 20-codon codes giving DNA/RNA the number is even higher. By choosing suitably the relative isometries it might be possible to obtain the maximal number of 60 different codons for the icosahedral genetic code. On the other hand, by a suitably choice of relative isometries one might have undesired common 3-chords. In any case, the earlier estimate 256 for the number of bio-harmonies [L12] suggested to correlate with "emotional" states of the basic biomolecules is expected to change.

Before going to estimates one must consider some delicacies related to the notion of 12-note scale as Hamiltonian cycle.

1. One can regard the cycles as purely geometric objects without orientation or assign to them orientation. For two different orientations the scales would run in opposite directions as scalings by 3/2 along single edge of the cycle. If two codes have common edge, the scaling must be same along it. If the orientation of the second cycle is changed, the common edge ceases to be common.

2. The basic note of the 12-note scale at cycle can be chosen arbitrarily: this corresponds to the choice of the key in music (one could of course argue that the key does not make sense in 12-note scale if one has tempered scale with notes comes as powers of $2^{1/2}$ scaling of ground note rather than Pythagorean scale with rational ratios of notes).

   The fusion of tetrahedron to icosahedron selects one particular triangular face and brings in one additional vertex outside the icosahedron, call it P. It would be natural to assign the ground note as P. The isometries not affecting P would correspond to those of icosahedron leaving the common face invariant and isometries of tetrahedron leaving P un-affected and continuable to icosahedral isometries. One would have subgroup of icosahedral group as allowed isometries acting on the cycles to be fused.

3. If one assigns note sequences to the cycle by quint rule, cycles C_1 and C_2 can have common triangle in geometric sense but if the distances of the vertices A, B, C of the triangles from P measured as the number of edges of cycle portion connecting them are not same along C_1 and C_2, the triangles correspond to different chords and are thus orthogonal in the proposed description as many-fermion states.

4. To sum up, the states associated with triangles would be characterize by the position of triangle (20 values), by the notes of the triangle characterized by the distances from P, and the number 0, 1, 2 of the edges belonging to the cycle and should make easier to find ortogonal basis.

Again one can make probabilistic estimates: cycles are treated as purely geometric entities without orientation and without assignment of notes to the triangles.

1. Given cycles C_1 and C_2 what is the probability that they have at least one common edge as purely geometric entities without the sequence of notes? There are 30 edges so that given edge is shared with probability 1/30. If the edges of cycles were chosen randomly (certainly not true), the probability of having a common edge for two cycles would be $P(1) = 12/30$. The assumption of note sequence reduces this probability dramatically.

2. By the above estimate each cycle contains at least two triangles with 2 edges at the cycle with minimal angle between them. One can call these these edge pairs V-corners. Assume that for cycle C_1 one has V-corner ABC at vertex A, call it $V_{1,A}$. What is the probability that one one of the V-corners of C_2 is located at A co-incides with ABC. The probability of V-corner of C_2 to locate at A is 1/12 and the probability that the edge of C_2 from B is BC is is 1/4 so that the probability of having common V-corner is 1/48. If C_2 contains n V-edges the probability is naively $n/48$.

   This estimate takes into account only geometry. The situation changes if one assumes that the cycles are oriented. In this case one can have common V-corner if the local orientations of C_1 and C_2 are opposite at the V-corner. If one assumes that the external vertex P of the tetrahedron defines the ground note then the number of edges connecting P to A defining distance $d(P, A)$ must be same for C_1 and C_2.

3. Given C_1 and C_2 (and vertices A with same distance $d(P, A)$) it might be possible to perform suitable isometry for C_2 that there is common V-corner. Therefore not all possible combinations of three code types allowing relative isometries need not maximal number of 3-chords.

   Remark: An interesting question is whether these can be allowed meaning that some codons are missing in the chemical realization of the dark codons in terms of ordinary DNA codons. Also the 1-1 pairing between dark DNA and and dark RNA would not be 1-1 if mediated by 3-chord resonance and one would have homonymy. This suggests that only codes without common chords can be allowed.

4. What about chords having 1 edge at cycle for two cycles C_1 and C_2? Let the edge be AB. As found, the naive probability for this is $P(1) = 12/30$. Both cycles must go through the third vertex C of the triangular face. The subsequent notes along cycle differ by a quint that is scaling of the frequency by factor 3/2. Notes are same if the numbers of the needed quints

are same for C_1 and C_2 For C_1 the number $n_B > 1$ of quints is known. In the approximation that possible portions of C_1 represent n-step non-self-intersecting random walks from B to C, one must estimate the number of all non-self-intersecting n-step-paths from B to C and find what is the number of the paths leading to C. One can go from A to C with n_A steps and similar estimate applies.

5. The third possibility is that the one has 3 common vertices A, B, C forming a triangular face such that neither cycle contains any of its edges.

The cautious conclusion is that it is plausible that one can find 3 cycles having no common chords if one allows relative rotations of the cycles and that this condition is necessary for realizing the absence of homonymies at dark level. The automatic orthogonality of the Hamiltonian cycles cannot be excluded but would allow also codes with codons containing more than 3 letters so that one could have kind of super-DNA. Whether they can be realized chemically depends on whether there are biomolecules resonating with the the n frequency triplets involved. Octave equivalence for frequencies might give hopes about chemical realization of several harmonies. Therefore the evolution might be seen as gradual emergence of molecules able to pair with DDNA and one can even imagine artificial evolution by tailoring the frequencies involved (maybe cyclotron frequencies).

Could harmonies form a Hilbert space

The condition that there are no common 3-chords brings in mind orthogonality and suggests that harmonies as Hamiltonian cycles could be defined as quantum states in suitable Hilbert space.

1. One could define inner product for Hamiltonian cycles as the number of common chords suitably normalized so that the norm of cycle of cycle equals to one. The number of common chords in the norm squared is 20 in the icosahedral case and 24 for the fusion of icosahedral and tetrahedral codes. Could Hilbert space picture for cycles make sense? The fusion of 2 (tRNA) or 3 (DNA) codes does not however naturally correspond to quantum superposition but rather tensor product.

2. Could one think that each cycle correspond to a 20-fermion product state with 3-chord characterizing the state of given triangle created by fermionic oscillator operator so that product P of 20 fermionic oscillators assignable to the triangles would create the harmony? The fusion of cycles C_1 and C_2 would be obtained by product P_1P_2. By fermionic statistics the resut would be zero if there are common cycles.

These considerations are purely formal and have no implications for what follows.

10.3.4 How the symmetries of the model of harmony could relate to those of the genetic code?

Genetic code has surprisingly strong symmetries. I have discussed a possible interpretation of these symmetries using analogies with particle physics and considered also a mechanism explaining their emergence earlier [K17, K19]. The proposal was that 3-letter code emerged as a fusion of 2-letter code with 16 codons and 1-letter coded with 4 codons. In the recent framework, a more natural option is that the third codon of 3-letter code was originally passive and became active via symmetry breaking distinguishing first between UC and AG pairs and later between U and C *resp.* A and G. Note that for the standard code the breaking is minimal and caused by odd number of Start and Stop codons.

1. For vertebrate code one half of codons has very high symmetry in the sense that the two first letters dictate the AA for 32 cases. Exception is UUU, which codes for Phe or Leu for some modifications of the standard code. UUU $\rightarrow$ Leu means breaking of maximal symmetry.

2. There is also a second symmetry, which I have referred to as isospin symmetry. It is only slightly broken. For general codons XYU and XYC code for same AA as also XYA and ad XYG. For the standard code this symmetry is broken only in columns containing initiation codon or stop. The Start codon AUG codes also for met. UGA and UGG code for Stop and

Trp. For the remaining codons one has slightly broken "isospin symmetry". The breaking of isospin symmetry is minimal for vertebrate code. The modifications of the code tend to break the isospin symmetry and even the maximal symmetry of 32 codons. This must be important.

If the model of genetic code based on music harmony [L12] is correct, the symmetries for the model of music harmony must relate to those of genetic code.

1. How the symmetries of the genetic code relate to the symmetries of icosahedron (60-element group) and tetrahedron (permutation group S_4 with 24 elements) in the model of bio-harmony? Icosahedral symmetry group has 60 elements and has sub-groups $Z_2, Z_4, Z_5, Z_6 = Z_2Z_3$. Note that there are two Z_2:s having rotation by π and reflection as generators.

   The gluing of tetrahedron to icosahedral along single face reduces its group of symmetries to S_3 leaving the point P not belonging to icosahedron invariant. S_3 has as subgroups reflection group $Z_{2,refl}$ and Z_4 consisting of rotations.

2. What is the counterpart for maximal symmetry in icosahedral and tetrahedral groups? Do the 3-chords for codon XYZ decompose to two-chord characterizing XY and a note characteriing Z= A,U,C,G, which can depend on XY. The symmetry relating UC pair and AC pair could correspond to $Z_{2,refl}$ reflection symmetry, which is shared by icosahedral and tetrahedral groups. For 32 icosahedral codons the action of $Z_{2,refl} \times Z_{2,rot}$ would be trivial so that AA would not depend on the third letter at all. For most of the remaining codons the action of the symmetry group on icosahedral codons would reduce to $Z_{2,rot}$ permuting the third letters U and C *resp.* A and G. At the level of frequencies the sums of frequencies for codons coding for the same AA sould be same modulo octave equivalence.

   The addition of tetrahedron brings in 4 tetrahedral codons with one of them shared with icosahedron. Icosahedral $Z_{2,rot}$ does not make sense for these codons. Intriguingly, there are 4 codons in vertebrate code which break isospin symmetry AUA and AUG coding for I and Met/start and UGA and UGG coding for Stop and Trp. If these codons correspond to the tetrahedral codons which cannot have $Z_{2,rot}$ as isospin symmetry, the breaking of $Z_{2,rot}$ would follow from the breaking of symmetry induced by the attachment of tetrahedron to icosahedron.

10.3.5 What distinguishes between codons and anti-codons and between DNA and RNA?

The icosahedral model should provide answer to several questions not considered yet.

1. The model for the genetic code in terms of dark proton sequences both DNA and RNA are predicted. This should be the case also in the icosahedral model. The 3-chords for DNA and RNA should be the same but there should be some inherent distinction between the two realizations.

2. Besides the active DNA strand there is also the inactive DNA strand (no transcription to mRNA) consisting of anti-codons. What does anti-strand correspond in the representation consisting of 3-chords? The chords assignable to the anti-strand should exist but there should be some difference between chords and anti-chords. Why this strand is inactive? mRNA is produced only via the pairing of RNA codons with active DNA strand. Could RNA_t as part of tRNA and counterpart of anti-RNA be unable to form stable strands in the recent biological environment and could lonely RNA_t codons fail to exist stably so that the transcription of DNA anti-strand to RNA_t strands would be impossible.

3. What does anti-DNA anti-RNA and anti-tRNA mean at the level of dark proton sequences?

I have approached these problems from particle physics point of view by using analogies and they might be helpful in the attempts to answer these questions [K19]. There are two mirror symmetries in the icosahedral harmony: 3-D reflection with respect to origin and change of the direction of the 12-note scale. Could these reflection symmetries help to understand the situation?

1. The symmetry mapping letters to antiletters (T $\leftrightarrow$ A, G $\leftrightarrow$ C) is mirror symmetry like charge-parity symmetry CP of particle physics equivalent with time reversal T by CPT theorem. CP is mysteriously broken: we have matter but where is the antimatter?

   The biological analogy with matter-antimatter asymmetry is that strand is active but anti-strand is passive - no transcription to mRNA. This would be the case if anti-RNA does snot exist as stable sequences. This would also explain why RNA does not replicate and does not form stable double helices.

2. Codons and conjugate letters for DNA are related by the CP like transformation (T $\leftrightarrow$ A, G $\leftrightarrow$ C). There should exist an icosahedral symmetry realizing this symmetry. Icosahedron allows also 3-D reflection through the origin as a symmetry (see `http://tinyurl.com/y8capjz7`). It permutes the opposite faces of icosahedron and extends the icosahedral rotation group with 60 elements to a group with 120 elements. The extended symmetry should preserve the set of 3-chords: they should be identical for DNA codon and anticodon.

   Harmony and anti-harmony for DNA would differ in that the attached tetrahedron would be at opposite face for the anti-codon representation since the reflection maps the tetrahedron to the opposite face. Could one see this as an analog of matter antimatter asymmetry? For double DNA strand anti-codons would correspond to icosahedron with tetrahedron attached to the opposite face. This symmetry should map the codons to their anticodons and there should be no fixed codon - this is indeed the case since there are no fixed faces.

   Icosahedral reflection should however leave the chords invariant apart from transponation by some power of 3/2 in order to leave the harmony invariant: codons and anticodons would be in different key in order to resonate. Icosahedral reflection would be an additional symmetry of the Hamiltonian cycles. The tetrahedron attached to the opposite face in reflection would be shifted back in transponation.

mRNA should have icosahedral realization with same 3-chords as DNA. What distinguishes mRNA from DNA at icosahedral level?

Could only mRNA exists as stable sequences and anti-mRNA fails to exist in this manner? This would be analog of CP breaking and the codons RNA_t in tRNA would correspond to anti-RNA_t existing only as single codon attached to AA. Could also the 4 tetrahedral anticodons for RNA_t (anti-tRNA) fail to exist (this would give 40 tRNA codons as also dark proton model predicts). Otherwise one would have 44 RNA_t codons.

DNA and mRNA differ only in single aspect: the letter T is replaced with letter U. How the replacement of U $\rightarrow$ T (and the replacement of riboses with de-oxy-riboses) is visible in the icosahedral harmony if the set of chords remains the same - perhaps modulo transponation by some number of quints?

Could the order of notes along the Hamiltonian cycle distinguish between DNA and RNA? The chords would remain the same but the order of notes in the chord would change.

1. If the reversed scale proceeded downwards in quarts (quint backwards, say C-G to C-G), the 3-chords would be same for the scales and the two scales are identical. Could one imagine that 3-chords are "played" as arpeggios! The order of arpeggio (upwards downwards in scale) would be opposite for up-chord and down-chord. RNA_t would define down-chords for mRNA up-chords but they would not form stable sequences and 4 anti-chords might be even missing.

2. If it proceeds in quints, the chords for the harmonies would not be same in general (for instance C-G upwards quint is replaced with C-F downwards quint). The scalings $(3/2)^k$ are replaced by scalings $(3/2)^{12-k}$ and the cycle becomes mirror image retaining its shape so that it is still a cycle and since the shape is preserved the symmetries are preserved too. Chords are in reflected positions and related by the map $(k_1, k_2, k_3) \rightarrow (12 - k_1, 12 - k_2, 12 - k_3)$. The chords are obviously different so that DNA and mRNA cannot differ in this manner.

   The scale and its quint-reversed counterpart differ much like major and quint scales as one easily finds (consider only the upwards scale Cmajor scale $CDEFG...$ in C major and the downwards Cminor scale $CB\flat A\flat G...$). They could therefore correspond to two different moods rather than mRNA-RNA.

3. TGD and TGD inspired theory of consciousness bringing observer part of physical system relies on zero energy ontology (ZEO). In ZEO the scale and its quint reversal could correspond to two different arrows of time for zero energy states. As self dies in state function reduction to the opposite boundary of causal diamond (CD), it is predicted to reincarnate with reversed arrow of time [L36]. Death is a sad event: could it be that the death of subself representing mental image is experienced by self as sad event and that in bio-harmony time reversal would change joy to sadness?

This relates in an interesting manner to the earlier speculations in TGD inspired view about pre-biotic life.

1. The proposal made in [K19] is that during RNA era preceding DNA era RNA replicated and AAs associated with pre-tRNA served as catalyst and later stole the stage so that RNA replication became translation. The greatest betrayal in the history of life! At this moment also DNA had to emerge. Otherwise RNA and life would have disappeared.

   Amusingly, also in cosmology CP symmetry was broken, when antimatter and matter annihilated and what remained was matter (there was slight imbalance originally).

2. Could one think that before the breaking of the analog of CP symmetry the tetrahedral part of the code was not present and the number of mRNA codons was 60. mRNA and anti-mRNA realized as mRNA_t had common chords related by icosahedral reflection symmetry. Also the 1st letter of mRNA_t was just like the other letters.

   In the transition A and C as 1st letters disappeared and were replaced with G,U and I (in Watson-Crick scenario). The 4 tetrahedral codons containing Start and Stop codons emerged in the transition.

   In the symmetry breaking DNA with opposite direction of the scale (the reversed scale proceeded downwards as quarts rather than quints) and arpeggios emerged. Perhaps this required the replacement of U with T and perhaps also of riboses with de-oxy-riboses.

3. Did the 4 additional tetrahedral codons responsible for the breaking of the analog of isospin symmetry (A $\leftrightarrow$ G and T $\leftrightarrow$ C) associated with the stop and Start codons emerge in this event so that 60-codon realization of the code was replaced with 64 codon realization. If Start and Stop emerged in this event the entire mRNA strand replicated before it.

4. Was the letter mRNA letter U replaced with DNA letter T in this transition. Did this make possible the existence DNA as double strands stable in the presence of nuclear or cell membrane but not stable as single strand. Did the 4 additional tetrahedral codons responsible for the breaking of the analog of isospin symmetry (A $\leftrightarrow$ G and T $\leftrightarrow$ C) associated with the stop and Start codons emerge in this transition. Before the transition the entire mRNA strand would have been able to replicate. mRNA-AA pairing was present and AA would have catalysed the replication.

5. Was the homonymy present in mRNA replication before the transition. The updated scenerio for mRNA-tRNA correspondence allows the replication albeit not in 1-1 manner (see `http://tinyurl.com/y73se8vs`). Was the letter I present at that period: was it part of both mRNA and rNA_t or of only RNA_t giving therefore rise to a leakage?

If RNA era in the proposed sense was realized, what happened before it?

1. One imagine that before RNA era the RNA_t - not necessary identical with its recent form - as a realization of 2-harmony (or perhaps of all 3 different types of 2-harmonies) with 40 codons was realized and was able to replicate with AAs serving as catalysts attached to RNA_t.

   Only the complementary RNA_t was able to appear as sequences: tetrahedral codons were absent. In the transition from 2-harmony to 3-harmony both DNA and full RNA emerged. Replication of RNA_t transformed to translation of AAs. This vision would be more in spirit with the idea about the gradual emergence of biological representations of the dark variants of biomolecules.

2. One could go even further and ask whether this period was preceded by a period during which pre-tRNA identifiable as single 20-codon representation choosable in 3 manners. Pre-tRNA $\leftrightarrow$ AA correspondence would have been 1-1. AAs would have decomposed to three types corresponding to these 3 choices. For instance for the code with Z_6 symmetry only 4 AAs would have been present. For the details of harmonies see the Appendix of [L12] (see `http://tinyurl.com/yad4tqwl`).

10.4 Context dependence from TGD point of view

The original idea was that context dependence and homonymy are absent at the level of dark variants of various codons and AAs and would result from the pairing with chemical counterparts of dark codons. More precisely: the horizontal dark DX-DY pairings would be context independent and would not depend on emotional state whereas the vertical DX-X pairings are induced by DX-DY pairings and induce X-Y pairings. This is obviously something new from the point of biology as chemistry paradigm.

It however turned out that the context dependence appears very naturally at the dark level. DtRNA bio-harmony allows naturally 3 different representations as 2-harmonies realized as sub-harmonies of 3-harmony associated with DNA and mRNA. One would have 3 basic context already at this level.

One can imagine at least 3-sources of context dependence and expression of emotions by gene expression.

1. Several bio-harmonies are possible and DX and X would couple by different resonant 3-chords for each harmony. It is of course possible that very few of these bioharmonies - perhaps only one - are realized at the level of DNA and mRNA. This would explain the uniqueness of DNA and mRNA codons in biological sense.

   If several bioharmonies are realized for DNA then both mRNA, RNA_t and AA must have resonance couplings to all these bioharmonies. For AA this is satisfied if $f_{XYZ} = f_1 + f_2 + f_3$ is same (perhaps modulo octave equivalence) for all harmonies involved or if AA has all all the frequencies f_{XYZ} as resonance frequencies. For mRNA $(f_1, f_2, f_3) \to (f_1, f_2, f_3)$ pairing would require even larger spectrum of resonant 3-chords at the level of chemistry. Hence it is quite possible that only single 3-harmony is realized for DDNA, DmRNA, and DAA. If several harmonies are present, the evolution would have gradually invented the biomolecules having the needed spectrum and would still be in progress.

2. The situation with DtRNA is different. The DmRNA-DtRNA pairings would involve 3 different unions of 2 20-chord harmonies. This choice implies context dependence already at dark DNA level and could be the fundamental reason for mRNA-tRNA homonymy. What is however important that the decomposing of tRNA to (RNA_t,AA) pairs guarantees automatically genetic code via $f_{XYZ} = f_1 + f_2 + f_3$ coupling. AA dictates the pairing unlike usually thought.

3. If the frequencies are cyclotron frequencies determined by the magnetic fields at flux tubes, the variation of magnetic field strength due to the variation of flux tube thickness changes the frequency scale. This could be also seen as emotional expression (in analogy with membrane potential in biology inducing variation of Josephson frequencies and varying the degree of alertness in neurons).

   The gradual variation of magnetic fields strengths during evolution could explain the slight differences in the genetic code. Evolution would be clearly in question in the sense that the symmetries of the code are maximal for the nuclear code. It will be found that also this mechanism is needed in order to understand all deviations of the code.

10.4.1 Context dependence as "emotional expression" at molecular level?

Using the attribute "emotional" certainly raises eyebrows and I will drop even the quotation marks in the following. Reader can freely add them.

Basic guide lines

Consider first the basicguidelines

1. One plausible possibility is that genetic code as DNA-AA pairing is unique in given context - whatever it is physically - but there exist what one might call dialects just like slight modifications of vertebrate genetic code. There is homonymy, which however disappears when context is taken into account: same mRNA can correspond to two AAs or AA and stop. The homonymy is associated with mRNA-tRNA pairing for the third mRNA letter which is many-to-one and 1-to-many. Which the actual choice depends on context as in ordinary language.

2. Wobble base pairing is the model explaining both the many-to-1 and 1-to-many pairings. An interesting finding is that for 32 codons the pairing does not depend on third letter at all. I have proposed long time ago a model in which 2-letter code emerged first and then fused with 1-letter code to give 3-letter code. A more plausible interpretation is as activation of the 3rd letter in 3-letter code. The wobble base pairing and homonymy would have emerged in this fusion of codes.

3. From the tables of Wikipedia at article (see `http://tinyurl.com/y73se8vs`) for standard code one can read when the pairing of the third letter is many-to-one and 1-to-many. If it is 1-to-many and unless the resulting tRNA anticodons correspond to the same AA, the outcome can be several AAs.

   This does not lead to 1-to-many mRNA $\rightarrow$ AA if the RNAs associated with tRNAs in mRNA $\rightarrow$ tRNA pairing couple with the same AA. The pairing between mRNA and AAs is 1-to-many rather rarely and could be accidental. It seems that there is a principle taking care that the deviations from the standard code get minimized.

4. The homonymy for mRNA-AA pairings is very rare. This suggests that it is accidental and disappeared during the evolution.

The origin of mRNA-tRNA homonymy and mRNA-AA homonymy

mRNA-tRNA homonymy is clearly exceptional and the proposal that tRNA bio-harmony corresponds to a fusion of 2 20-chord codes together with the fact that there are 3 basic types of these codes could explain this.

1. Suppose that DtRNA harmony corresponds to a sub-harmony of full bio-harmony for DDNA and DRNA as a fusion of two sub-cycles from the union of 3 cycles defining DDNA and DRNA harmony. One can make this choice in 3 manners corresponding to the choices (Z_6, Z_4), (Z_6, Z_2) and Z_4, Z_2. These 3 basic choices would naturally explain the DtRNA-tRNA homonymy without the dependence on emotional state. This would not however explain the deviations from the standard code.

   In the case DtRNA- tRNA pairing it is enough that tRNA couples resonantly only to the 3-chord representatives associated with one 2-harmony appearing as sub-harmony of 3-harmony that is selected and defines the context. This obviously allows larger number of tRNAs satisfying the resonance conditions. This could relate to the homonymy.

   The function of tRNA as an agent transferring DAA-AA pair and attaching it to DmRNA-mRNA pair. Hence tRNA homonymy is desirable - it can happen that the concentration of particular certain kind of tRNA is low so that second kind of tRNA coupling to same mRNA can handle the job.

2. tRNA homonyms for the first anticodon of tRNA would reflect the emotional state of DDNA/mRNA. Why only the third? This might relate to the idea about fusion of 2-letter codes and 1-letter codes. For 2-letter code there would be no "emotional expression" and no context dependence. The emergence or perhaps better, the activation of additional letter at the level of chemical expression, would have brought in the chemical emotional expression.

Consider now mRNA-AA homonymy. This homonymy is rather rare and could be accidental.

1. If AA couples to the sum $f_{XYZ} = f_1 + f_2 + f_3$ of the frequencies characterizing the codon $X_1Y_1Z_1$, it can happen that one has $f_{X_1Y_1Z_1} = f_{X_2Y_2Z_2}$ modulo octave multiple so that besides codon $X_1Y_1Z_1$ also the wrong codon $X_2Y_2Z_2$ codes for the same AA. Of course, this condition might hold true only approximately. This could explain mRNA-AA homonymies as accidental.

2. There is however an objection against the proposal. If the frequencies f_{XYZ} are identical in octave equivalence for all codons coding for AA, the accidental degeneracy would suggests that the entire mRNA multiplet containing $X_2Y_2Z_2$ codes for AA. Typically however only one member of the mRA multiplet codes for wrong AA.

   Should one give up the idea that the members of mRNA multiplet satisfy $f_{X_1Y_1Z_1} = f_{X_2Y_2Z_2}$. If so, AA would have the frequencies f_{XYZ} of mRNA multiplet as distinct resonance frequencies. For instance, could one think that the A-G and T-C breakings at the level of frequencies are present although they are not large enough to make themselves visible in the mRNA-AA correspondence (say for the mRNA 4-plets coding for same AA). This is the case if AA has all these frequencies as resonance frequencies. Also the number of octaves distinguishing between $X_1Y_1Z_1$ and $X_2Y_2Z_2$ matters somewhat. In this case the accidental resonance condition for wrong AA could be satisfied for single member of mRNA multiplet only.

A concrete objection against the model

One can try to understand the possible dependence of code on the emotional state by looking the numbers of 3-harmonies obtained as fusion of Z_6, Z_4 and Z_2 symmetries. One can find explicit tables for the codes in the Appendix of [L12] (see `http://tinyurl.com/yad4tqwl`).

1. A crucially important thing to notice is that Z_6 harmony is unique. This harmony allows 3 6-plets for which 6 DNAs code for single AA. There is also one doublet. Therefore the codons associated 3 6-plets and doublet should always code the same AA unless the magnetic fields at flux tubes determining the cyclotron frequencies van vary. It is easy to verify that this prediction is correct for the nuclear code.

   For non-nuclear codes the situation is different. There are 3 6-plets and they code for Leu, Ser, and Arg. These 6-plets should be stable under the modifications of the standard code. This rule is however broken in at least two cases:

   (a) For CUG coding for Ser instead of Leu. Ser is coded usually by UCG. Both DAA and AA couple to the sum $f_{XYZ} = f_1 + f_2 + f_3$ of the 3-chord frequencies. The simplest explanation already discussed is that DSer and DLeu have accidentally $f_{CUG} = f_{UCG}$ modulo octave multiple. T

   (b) UUG coding for Stop rather than Leu. Stop is coded usually by UGG. Accidental degeneracy would be the explanation also now. Stop identified as release factor FR1 or FR2 playing the role of AA and possibly having also dark AA counterpart would have $f_{UGG} = f_{UUG}$.

2. All deviations from the standard code could be determined solely by the accidental degeneracies for the frequencies f_{XYZ} associated with two codons coding for different AAs or AA and stop. For standard code they would have been eliminated almost completely by evolution: as noticed earlier, even in human mitochondrial code there is this kind of homonymy.

3. For 3-chords with Z_4 as isometry group one has 2 different harmonies, which means non-trivial conditions on DNA and mRNA since the 3-chords of all these harmonies must act as resonance chords. In principle homonymy becomes possible for DDNA $\rightarrow$ DNA and DmRNA $\rightarrow$ mRNA pairings but is not realized. Either coupling to both harmonies is possible or there are no DNAs or mRNAs coupling resonantly to all 3-chords of either harmonies so that only 1 harmony is realized completely. This is important if one requires uniqueness of the genetic code.

4. For 3-chords having Z_{rot} isometries there are 3 harmonies and for Z_{refl} 5 harmonies. This gives increasingly stronger conditions on resonant couplings. The uniqueness of the code suggests that only a subset of possible harmonies is possible. Also the probability of homonymy for DAA-AA pairing increases and might explain 21st and 22nd AAs Pyl and Sec coupling to non-standard representation. Deviations typically occur for the doublets as indeed found.

What is interesting that if one loosens the conditions and allows different couplings and allows several 3-harmonies, it is in principle possible to have larger number of DNA and mRNA codons than usually. Also analogs of AAs can be considered. Frequency coding relates interestingly to extended genetic codes with 4 or 5 codons (see `http://tinyurl.com/ycsfgu7n`) and nucleic acid analogues (see `http://tinyurl.com/y8tj8hsm`).

10.4.2 Is the notion of reading frame consistent with the proposed realizations of the genetic code?

Reading frame (see `http://tinyurl.com/yb6wr3d7`) represents also a context dependence of the code. Reading frame begins with the Start codon and new reading frame can begin at second or third letter of codon. There must be also Stop after $3 \times n$ letters also in the new reading frame.

Shifting of reading frame by 1 or 2 units can take place for viral, prokaryote, and mitochondrial genomes but for some reason not in nuclear genome. Shift makes sense if the first codon is Start codon. For human genome MT-AOT8 and MT-ATP6 are examples of reading frames for mitochondrial genes coding for different proteins. The interesting question is why the shift occurs only at the level of viruses, prokaryotes, and mitochondria and chloroplasts.

Does the notion of reading frame make sense for the two models of genetic code? Consider first the representation of 64 codons as 3-chords. If all 64 codons are are realized as chords, shift does not produce chords not belonging to the harmony. Since the notes of chords cannot correspond to the letters the shift is highly non-trivial since it is not only shifted decomposition of notes to triplets but change also the notes.

Is this possible at the level of DmRNA? At the dark level code words do not have decomposition to letters. Dark proton triplets should re-organize in a new manner into triplets. If the dark protons inside proton triplet are connected by colored bonds to form color singlet, the shift would produce colored 3-proton states unless also the color structure of the states is re-organized so that it is consistent with the shift at the level of codons. Kind of phase transition would take place and induce the change of the reading frame.

Chapter 11

About the Correspondence of Dark Nuclear Genetic Code and Ordinary Genetic Code

11.1 Introduction

The idea about the realization of genetic code in terms of dark proton sequences giving rise to dark nuclei is one of the key ideas of TGD inspired quantum biology [L21]. This vision was inspired by the totally unexpected observation that the states of three dark protons (or quarks) can be classified to 4 classes in which the number of states are same as those of DNA, RNA, tRNA, and amino-acids. Even more, it is possible to identify genetic code as a natural correspondence between the dark counterparts of DNA/RNA codons and dark amino-acids and the numbers of DNAs/RNAs coding given amino-acid are same as in the vertebrate code [L21]. What is new is that the dark codons do not reduce to ordered products of letters.

During years I have considered several alternatives for the representations of genetic code. For instance, one can consider the possibility that the letters of the genetic code correspond to the four spin-isospin states of nucleon or quark or for spin states of electron pair. Ordering of the letters as states is required and this is problematic from the point of view of tensor product unless the ordering reflects spatial ordering for the positions of particles representing the letters. One representation in terms of 3-chords formed by 3-photon states formed from dark photons emerges from the model of music harmony [L12]. By octave equivalence the ordering of the notes is not needed.

11.1.1 Insights

The above observations inspire several speculative insights.

1. The emergence of dark nuclei identified as dark proton sequences would relate to Pollack's effect in which irradiation of water generates in presence of gel phase bounding the water what Pollack calls exclusion zones (EZs). EZs are negatively charged and water has effective stoichiometry $H_{1.5}O$. EZs deserve their name: somehow they manage to get rid of various impurities: this might be very important if EZs serve as regions carrying biologically important information. The protons of water molecules must go somewhere and the proposal is that they go to the magnetic body of some system consisting of flux tubes. The flux tubes contain the dark protons as sequences identifiable as dark nuclei.

2. Since nuclear physics precedes chemistry, one can argue that prebiotic life is based on these dark biomolecules serving as a template for ordinary biomolecules. To some degree biochemistry would be shadow dynamics and dark dynamics would be extremely simple as compared to the biochemistry induced by it. In particular, DNA replication, transcription, and translation would be induced by their dark variants. One can even extend this vision: perhaps

also ordinary nuclear physics and its scaled up counterpart explaining "cold fusion" are parts of evolutionary hierarchy of nuclear physics in various scales.

3. Nature could have a kind of R&D lab allowing to test various new candidates for genes by using transcription and translation at the level of dark counterparts of the ordinary basic biomolecules.

11.1.2 Conditions on the model

The model must satisfy stringent conditions.

1. Both the basis A, T, C, G and A, U, C, G as basic chemical building bricks of RNA and DNA must have emerged without the help of enzymes and ribozymes. It is known that the biochemical pathway known as pentose-phosphate pathway (see `http://tinyurl.com/y9akkwok`) generates both ribose and ribose-5-phosphate defining the basic building brick of RNA. In DNA ribose is replaced with de-oxiribose obtained by removing one oxygen.

   Pyrimidines U, T, and C with single aromatic ring are are reported by NASA to be generated under outer space conditions (see `http://tinyurl.com/y7sh9zk4`). Carell et al [I73] (see `http://tinyurl.com/z65kpyo`) have identified a mechanism leading to the generation of purines A and G, which besides pyrimidines A,T (U) are the basic building bricks of DNA and RNA. The crucial step is to make the solution involved slightly acidic by adding protons. TGD inspired model for the mechanism involves dark protons [L24] [K19].

   Basic amino-acids are generated in the Miller-Urey type experiments (see `http://tinyurl.com/4q2arv`). Also nucleobases have been genererated in Miller-Urey type experiments [I79].

   Therefore the basic building bricks can emerge without help of enzymes and ribozymes so that the presence of dark nuclei could lead to the emergence of the basic biopolymers and tRNA.

2. Genetic code as a correspondence between RNA and corresponding dark proton sequences must emerge. Same true for DNA and also amino-acids and their dark counterparts. The basic idea is that metabolic energy transfer between biomolecules and their dark variants must be possible. This requires transitions with same transition energies so that resonance becomes possible. This is also essential for the pairing of DNA and dark DNA and also for the pairing of say dark DNA and dark RNA. The resonance condition could explain why just the known basic biomolecules are selected from a huge variety of candidates possible in ordinary biochemistry and there would be no need to assume that life as we know it emerges as a random accident.

3. Metabolic energy transfer between molecules and their dark variants must be possible by resonance condition. The dark nuclear energy scale associated with biomolecule could correspond to the metabolic energy scale of .5 eV. This condition fixes the model to a high extent but also other dark nuclear scales with their own metabolic energy quanta are possible. In fact, the dark nuclear binding energy for $k = 151$ scaled up from the typical value of the ordinary nuclear binding energy about 1 MeV is .5 eV.

11.1.3 Vision

The basic problem in the understanding of the prebiotic evolution is how DNA, RNA, amino-acids and tRNA and perhaps even cell membrane and microtubules . The individual nucleotides and amino-acids emerge without the help of enzymes or ribozymes but the mystery is how their polymers emerged. If the dark variants of these molecules served as templates for their generation one avoids this hen-and-egg problem. The problem how just the biomolecules were picked up from a huge variety of candidates allowed by chemistry could be solved by the resonance condition making possible metabolic energy transfer between biomolecules and dark nuclei.

The basic question is to what p-adic length scales $L(k)$ DNA, RNA and amino-acids correspond. The original hypothesis was that the p-adic length scale assignable to dark DNA is consistent with the radius of ordinary DNA. It however turned out that this implies that the

binding energy scale of corresponding dark nuclear physics is too high for the recent biology. Also the assumption that the dark variant of DNA double strand is horizontally scaled up variant of ordinary DNA strand excludes this identification since it requires that the horizontal size scale of dark DNA strand is larger than that of ordinary DNA strand.

DNA coil has radius $L(151) = 10$ nm and this suggests that dark DNA radius does not correspond to the radius of ordinary DNA (as assumed in the original version of this text) but to the p-adic length scale $L(151)$, where $k = 151$ corresponds to first Gaussian Mersenne prime belonging to the group $k = 151, 157, 163, 167$. The primes $k > 151$ would correspond to higher level coilings of DNA. From this hypothesis one ends up to the proposal that RNA, tRNA, and amino-acids correspond to $k = 149$. This picture follows essentially from the contraints posed by various biological anomalies.

Also the smaller primes $k = 127, 131, 137, 139$ can be present in pre-biotic evolutions. This hierarchy of dark nuclear physics leads to a vision about how prebiotic evolution led via RNA era to the recent biology. Unidentified infrared bands (UIBs) from interstellar space identified in terms of transition energies of dark nuclear physics support this vision and one can compare it to PAH world hypothesis.

The vision about dark matter as a controller of biomatter leads to ask whether cell membrane and microtubules could correspond to 2-D analogs of RNA strands associated with dark RNA codons forming lattice like structures related to by radial scaling to their counterparts at the level of ordinary biomatter. This is supported by p-adic length scale hypothesis and thermodynamical considerations. These 2-D structures could represent 2-D variants of 1-D structures represented by DNA, RNA, and amino-acids with each node of lattice representing code letter.

Thermal constraints allow cell membrane of thickness about 5 nm as am additional realization of $k = 149$ level with $n = 2^{22}$ in terms of lipids as analogs of RNA codons. For $k = 149$ metabolic energy quantum is predicted to be .5 eV. The thickness of neuronal membrane in the range 8-10 nm and could correspond to $k = 151$ and $n = 2^{23}$ in accordance with the idea that it corresponds to higher level in the cellular evolution reflecting that of dark nuclear physics. The energy quantum of ordinary Josephson radiation is just at the verge of thermal threshold. This could be understood in terms of minimization of metabolic resources. For bosonic singly charged ions the Josephson energy would be below the thermal threshold. The notion of generalized Josephson junction saves the situation. For massive particles associated with flux tubes the thermal energy $T/2$ is below the potential energy defined by action potential and that of metabolic energy quantum.

Also microtubules could correspond to $k = 151$ realization for which metabolic energy quantum is $E_{ex}(151) = .25eV$. Of course, the replacement of $E_{ex} = 1$ MeV for ordinary nuclei with $E_{ex} = 2$ MeV would give $E_{ex}(151) = .5$ eV so that one must take these estimates as order of magnitude estimates only. Also a proposal for how microtubules could realize genetic code with the 2 conformations of tubulin dimers and 32 charges associated with ATP and ADP accompanying the dimer thus realizing the analogs of 64 analogs of RNA codons is made.

The great vision would be that hierarchy of dark variants of DNA, RNA, amino-acids and their replication, transcription, and translation would be behind biological replication in various scales. Ordinary bio-chemistry would be shadow dynamics doing its best to mimic what happens at the level of dark matter. The reduction of bio-physics to that of dark matter level would mean a huge simplification of the vision about living matter.

11.2 About dark variants of DNA, RNA, and amino-acids

To make progress one must construct a concrete model for the dark nuclei. The recent picture relies strongly on various anomalies to which TGD provides a solution. The TGD inspired model for "cold fusion" leads to the notion of dark nuclear physics - actually hierarchy of them labelle by the values of $h_{eff}/h = n$ and corresponding p-adic length scales. Second basic idea [L15] is that cylindrical variants of EZs discovered by Pollack [L15] give rise to the dark counterparts of DNA, RNA, and amino-acids as dark proton sequences. tRNAs would be analogs of tritium and ^{3}He. Pollack effect serves as a strong constraint for the model. Also the effects of ELF em fields on vertebrate brain [J8] combined with the rather recent finding about clustering of RNA II polymerase molecules [I74] exhibiting Comorosan effect [I134] provide valuable constraints on

the model [L40]. The outcome of the arguments is that single strand of DNA, mRNA, tRNA and amino-acids most naturally correspond to $k = 149$ and double stranded DNA to $k = 151$.

Remark: The following argumentation is kind of Sherlock-Holmes-ing using all possible hints as constraints to select between imagined options rather than glorious march from axioms to theorems and thus not science in the usual sense.

11.2.1 Dark variant of DNA

Concerning the identification of the size scale of dark DNA one can consider several options. The first guess was that the scale is same as for ordinary DNA: L(141)=.34 nm obtained by scaling from the distance of protons in the $k = 127$ dark nucleus implicated by the findings of Holmlid et al [C1, L26] [L17]. It however turns out that the p-adic length scale assignable to dark DNA is most naturally $k = 151$ corresponding to the thickness 10 nm of DNA coil. The hypothesis that the integer k labelling p-adic length scale is prime is attractive working hypothesis leaving very few options under consideration. The options $k = 137$ and $k = 149$ are excluded since the pairing of dark DNA and ordinary DNA would not be possible without the coiling of ordinary RNA around dark DNA. This leaves only options for which $k \geq 149$ for prime values of k.

Remark: The p-adic length scale associated with a system is defined to be $L(k)$ if the size of the system is in the half open interval $[L(k), L(k+1))$. One can also consider the possibility that p-adic length scale corresponds to the upper end of $[L(k-1), L(k))$.

General considerations

Consider first some background.

1. The TGD based model leads to the proposal for a formation of this kind of dark nuclear strings such that the distance between protons is rather precisely electron Compton length $L_e \simeq .4 \times 10^{-12}$ meters explains "cold fusion" in terms of dark nucleosynthesis which should have preceded ordinary nucleosynthesis by heating the material to the temperature required by it [L29] [K74].

   Dark nucleosynthesis would have produced part of heavier nuclei outside stars. The binding energy scale for dark nuclear physics would be scaled down like 1/length and 2.6 MeV binding energy per nucleon for ^{3}He of the ordinary nuclei would be scaled down by a factor 2^{-11} to 1.3 keV. Note however that it is excitation energies of order 1 MeV what matters and would scale down to .5 keV. This level does not yet correspond to biology as we know it but could be one step in the evolutionary hierarchy leading from nuclear physics also based on nuclear strings to biology involving increase of Planck constant $h_{eff}/h = n$ identifiably as the dimension of algebraic extension of rationals characterizing the complexity of the dynamics.

2. These dark nuclei have $h_{eff}/h = n = 2^{11}$ (or near to it) and cannot be those responsible for the dark variants of biomolecules since the distances of dark protons given by electron Compton length are much shorter than the distance between DNA nucleotides about .34 nm, which is roughly 142 times the electron Compton length 2.4×10^{-3} nm.

3. The distance between the dark protons appearing as counterparts of DNA nucleotides should be larger than that between ordinary DNA nucleotides. The simplest assumption that dark DNA coil is a horizontally scaled variant of DNA coil with same twisting angle so that DNA nucleotides are projected horizontally to their dark counterparts at the surface of a cylinder. Once the p-adic length scale of this cylinder is given, the distance between dark protons is fixed by p-adic scaling from the distance between dark protons for $k = 127$ case - that is electron Compton length. In the case of uncoiled RNA/AA one could have also a coil rotating around the ordinary RNA/AA.

   The distance between dark nucleotides must be longer than the the distance $3 \times .34 \sim 1$ nm taken by single ordinary DNA codon. If k is prime this leaves only $k = 149$ or $k = 151$ into consideration.

4. The negative charge of DNA and RNA assignable to one oxygen of phosphate combining with ribose and DNA/RNA base could come from the tubular EZ formed in the formation

of DNA. The negative charge of phosphates and the positive charge of dark protons could guarantee the stability of pairs of dark proton sequences and ordinary RNA and DNA.

DNA strand has radius of $R = 1$ nm. The Debye length R_D of DNA gives rough idea about the scale above which the negative charge of DNA nucleotides associated with the phosphates screened. R_D should be longer than R: otherwise it is not possible to speak about charge of DNA only atomic length scales. One should have $R_D > R$: otherwise it does not make sense to assign negative DNA charge except in atomic length scales. The simplest option is that dark DNA has size scale $L(151)$.

Remark: The rough estimates depend on how one identifies p-adic length scale. For the identification as $L(k) = \sqrt{5}L_e(k)$ motivated by the mass formula for electron, one would have $L(k) = \sqrt{5}L_e(k)$ giving $L(141) = 0.67$ nm. With this interpretation the estimate for the screening radius would be still shorter than R.

Remark: Scaled up hadron physics would be associated with flux tubes of the magnetic body of the codon at which one would have nucleons as 3-quark color singlets. I have already earlier proposed that scaled variants of hadron physics [K21] appear in TGD inspired biology. One motivation comes from honeybee dance [A15]!

The pairing dark AAs with positive charge with ordinary AAs might lead to problems since 16 AAs are neutral. The only charged AA residues are Lys (+), Arg (+), Asp (-) and Glu (-).

1. The formation mechanism for dark proton sequences gives for dark AAs a large positive charge. AAs are however not accompanied by negatively charged phosphate ions. Does charge neutrality require that the dark bonds between dark proton has negative charge so that one has effectively neutron?

   Dark weak interactions correspond to large value of n [L29] so that in DNA length scale their proceed as fast as electromagnetic interactions (weak bosons would behave like massless particles below scaled up weak scale). This could make possible β decays changing the charges of the bonds between dark protons or dark neutrons [L29] and lead to a stability by β emission.

2. Proteins in water environment have a charge due to protons or electrons attaching to them. This charge depends on pH and becomes negative above certain critical pH. One might think that the limit of very large pH (no protons) corresponds to the situation in which the electrons of EZ attach to AAs.

Dark codons do not have decomposition to letters whereas ordinary codons have. In a well-defined sense one could say that dark code is "holistic" whereas the ordinary code is "reductionistic".

1. This brings in mind western written language in which words decompose to letters. In some eastern languages the symbols of written language correspond to entire words. Do these differences correspond at deeper level to ordinary and dark genes. Could the analytic and holistic aspects of cognition relate to the differences between ordinary and dark code.

2. One cannot exclude the entanglement between codons and evolution as emergence of entanglement even suggests this. Could this kind of entanglement give rise to basic units of DNA, in particular genes and introns. Could the decomposition of gene into coding regions and introns correspond to a decomposition to unentangled products of internally entangled pieces. This would increase exponentially the degrees of freedom involved and explain why organisms with practically the same code can be at so different evolutionary levels. In the splicing process when intronic portions are cut out from DNA sequence. Do the remaining pieces of RNA get entangled or does the decomposition of dark RNA to unentangled pieces have some meaning? Note that also ordinary RNA would be entangled or entangled. Could introns provide the means for decomposing the coding RNA to unentangled pieces.

3. The most natural possibility is that entanglement contains superposition of codon sequences in which each sequence codes for the same AA. The chemical codons appearing in the superposition have different masses and chemical properties but in zero energy ontology (ZEO)

this is possible. Situation would be like for a superconductor in which coherent state means superposition of states with different numbers of Cooper pairs and thus different fermion number in standard ontology but in ZEO this problem disappears.

Why one must have $k = 151$ for dark DNA

It was already found that for prime values of k the options $k < 149$ are not possible for dark DNA since ordinary DNA should coil around dark DNA. There is also second objection against prime $k < 149$ from energetics inspiring the hypothesis DNA corresponds to $k = 151$.

1. The scaling of the dark nuclear binding energy $E_b \sim 7$ MeV per nucleon as $L(107)/L(k)$ predicts very high binding energies for primes $k < 149$. For instance, $k = 139$ would correspond to the scaled binding energy $E_b(139) = E_b L(107)/L(139)$, $E_b \sim 7$ MeV, which is typical nuclear binding energy. This gives $E_b(139) = E_b/2^{(139-107)/2} = .14$ keV. For $k = 139$ the typical nuclear excitation energy $E_{ex} = 1$ MeV scales dow to 20 eV, which is still very high but could correspond to energies of atomic transitions. For $k = 151$ it E_b scales down to 3.5 eV. The typical dark excitation energy for $k = 151$ is $E_{ex}(151) = .5$ eV and the identification as a nominal value of metabolic energy quantum is attractive. Dark nuclear physics might therefore control biochemistry using dark nuclear transitions as a tool to provide desire energy currency.

2. The TGD based explanation of Pollack effect provides a consistency test for the idea [L15] [L15]. In Pollack effect IR light (besides either kinds of energy feeds) induces the formation of negative charged exclusion zones (EZs) in water bounded by gel phase. In TGD based model this would correspond to the formation of dark proton sequences at magnetic flux tubes. The scale of dark nuclear binding energy would be most naturally in eV scale. The binding energy scale of hydrogen atoms in water molecules is about 5 eV which suggests that the binding energy scale for dark protons sequences is smaller since otherwise energy would be liberated. This would suggest $k = 149$ as will be found.

3. One can imagine that an external perturbation induces

   (a) a transition in which the proton bound to water molecule transforms to its dark variant in higher energy state or

   (b) that the proton goes over a potential wall, whose height is measured in eV:s.

   If the dark nuclear binding energy is higher than the binding energy of proton in water molecule, the process should liberate energy and could occur spontaneously unless high potential wall prevents it. Hence the first option seems the only realistic one. Note that one could consider the cancellation of dark nuclear binding energy and repulsive Coulomb energy which scale in the same manner as function of p-adic length scale so that still the net energy would scale increase in shorter p-adic length scales.

Pollack effect suggests that if k is prime, one must have $k = 149$ for dark proton sequences formed in Pollack effect.

1. For $k = 149$ one has $E_b(151) \sim E_b/2^{(149-107)/2} = 3.5$ eV for $E_b = 7$ MeV, which is in UV range slightly above the visible range. The binding energy of hydrogen atom in water is about 5 eV which would require the incoming radiation to have energy 1.5 eV which is indeed in IR range. This option looks therefore realistic.

2. For $k = 151$ one would have $E_b(151) \sim 7MeV/2^{(151-107)/2} = 1.75$ eV, which just above the IR energy range. Now the energy needed to transform ordinary protons to dark protons in Pollack effect would be in UV range so that this options seems to be excluded.

This argument suggests that dark proton sequences generated in Pollack effect are analogs of single DNA strand, which would naturally correspond to $L(149) = L(151)/2$. Also RNA would naturally correspond to this scale.

1. $L(151) \simeq 10$ nm is the thickness of coiled DNA double strand. The size scale of dark nucleons would be $L(151)$ and the dark DNA strand should be horizontally scaled variant of ordinary DNA strand by a scaling factor $\lambda \sim L(151)/.33$ nm $= 30$. DNA double strand would be obtained by a transversal scaling from the ordinary DNA double strand.

2. The higher coilings of DNA could correspond to higher horizontally scaled variants of DNA corresponding to $k = 157, 163, 167$. $k = 167$ would correspond to nuclear membrane length scale of 2.5 μm. The emergence of nuclear membrane in $k = 151$ length scale would have been accompanied by the emergence of dark DNA in this scale. Cell membrane could correspond to $k = 173$ and p-adic length scale 17.6 μm. Neurons have size varying from 4-100 micrometers (the definition of size depends on whether one includes axons) and might correspond to $k = 179, 181$ and length scales of .16 mm and perhaps even .32 mm.

The only justification for this speculative picture is that it is consistent with the other basic ideas about TGD inspired quantum biology.

1. Cisse et al [I74] found that RNA II polymerase molecules cluster during transcription and their dynamics involves multiples of the time scale $\tau = 5$ seconds. Comorosan reported long time ago that just these time scales are universal bio-catalysis [I134]. The TGD inspired model [L40] for the findings of Cisse et al allows to sharpen the TGD based view about quantum biology considerably.

2. The basic parameter of the model is the value of gravitational Planck constant $\hbar_{gr} = GM_D m/v_0$ assigned to magnetic flux tubes mediating gravitational interactions. Already earlier work gives estimates for the value M_D of dark mass and velocity parameter v_0 and the model leads to the same estimates. The identification of the values of τ as Josephson periods assuming the potential difference V along flux tubes connecting reacting molecules is universal and same as over neuronal membrane fixed the value of h_{gr}. The value of V along flux tube serving as Josephson junction would be universal and equal to membrane potential. Josephson radiation would have energies coming as multiples ot ZeV just above the thermal energy at physiological temperatures fixed by the membrane potential.

3. The model forces the conclusion that the endogenous magnetic field B_{end} has at its upper bound $B_{end} = .2$ Gauss deduced from the findings of Blackman about effects of ELF em fields on vertebrate brain [J8]. The earlier ad hoc hypothesis was that $B_{end} = .2$ Gauss is minimum value of B_{end}. Furthermore, for the required value of h_{gr} $B_{end} = .2$ Gauss corresponds to dark cyclotron energy of .12 keV, which is surprisingly large energy at the upper end of UV band: the earlier intuitive guess was that energy scale is in visible range.

   Also harmonics of cyclotron frequencies were found to have effects so that really large energy scales are involved with the interaction of ELF radiation and one can ask whether this picture really makes sense. This raises a question about the mechanism of the interaction of ELF em radiation with living matter. One also wonder why the ELF radiation has effects on both behavior and physiology.

   Assume

   (a) that dark photons with energies coming as multiples of .12 keV are in question,

   (b) that these dark photons excite dark cyclotron states in the cellular length scale deduced from flux quantization and

   (c) that the dark cyclotron photons radiated as the excited cyclotron states return to the ground states perform some control action on ordinary DNA coil - this is in accordance with the basic vision about the role of magnetic body.

   X rays have energy range varying from 100 eV to 100 keV and wavelengths varying from 10 nm to .01 nm. The wavelength of an ordinary photon resulting from dark photon with energy of .12 keV would be of order 10 nm, the radius of DNA coil for $k = 151$!

   Could this energy induce an analog of standing em wave in transversal degrees of freedom of DNA perhaps transformable to many phonon state with very large number of photos and

thus classical acoustic wave? This would allow to understand how cyclotron harmonics can have non-trivial effects. The effects of ELF radiation on behavior and physiology could be understood as gene expression induced by the irradiation.

Both dark cyclotron radiation and radiation generated in dark nuclear transitions could have biological effects

1. Can one relate energy scale of .12 keV associated with dark cyclotron radiation to atomic physics? The ionization energies behave as Z_{eff}^2/n^2, where Z_{eff} is nuclear charge minus the charge of the closed shells. Z_{eff} is also reduced by electronic screening by other valence electrons. The binding energies of valence electrons decrease with the principal quantum number n so that only $n = 2$ row of the periodic table might allow so high ionization energies for valence electrons.

   Oxygen is certainly the first candidate to consider. The ionization energy for oxygen is .12 eV from an estimate assuming that the effective nuclear charge is 6 (with the contribution of 2 valence electrons subtracted). The actual value is 68.9 eV: the reduction is due to electron screening. This value is smaller than the estimate estimate for $E_b = .12$ keV and since harmonics of this energy are involved, the interpretation in terms of ionization does not make sense.

2. Not only oxygen but also heavier elements are ionized in living matter and at least to me this has remained more or less a mystery. Could dark photons emitted by dark nuclei of MB perform control by inducing the transitions and even ionization of oxygen and other biologically important atoms. The process could proceed also in opposite direction. The energy scale would correspond to that of nuclear excitations scaled down by the above ratio of p-adic length scales. If the energy scale of ordinary nuclear excitations is taken to be about 1 MeV, the dark energy scale for $k = 127$ assignable to the dark nuclei created in "cold fusion" is keV. For $k = 131$ the scale would be 250 eV and above the ionization energy scales for valence electrons. For $k = 137$ the scale would be 17 keV. These dark nuclear transitions could generate dark photons inducing transitions of atoms and even ionizations.

11.2.2 What about dark variants of RNA, tRNA, and AAs?

Also RNA and AAs should have dark variants and one should understand their role. Suppose that the integer k characterizing the p-adic length scale is prime. The vision about RNA era preceding DNA era suggests that RNA accompanying dark RNA is at lower level in the evolution, and hence the value of h_{eff} is smaller for dark RNA than for dark DNA. Also the p-adic length scale for RNA would be shorter.

1. The most natural option is that RNA corresponds to $k = 149$ as also single DNA strand. This would conform with the above suggestion that the Pollack effect generates $k = 149$ dark proton sequence (dark RNA?). DNA double strand would correspond to $k = 151$.

   The emergence of $k = 151$ level would mean the emergence of structures with scale characterized by $L(151)$. This includes DNA double strand forming a coil with thickness $L(151)$ and nuclear and cell membranes. During RNA era these structures would have been absent.Both DNA double strand and cell membrane have binary structures. Therefore single DNA strand and lipid layer could correspond to $k = 149$. In transcription DNA opens and double strand becomes pair of strands having naturally $k = 149$. Therefore mRNA should have also $k = 149$.

2. If AAs correspond to $k = 149$ then also tRNA should correspond to $k = 149$. On the other hand, tRNA does not form strands and should be more elementary structure than RNA. Could tRNA corresponds to $k = 139$ or $k = 137$? This would require that also the attached AA would correspond to $k = 139$ or $k = 137$, which does not look plausible.

   Remark: TGD vision assumes tRNA was present already at RNA era and the role of AA in tRNA was to catalyze RNA replication. In fact, RNA could have been just tRNA at very early stages.

What about AAs? The following arguments suggest that one has $k = 149$ for both AAs and RNA.

1. For dark AAs one can imagine p-adic evolutionary hierarchy analogous to that for DNA. In TGD inspired vision AA sequences emerged together with DNA. Proteins can appear also as coils. Since mRNA pairs with single DNA strand and AAs with mRNA, it seems that AAs should correspond to $k \geq 149$?

2. One could however argue that AAs are building bricks rather than information molecules and k could be rather small for dark AAs. Dark AAs should pair with proteins. Pairing without coiling is possible only if the length per letter is same as the length per AA and thus same as for DNA letter, which is longer than the length taken by $k = 139$ dark proton. Also this suggests $k = 149$ for dark AAs and their coiling around the ordinary AAs.

11.2.3 Clustering of RNA polymerase molecules and Comorosan effect

Once again I had good luck: I received a link (see `http://tinyurl.com/y7bego83`) to a highly interesting popular article telling about the work by Ibrahim Cisse at MIT and his colleagues [I74] (see `http://tinyurl.com/y9wzt5yl`) about the clustering of RNA polymerase proteins in the transcription of RNA. Similar clustering has been observed already earlier and interpreted as a phase separation giving rise to protein droplets [L47]. Now this interpretation is not proposed by experiments but they say that it is quite possible but they cannot prove it.

I have already earlier discussed the coalescence of proteins into droplets as this kind of process in TGD framework [K75] [L47]. The basic TGD based ideas is that proteins - and biomolecules in general - are connected by flux tubes characterized by the value of Planck constant $h_{eff} = n \times h_0$ for the dark particles at the flux tube. The higher the value of n is the larger the energy of given state. For instance, the binding energies of atoms decrease like $1/n^2$. Therefore the formation of the molecular cluster liberates energy usable as metabolic energy.

Remark: h_0 is the minimal value of h_{eff}. The best guess is that ordinary Planck constant equals to $h = 6h_0$ [L23, L42] (see `http://tinyurl.com/goruuzm` and `http://tinyurl.com/y9jxyjns`.

TGD view about the findings

Gene control switches - such as RNA II polymerases in DNA transcription to RNA - are found to form clusters called super-enhancers. Also so called Mediator proteins form clusters. In both cases the number of members is in the range 200-400. The clusters are stable but individual molecules spend very brief time in them. Clusters have average lifetime of $5.1 \pm .4$ seconds.

Why the clustering should take place? Why large number of these proteins are present although single one would be enough in the standard picture. In TGD framework one can imagine several explanations. One can imagine at least following reasons.

1. If the initiation of transcription is quantum process involving state function reduction, clustering could allow to make this process process deterministic at the level of single gene in spite of the non-determinism of state function reduction. Suppose that the initiation of transcription is one particular outcome of state function reduction. If there is only single RNA II polymerase able to make only single trial, the changes to initiate the transcription are low. This could be the case if the protein provides metabolic energy to initiate the process and becomes too "tired" to try again immediately. In nerve pulse transmission there is analogous situation: after the passing of the nerve pulse generation the neuron has dead time period. As a matter of fact, it turns out that the analogy could be much deeper.

   How to achieve the initiation with certainty in this kind of situation? Suppose that the other outcomes do not affect the situation appreciably. If one particular RNA polymerase fails to initiate it, the others can try. If the number of RNA transcriptase molecule is large enough, the transcription is bound to begin eventually! This is much like in fairy tales about princess and suitors trying to kill the dragon to get the hand of princess. Eventually comes the penniless swineherd.

2. If the initiation of transcription requires large amount of metabolic energy then only some minimal number of N of RNA II polymerase molecules might be able to provide it collectively. The collective formed by N molecules could correspond to a formation of magnetic body (MB) with a large value of $h_{eff} = n \times h_0$ and controlling the molecules and inducing its coherent behavior. The molecules would be connected by magnetic flux tubes.

3. If the rate for occurrence is determined by an amplitude which is superposition of amplitudes assignable to individual proteins the the rate is proportional to N^2, N the number of RNA II polymerase molecules. The process for the cluster is reported to to be surprisingly fast as compared to the expectations - something like 20 seconds. The earlier studies have suggests that single RNA polymerase stays at the DNA for minutes to hours.

   Clustering could allow to speed up bio-catalysis besides the mechanism allowing to find molecules to find by a reduction of $h_{eff}/h = n$ for the bonds connecting the reactants and the associated liberation of metabolic energy allowing to kick the reactants over the potential wall hindering the reaction.

Concerning the process of clustering there are two alternative options both relying on the model of liquid phase explaining Maxwell's rule assuming the presence of flux tube bonds in liquid and of water explaining its numerous anomalies in terms of flux tubes which can be also dark (see `http://tinyurl.com/ydhknc2c`).

1. **Option I**: Molecules could form in the initial situation a phase analogous to vapour phase and there would be very few flux tube bonds between them. The phase transition would create liquid phase as flux tube loops assignable to molecules would reconnect form flux tube pairs connecting the molecules to a tensor network giving rise to quantum liquid phase. The larger then value of n, the longer the bonds between molecules would be. This kind of model [L32] (see `http://tinyurl.com/yassnhzb`) is used to explain the strange findings that a system consisting of plastic balls seems to show primitive features of life such as metabolism.

2. **Option II**: The molecules are in the initial state connected by flux tubes and form a kind of liquid phase and the clustering reduces the value of $h_{eff}/h = n$ and therefore the lengths of flux tubes. This would liberate dark energy as metabolic energy going to the initiation of the transcription. One could indeed argue that connectedness in the initial state with large enough value of n is necessary since the protein cluster must have high enough "IQ" to perform intelligent intentional actions.

Protein blobs are said to be drawn together by the "floppy" bits (pieces) of intrinsically disordered proteins. What could this mean in the proposed picture? Disorder would mean absence of correlations between building bricks of floppy parts of the proteins in translational degrees of freedom.

1. Could floppiness correspond to low string tension assignable to long flux loops with large n assignable to the building bricks of "floppy" pieces of protein? Could reconnection for these loops give rise to pairs of flux tubes connecting the proteins in the transition to liquid phase (Option I)? Floppiness would also make possible to scan the environment by flux loops to get in touch with the flux loops of other molecules and in the case of hit (cyclotron resonance) induce reconnection.

2. In spite of floppiness in this sense, one could have quantum correlations between the internal quantum numbers of the building bricks of the floppy pieces. This would also increase the value of n serving as molecular IQ and provide molecule with higher metabolic energy liberated in the catalysis.

About Comorosan effect and clustering of RNA II polymerase proteins

What about the interpretation of the time scales τ equal 5, 10, and 20 seconds appearing in the clustering of RNA II polymerase proteins and Mediator proteins? What is intriguing that so called Comorosan effect [I134, I66] involves time scale of 5 seconds and its multiples claimed by Comorosan long time ago to be universal time scales in biology. The origin of these time

scales has remained more or less a mystery although I have considered several TGD inspired explanations for this time scale is based on the notion of gravitational Planck constant [K59] (see `http://tinyurl.com/yb8fw3kq`).

One can consider several starting point ideas, which need not be mutually exclusive.

1. The time scales τ associated with RNA II polymerase and perhaps more general bio-catalytic systems as Comorosan's claims suggest could correspond to the durations of processes ending with "big" state function reduction. In zero energy ontology (ZEO) there are two kinds of state function reductions [L36]. "Small" state function reductions - analogs of weak measurements - leave the passive boundary of causal diamond (CD) unaffected and thus give rise to self as generalized Zeno effect. The states at the active boundary change by a sequence of unitary time evolutions followed by measurements inducing also time localization of the active boundary of CD but not affecting passive boundary. The size of CD increases and gives rise to flow of time defined as the temporal distance between the tips of CD. Large reductions change the roles of the passive and active boundaries and mean death of self. The process with duration of τ could correspond to a life-time of self assignable to CD.

   Remark: It is not quite clear whether CD can disappear and generated from vacuum. In principle this is possible and the generation of mental images as sub-selves and sub-CDs could correspond to this kind of process.

2. In [K59] I proposed that Josephson junctions are formed between reacting molecules in bio-catalysis. These could correspond to the shortened flux tubes. The difference $E_J = ZeV$ of Coulomb energy of Cooper pair over flux tube defining Josephson junction between molecules would correspond to Josephson frequency $f_J = 2eV/h_{eff}$. If this frequency corresponds to $\tau_J = 5$ seconds, h_{eff} should be rather large since E_J is expected to be above thermal energy at physiological temperature.

   Could Josephson radiation serve as a kind of of synchronizing clock for the state function reductions so that its role would be analogous to that of EEG in case of brain? A more plausible option is that Josephson radiation is a reaction to the presence of cyclotron radiation generated at MB and performing control actions at the biological body (BB) defined in very general sense. In the case of brain dark cyclotron radiation would generate EEG rhythms responsible for control via genome and dark generalized Josephson radiation modulated by nerve pulse patterns would mediate sensory input to the MB at EEG frequencies.

   A good guess motivated by the proposed universality of the Comorosan periods is that the energy in question does not depend on the catalytic system and corresponds to Josephson energy for protein through cell membrane acting as Josephson junction and giving to ionic channel or pump. The flux tubes themselves have universal properties.

3. The hypothesis $\hbar_{eff} = \hbar_{gr} = GMm/\beta_0 c$ of Nottale [E5] for the value of gravitational Planck constant [K45, K37, K76, K75] gives large $\hbar$. Here $v_0 = \beta_0 c$ has dimensions of velocity. For dark cyclotron photons this gives large energy $E_c \propto \hbar_{gr}$ and for dark Josephson photons small frequency $f_J \propto 1/h_{gr}$. Josephson time scale τ_f would be proportional to the mass m of the charged particle and therefore to mass number A of ion involved: $f_J \propto A$ possibly explaining the appearance of multiples of 5 second time scale. Cyclotron time scale does not depend on the mass of the charged particle at all and now sub-harmonics of τ_c are natural.

The time scales assignable to CD or the lifetime-time of self in question could correspond to either cyclotron of Josephson time scale τ.

1. If one requires that the multiplies of the time scale 5 seconds are possible, Josephson radiation is favoured since the Josephson time scale proportional to $h_{gr} \propto m \propto A$, A mass number of ion.

   The problem is that the values $A = 2, 3, 4, 5$ are not plausible for ordinary nuclei in living matter. Dark nuclei at magnetic flux tubes consisting of dark proton sequences could however have arbitrary number of dark protons and if dark nuclei appear at flux tubes defining Josephson junctions, one would have the desired hierarchy.

2. Although cyclotron frequencies do not have sub-harmonics naturally, MB could adapt to the situation by changing the thickness of its flux tubes and by flux conservation the magnetic field strength to which f_c is proportional to. This would allow MB to produce cyclotron radiation with the same frequency as Josephson radiation and MB and BB would be in resonant coupling.

Consider now the model quantitatively.

1. For $\hbar_{eff} = \hbar_{gr}$ one has

$$r = \frac{\hbar_{gr}}{\hbar} = \frac{GM_D m}{c\beta_0} = 4.5 \times 10^{14} \times \frac{m}{m_p}\frac{y}{\beta_0} \quad .$$

Here $y = M_D/M_E$ gives the ratio of dark mass M_D to the Earth mass M_E. One can consider 2 favoured values for m corresponding to proton mass m_p and electron mass m_e.

2. $E = h_{eff} f$ gives the concrete relationship $f = (E/eV) \times 2.4 \times 10^{14} \times (h/h_{eff})$ Hz between frequencies and energies. This gives

$$x = \frac{E}{eV} = 0.4 \times r \times \frac{f}{10^{14} Hz} \quad .$$

3. If the cyclotron frequency $f_c = 300$ Hz of proton for $B_{end} = .2$ Gauss corresponds to bio-photon energy of x eV, one obtains the condition

$$r = \frac{GM_D m_p}{\hbar\beta_0} \simeq .83 \times 10^{12} x \quad .$$

Note that the cyclotron energy does not depend on the mass of the charged particle. One obtains for the relation between Josephson energy and Josephson frequency the condition

$$x = \frac{E_J}{eV} = 0.4 \times .83 \times 10^{-2} \times \frac{m}{m_p} \times x\frac{f_J}{Hz} \quad , \quad E_J = ZeV \quad .$$

One should not confuse eV in ZeV with unit of energy. Note also that the value of Josephson energy does not depend on h_{eff} so that there is no actual mass dependence involved.

For proton one would give a hierarchy of time scales as A-multiples of $\tau(p)$ and is therefore more natural so that it is natural to consider this case first.

1. For $f_J = .2$ Hz corresponding to the Comorosan time scale of $\tau = 5$ seconds this would give $ZeV = .66x$ meV. This is above thermal energy $E_{th} = T = 27.5$ meV at $T = 25$ Celsius for $x > 42$. For *ordinary* photon ($h_{eff} = h$) proton cyclotron frequency $f_c(p)$ would correspond for $x > 42$ to EUV energy $E > 42$ eV and to wavelength of $\lambda < 31$ nm.

The energy scale of Josephson junctions formed by proteins through cell membrane of thickness $L(151) = 10$ nm is slightly above thermal energy, which suggests $x \simeq 120$ allowing to identify $L(151) = 10$ nm as the length scale of the flux tube portion connecting the reactants. This would give $E \simeq 120$ eV - the upper bound of EUV range. For $x = 120$ one would have $GM_E m_p y/v_0 \simeq 10^{14}$ requiring $\beta_0/y \simeq 2.2$. The earlier estimates [K75] for the mass M_D give $y \sim 2 \times 10^{-4}$ giving $\beta_0 \sim 4.4 \times 10^{-4}$. This is rather near to $\beta_0 = 2^{-11} \sim m_e/m_p$ obtained also in the model for the orbits of inner planets as Bohr orbits.

For ion with mass number A this would predict $\tau_A = A \times \tau_p = A \times 5$ seconds so that also multiples of the 5 second time scale would appear. These multiples were indeed found by Comoran and appear also in the case of RNA II polymerase.

2. For proton one would thus have 2 biological extremes - EUV energy scale associated with cyclotron radiation and thermal energy scale assignable to Josephson radiation. Both would be assignable to dark photons with $h_{eff} = h_{gr}$ with very long wavelength. Dark and ordinary photons of both kind would be able to transform to each other meaning a coupling between very long lengths scales assignable to MB and short wavelengths/time scales assignable to BB.

   The energy scale of dark Josephson photons would be that assignable with Josephson junctions of length 10 nm with long wavelengths and energies slightly above E_{th} at physiological temperature. The EUV energy scale would be 120 eV for dark cyclotron photons of highest energy would be fixed by flux tube length of 10 nm.

   For lower cyclotron energies forced by the presence of bio-photons in the range containing visible [K65, K66] and UV and obtained for B_{end} below .2 Gauss, the Josephson photons would have energies below E_{th}. That the possible values of B_{end} are below the nominal value $B_{end} = .2$ Gauss deduced from the experiments of Blackman [J8] does not conform with the earlier ad hoc assumption that B_{end} represents lower bound. This does not change the earlier conclusions.

   Could the 120 eV energy scale have some physical meaning in TGD framework? The corresponding wavelength for ordinary photons corresponds to the scale $L(151) = 10$ nm which correspond to the thickness of DNA double strand. Dark DNA having dark proton triplets as codons could correspond to either $k = 149$ or $k = 151$. The energetics of Pollack effect suggests that $k = 149$ is realized in water even during prebiotic period [L38] (see `http://tinyurl.com/yalny39x`). In the effect discovered by Blackman the ELF photons would transform dark cyclotron photons having $h_{eff} = h_{gr}$ and energy about .12 keV. They would induce cyclotron transitions at flux tubes of B_{end} with thickness of order cell size scale. These states would decay back to previous states and the dark photons transformed to ordinary photons absorbed by ordinary DNA with coil structure with thickness of 10 nm. Kind of standing waves would be formed. These waves could transform to acoustic waves and induce the observed effects. Quite generally, dark cyclotron photons would control the dynamics of ordinary DNA by this mechanism.

   It is natural to assume that $B_{end} = .2$ Gauss corresponds to the upper bound for B_{end} since magnetic fields are expected to weaken farther from the Earth's surface: weakening could correspond to thickening of flux tubes reducing the field intensity by flux conservation. The model for hearing [K43] requires cyclotron frequencies considerably above proton's cyclotron frequency in $B_{end} = .2$ Gauss. This requires that audible frequencies are mapped to electron's cyclotron frequency having upper bound $f_c(e) = (m_p/m_e)f_c(p) \simeq 6 \times 10^5$ Hz. This frequency is indeed above the range of audible frequencies even for bats.

For electron one has $h_{gr}(e) = (m_e/mp) \times h_{gr}(p) \simeq 5.3 \times 10^{-4} h_{gr}(p)$, $\hbar_{gr}(p)/\hbar = 4.5 \times 10^{14}/\beta_0$. Since Josephson energy remains invariant, the Josephson time scales up from $\tau(p) = 5$ seconds to $\tau(e) = (m_e/m_p)\tau(p) \simeq 2.5$ milliseconds, which is the time scale assignable to nerve pulses [K44, K15].

To sum up, the model suggests that the idealization of flux tubes as kind of universal Josephson junctions. The model is consistent with bio-photon hypothesis. The constraints on $h_{gr} = GM_D m/v_0$ are consistent with the earlier views and allows to assign Comorosan time scale 5 seconds to proton and nerve pulse time scale to electron as Josephson time scales. This inspires the question whether the dynamics of bio-catalysis and nerve pulse generation be seen as scaled variants of each other at quantum level? This would not be surprising if MB controls the dynamics. The earlier assumption that $B_{end} = 0.2$ Gauss is minimal value for B_{end} must be replaced with the assumption that it is maximal value of B_{end}.

11.3 TGD view about the emergence of chemical life

Consider first the basic assumptions.

1. Dark DNA, RNA,... emerged before chemistry and serve as templates for ordinary DNA,

RNA,... The replication, transcription, and translation for ordinary DNA, RNA,... are induced by the corresponding processes for their dark counterparts.

2. Dark proton sequences are associated with tubular EZs in water generated by Pollack effect.

3. The amount of entanglement measured by entanglement negentropy (having a well-defined meaning in adelic physics [L34]) is expected to increase gradually during evolution. Hence one expects generation of more and more entangled sequences of dark nucleons. At the bottom - perhaps ordinary nuclear physics - one would have the product states of dark nucleons. Perhaps dark nuclear physics with $n = 2^{11}$ came next. After that came $n = 2^{18}$ dark nuclear physics. But which came first: dark variants amino-acids, tRNA, RNA, or DNA and their chemical counterparts? And could one see even genes as entangled codon sequences coding for the same protein?

11.3.1 The quantum vision about the prebiotic evolution

The following vision about quantal prebiotic evolution beginning from amino-acids suggests itself. The basic idea is that all processes took place at dark level and induced the processes for ordinary biomolecules in water environment. Even the enzyme and ribozyme actions essential in recent biology would be replaced with corresponding actions at dark level and biochemistry would reduce to shadow dynamics.

1. Amino-acids are easiest to produce (as Miller-Urey experiment demonstrated (see `http://tinyurl.com/4q2arv`)) requiring no enzymatic action and there is just single chemical amino-acid per dark RNAs coding for it. Therefore the pairs of amino-acids and their dark variants could have emerged first. Note that proteins were not yet present.

   Remark: Vivo-vitro difference could mean that dark partner of biomolecule is present in vivo and missing in vitro.

2. DNA requires cell membrane. This requires RNA emerged after amino-acids. This implies that dark variants of dark tRNA, their pairing with tRNA and the pairing of dark RNA with RNA emerged next?

   This picture supports that the old TGD inspired idea about the role of tRNA during RNA era. Dark tRNA would have made possible the replication of dark RNA sequences (rather than the translation of RNA to amino-acid sequence) during this era. The dark amino-acid of dark tRNA would have served as a catalyst inducing the addition of dark RNA codon to the growing RNA sequence. No chemical transcription machinery nor DNA was needed at this stage. This would solve one hen-or-egg problem.

3. After that a revolution would have occurred. For some reason dark amino-acids began to attach to the growing sequence of amino-acids and dark RNA codon was left alone. What prevented dark RNA codon to attach to the growing dark RNA sequence? Was it the emerging entanglement between dark codons giving rise to genes as entangled pieces of DNA that made this impossible.

   This means entanglement also between the ordinary codons, which makes sense only in ZEO. If possible at all this entanglement should respect genetic code so that entangled superposition would involve only codons coding for the same amino-acid so that the translation to a single amino-acid sequence rather than their quantum superposition is possible. If more general superpositions are allowed the translation process would be like state function reduction to amino-acid sequence.

4. At this step the replication of both dark and ordinary RNA was lost and it seems that dark DNA-DNA pairs replicating dark DNA and transcribing it to dark RNA and inducing corresponding process at the level of chemistry must have emerged at the same time.

   The emergence of DNA requires also the emergence of cell membrane. Could the emergence of cell membrane relate to the emergence of dark nuclei in the p-adic length scale $L(k)$, $k = 149$ and could the double layered structure of cell membrane serve as an analog for that of DNA double strand? Could lipid layers correspond to 2-D analogs of DNA strand with lipids taking the role of codons?

5. Could the full genetic code emerged in step-wise manner as proposed earlier [K17, K53]? Genetic code can be seen in a good approximation as a fusion of 16-letter code and 4-letter code. This might be understood if the entanglement of dark codons emerges first as entanglement of only two first letters.

What gave rise to the correspondences between dark DNA, RNA, tRNA, amino-acids and their dark variants? How the amino-acids and nucleotide bases were selected?

1. The basic principle would be the condition that metabolic energy can be transferred between chemical and dark levels. This is possible if there identical transition energies in the spectra of biomolecules and their dark variants making possible resonance.

2. Metabolic energy quantum in the range .4-.5 eV should correspond to the excitation energy scale of dark dark nuclear physics if $E_{ex} = 1$ MeV is taken as the estimate for a typical nuclear excitation energy. Hydrogen bonds also correspond to this energy scale but this might be just what is needed to give rise to coherent metabolic activity.

   The original proposal was that dark DNA associated with ordinary DNA corresponds to $k = 141$ assignable to the ordinary DNA but this proposal predicts $E_{ex}(141) = 16$ eV. This proposal turned out to be unrealistic also in other respects. $k = 149$ assignable to dark RNA predicts $E_{ex}(149) = .5$ eV and is a more plausible option in many other aspects. Also lower values of k than $k = 149, 151$ might be present - at least during the prebiotic stage. Pollack's findings however support the view that the irradiation of water with IR light generates dark proton sequences with $k = 149$. Does this mean that the evolutionary level of water is raised to $k = 151$ in presence of gel phase binding the water sample? Note that "cold fusion" [L17, L29] might be interpreted as creation of $k = 127$ dark proton sequences.

To sum up: for DNA,RNA, and tRNA the emergence of entanglement would have created the chemical counterparts of quantum superpositions: ZEO is necessary since in positive energy ontology superpositions are highly implausible.

There are some questions to ponder.

1. Why the decomposition into triplets? Does resonance condition for the metabolic energy transfer select triplets as basic units and also the RNA-amino-acid correspondence? Do also intronic regions have triplets as basic units?

   One ends up to a prediction of vertebrate genetic code also from a model of music harmony [L12]. In fact, the model explains also its slight variation and the 2 additional amino-acids. Could this help to understand why the triplet code is so unique.

2. Could one imagine that also quarks and antiquarks were involved? Could dark nucleon pair with dark quark with same spin and isospin and color confinement forces dark proton triplets? Dark quarks indeed define a representation for A,T,C, G. In the model of topological computation [K17, K53]. I have actually speculated with the possibility that dark quarks and antiquarks are paired with ordinary DNA codons.

3. Could dark conjugate protons or their triplets of parallel dark DNA strands form Cooper pairs or does pairing of dark protons triplets (their conjugates) with dark quarks (anti-quarks) give rise to bosonic states?

11.3.2 Unidentified Infrared Bands as a test for the proposal

Unidentified Infrared Bands (UIBs) are an ill-understood phenomenon associated with radiation coming from interstellar space. There are also other analogous phenomena having no explanation in terms of molecular transitions [**?**] and one can ask whether they could be seen as signatures of dark nuclear physics.

1. UIBs are observed around bands around IR energies $E \in \{.11, .20, .375\}$ eV.

2. Poly-aromatic hydrocarbons (PAHs) (see `http://tinyurl.com/atx4t9a`) are known to generate UIBs [**?**]. Therefore the UIBs from interstellar space could originate from PAHs.

TGD based models for UIBs

TGD suggests several explanations for UIBs involving new physics related to the p-adic length scale hypothesis and $h_{eff}/h = n$ hierarchy.

1. For years ago I discussed a model for UIBs based on p-adic length scale hypothesis [**?**]. The idea was that protons "drop" from atomic space-time sheet with $k = 137$ to a larger space-time sheet to $k_1 > 137$ space-time sheet and the difference of zero point kinetic energies is liberated as radiation [**?**]. The proposal was that the zero point kinetic energies give rise to a hierarchy of metabolic energy quanta.

   Second possibility is phase transition in which the size of the $k = 137$ space-time sheet increases to $k_1 > 137$ and liberates the difference of zero point kinetic energy. For the third option energy preserving phase transition increasing $h_{eff}/h = n$ by a factor $(k_1 - k)/2$ followed by a phase transition reducing the value of h_{eff} back to the initial one but without change of the size of the space-time sheet would liberate the difference of zero point kinetic energies.

2. Could dark nuclear transitions explain UIBs? For $k = 149$ as the p-adic length scale of DNA letters would give nuclear energy scale $E = .5$ eV equal to the metabolic energy quantum by scaling 1 MeV for the ordinary nuclei by factor $2^{149-107}/2 = 2^{21}$ (here the original version of text contained error: this claim was made for $k = 141$). This energy has correct order of magnitude but is too high an energy for UIBs but there are of course also smaller energies possible for the nuclear excitations possibly explaining the UIBs.

3. What about hydrogen bonds? The strength of hydrogen bond - essentially the bond energy - is in the range .4-.5 eV -, which as such does not correspond to the average UIB energy, which come approximately as three lowest powers of two. The range of bond energies is .1 eV is smaller than the smallest UIB energy .11 eV.

   UIBs can be associated with hydrogen bonds if there are states of bond with higher bond energy. They could correspond to higher values of $n = h_{eff}/h$ for the de-localized dark proton associated with the bond (analogous to de-localized valence electron). For instance, if the energy of the bond corresponds to the cyclotron energy of proton in a magnetic field associated with the bond, it is proportional to n.

   The photon energies come approximately as powers of 2. If the favored values of n are in bands around $n = 2^k$ favored by the p-adic length scale hypothesis, one has hopes of understanding the band structure in terms of transitions reducing the value of k.

Membrane potential (see `http://tinyurl.com/chylvs9`) plays a key role in metabolism and one can wonder whether UIBs might relate to the potential energies defining energies $E_J = ZeV$ of Josephson photons associated with membrane if it acts like Josephson junction like structures associated with the prebiotic lifeforms.

1. Membrane potential energy varies in the range (.04, .08) eV (cell interior is negatively charged). Excitable cells (able to generate action potentials) include neurons, muscle cells, endocrine cells, and some plant cells. The average value for them is around .06 eV and further depolarization makes these cell more excitable. This suggests that the instability is caused by thermal radiation with nearly the same energy. The threshold for the generation of the action potential E_{act} is in the range $(.050, .055)$ eV. Interestingly, during ageing neurons become more hyperpolarized and therefore less excitable. In photoreceptors the resting potential energy can be as low as .03 eV making them very sensitive to light.

2. In TGD inspired quantum biology axonal membrane can be seen as a generalized Josephson junction [K41, K42, K44] decomposing nanoscopically to Josephson junctions defined by cell membrane proteins. The protein as junction would correspond to a magnetic flux tube along which various charged particles with $h_{eff} = n \times h$ flow possibly as supra currents. As a special case cell membrane acts like an ordinary Josephson junction. In this case the increment of the electrostatic energy of the Cooper pair over membrane given by $E_J = 2eV$ defines the energy of the smallest quantum of Josephson radiation.

The intensity of thermal radiation at temperature T as function of photon energy Ehas a peak at $E \simeq 3T$, which for room temperature about $T = .03$ eV gives $E_{max} = .09$ eV. The energy ZeV of Cooper pair should be larger than E_{max}. For critical action potential one has $E_{act} = 0.1$ eV, which is slightly above $E_{max} = .09$ eV so that the action potential has minimal value and thus minimizes metabolic energy costs and implies quantum criticality with temperature as a critical parameter.

Note however that for energies below E_{max} the intensity of thermal radiation decreases so that also these energies might serve as Josephson energies: this and the fact that incoming photons have intensity higher than termal background at this energy could explain why some photoreceptors can have $eV = .03$ eV.

3. Could also Josephson radiation relate to UIBs? The Josephson energy of Cooper pair for the membrane potential is around $E_J = 0.1$ eV, which corresponds to the lowest UIB band, which could thus correspond to action potential .05 eV of excitable membrane. The higher bands would correspond roughly to two octaves suggesting that the action potentials in these case are roughly .1 eV and .2 eV. Quantum criticality would suggest that temperatures scale like the energies of the bands slightly higher than $E_{max} \simeq 3T$.

Metabolic energy transfer between magnetic body and biological body (defined in very general sense for any system) is possible if the spectra of transition energies share common transition energies. Therefore the spectrum of transition energies assignable to hydrogen bonds could have many transition energies common with that assignable to dark nuclear transitions and second and third explanation could be consistent with each other.

Model for hydrogen bond

The explanations of UIBs in terms of hydrogen bonds encourages to consider a concrete model for the hydrogen bond as flux tube. This suggests a connection with metabolism at cellular level involving transfer of protons through cell membrane against potential gradient assumed to take place as dark protons carrying the metabolic energy and providing it to ADP-ATP process after their return.

1. The simplest model for the proton inside flux tube is as particle in 1-D flux tube with magnetic field. Unless the magnetic field strength and/or n is very large, the kinetic energy in the direction of flux tube dominates and phase transition would change the scale of kinetic energy proportional to n^2 for fixed flux tube length. For $n = 2^k$ this would give too strong dependence of photon energies on k.

2. On the other hand, if the flux tubes are flux loops of the magnetic body of molecule their lengths naturally scale as n and the longitudinal kinetic energy is not affected in the transition. The cyclotron energy proportional to n would change and for $n \sim 2^k$ one obtains qualitatively correct behavior.

   For proton in magnetic field of $B_{end} = .2$ Gauss the cyclotron frequency is 300 Hz and corresponds to $E_c(B_{end}) = 1.2 \times 10^{-12}$ eV. The identification of $E_c(B) = .5$ eVs would give $E_c(B) = n(B/B_{end}) \times E_c(B_{end}) = E_c(B) = .5$ eV. An estimate for B for the flux tube of hydrogen bond comes from flux quantization: $eBS = 1$ holds true for unit quantum of flux and for flux tube radius of one Angstrom this would give $B/B_{end} \sim 5 \times 10^8$. This gives the estimate $n \sim 10^8 \sim 2^{27}$. The rather large value conforms with the general vision for the values of n for dark protons whereas dark electrons of valence bonds would have much smaller values. The emergence of dark protons could be seen as the transition from chemistry already involving n as characterizer of valence bonds [L31] to bio-chemistry.

3. The identification of the metabolic energy quantum in terms of cyclotron energy could apply also in the case of cellular metabolism. The model for the generation of ATP from ADP assumes that protons are pumped by the energy coming from nutrient molecules against the membrane potential.

   The membrane potential correspond to energy of .05 eV but metabolic energy quantum is 10 times larger. This looks like an inconsistency, which in thermodynamical approach is resolved

by introducing of chemical potentials. In genuine quantum approach the introduction of thermodynamics quantities is not allowed.

The general vision about metabolic energy as a tool to increase $h_{eff}/h = n$ defining kind of molecular IQ suggests that the transformation to dark proton at magnetic flux tube along which proton can travel through the membrane is responsible for the most of the energy needed for pumping. After the dark proton has returned through cell membrane it transforms to ordinary proton and liberates the metabolic energy and makes possible ADP-APT transformation.

The above model assumes that the lengths of hydrogen bonds as flux loops scale like n. This makes possible the reconnection of flux loops coming from opposite sides of the membrane to pair of flux tubes along which dark protons can flow. Similar picture applies also to other biologically important ions.

The general view about superconductivity in TGD Universe [K41, K42] suggests that reconnection can give rise to a Cooper pairs of protons with members at separate flux tubes. Also Cooper pairs of electrons and biologically important ions could form by the same mechanism.

11.3.3 PAH world hypothesis from TGD point of view

The so called PAH world hypothesis (see `http://tinyurl.com/ycxm9zes`) has been proposed as a prebiotic era preceding RNA world. As a matter of fact, PAH world hypothesis inspired more a detailed development of TGD based model for dark nuclei.

Let us first list some properties of poly-aromatic hydrocarbons (PAHs) (see `http://tinyurl.com/atx4t9a`).

1. PAHS consist of aromatic rings glued together along sides. By definition aromatic rings have delocalized electrons. In benzene, which is the classical and simplest example of PAH, the electronic state is quantum superposition of states in which bonds and double bonds alternate along the ring but are shifted by 60 degrees with respect to each other. Naphtalene has two aromatic rings and anthracene and pnenanthtrene have 3 rings.

2. PAHs are very stable non-charged non-polar molecules and are very common in Earth. They are found in coal and tar deposits and produced in an incomplete combustion of organic matter. PAHs are poisonous. For instance, tobacco smoke contains PAHs with carcinogenic effects. The stability of PAHs motivates the belief that a large fraction of carbon in the interstellar space consists of PAHs.

3. Benzene in difficult to detect in in the interstellar space since the rotational symmetry does not allow to detect rotational transitions. Recently however nitrobenzene was detected so that benzene and more complex PAHs presumably exist in interstellar space (see `http://tinyurl.com/yap9ksrg`).

Benzene and more complex PAHs can give rise to more complex aromatic by hydrogenation, oxidation, carboxylation, and nitrogenation and led also to the basic building bricks of DNA and amino-acids and PAHs are proposed to have played important role in prebiotic life.

1. PAH world hypothesis states that the polymer like sequences of PAHs serve as scaffoldings for the formation of RNA like polymers (see `http://tinyurl.com/ycxm9zes`). The key motivation is that the distances between PAHs are same as between RNA and DNA bases: 3.4 nm. The proposal is that during PAH era RNA nucleosides A, U, C, G were attached to PAHs by hydrogen bonds.

2. Second hypothesis is that formaldehyde molecules [(H_2C)=O] formed valence bonds with RNA bases and with each other giving rise to sequences analogous to the phosphate-ribose backbone of RNA. The sequence of disjoint CO=:s was replaced with the sequence ..(C-R)-O-(C-R)-O-.. with R denoting the RNA nucleoside. After this hydrogen bonds were split and the predecessor of RNA was detached from the PAH scaffolding. Later the pre-RNA strands were folded to form double pre-RNA strands similar to ribozymes. The problem is to understand how the formaldehyde backbone was replaces with more stable phosphate-ribose backbone.

In TGD framework dark nuclei would serve as scaffolding, which however does not detach from the corresponding biomolecules. The distances between dark variants of biomolecules would explain why the two distances are the same. Very many molecules, including PAHs, can attach around dark RNA/DNA and the periodic structure would be reflect the properties of dark nuclei. This could explain UIBs as emission bands of both dark nuclei and hydrogen bonds essential for the pairing and the transfer of metabolic energy between ordinary and dark biomolecules. Also in DNA double strand hydrogen bonds could serve similar function. If thermal radiation excites higher energy states of nuclei, the emission of UIBs depends on temperature. Perhaps this could be tested.

UIBs could therefore serve as a direct signature of dark nuclear physics. If dark nuclei are not associated with PAHs in vitro or in an environment not containing water, UIBs would be absent.

11.3.4 Did RNA replicate in codon-wise manner during RNA era?

11.3.5 Did RNA replicate in codon-wise manner during RNA era?

There was an interesting popular article in Spacedaily with title "*Scientists crack how primordial life on Earth might have replicated itself*" (see `http://tinyurl.com/y92ng5vd`). The research paper [I91] is titled "*Ribozyme-catalysed RNA synthesis using triplet building blocks*" and published in eLife (see `http://tinyurl.com/ya5qyjfn`).

It is possible to replicate unfolded RNA strands in Lab by using enzymes known as ribozymes, which are RNA counterparts of enzymes, which are amino-adic sequences. In the presence of folding the replication is however impossible. Since ribozymes are in general folded, they cannot thus catalyze their own replication in this manner. The researchers however discovered that the replication using RNA triplets - genetic codons - as basic unit can be carried out in laboratory even for the folded RNA strands and with rather low error rate. Also the ribozyme involved can thus replicate in codon-wise manner. For units longer than 3 nucleotides the replication becomes prone to errors.

These findings are highly interesting in TGD framework. In TGD the chemical realization of genetic code is not fundamental. Rather, dark matter level would provide the fundamental realizations of analogs of DNA, RNA, tRNA, and amino-acids as dark proton sequences giving rise to dark nuclei at magnetic flux tubes [L38] (see `http://tinyurl.com/yalny39x`). Also ordinary nuclei correspond in TGD Universe to sequences of protons and neutrons forming string like entities assignable to magnetic flux tubes.

The basic unit representing DNA, RNA and tRNA codon and amino-acid would consist of 3 entangled dark protons. The essential aspect is that by entanglement the dark codons do not decompose to products of letters. This is like words of some languages, which do not allow decomposition to letters. This representation is holistic. As we learn to read and write, we learn the more analytic western view about words as letter sequences. Could the same hold true in evolution so that RNA triplets would have come first as entities pairing with dark RNA codons from from dark proton triplets as a whole? Later DNA codons would have emerged and paired with dark DNA codons. Now the coupling would have have been letter by letter in DNA replication and transcription to mRNA.

It is intriguing that tRNA consists of RNA triplets combined from amino-acids and analogs of mRNA triplets! The translation of mRNA to amino-acids having no 3-letter decomposition alone forces the holistic view but one can ask whether something deeper is involved. This might be the case. I have been wondering whether during RNA era RNA replicated using a prebiotic form of translational machinery, which replicated mRNA rather than translated RNA to protein formed from amino-acids (AAs) with AA serving as a catalyst.

1. During RNA era amino-acids associated with pre-tRNA molecules would served as catalysts for replication of RNA codons. The linguistic mode would have been "holistic" during RNA era in accordance with the findings of the above experiments. RNA codon would have been the basic unit.

2. This would have led to a smaller number of RNAs since RNA and RNA like molecules in tRNA are not in 1-1 correspondence. A more realistic option could have been replication of

subset of RNA molecules appearing in tRNA in this manner.

3. Then a great evolutionary leap leading from RNA era to DNA era would have occurred. AA catalyzed replication of RNA would have transformed to a translation of RNA to proteins and the roles of RNA and AA in tRNA would have changed. [Perhaps the increase of h_{eff} in some relevant structure as quantum criticality was reached led to the revolution]

4. At this step also (subset of) DNA and its transcription to (a subset of) mRNA corresponding to tRNA had to emerge to produce mRNA in transcription. In the recent biology DNA replicates and is transcribed nucleotide by nucleotide rather than using codon as a unit so that helicases and DNA and RNA polymerases catalyzing replication and transcription should have emerged at this step. The ability of DNA to unwind with the help of helicase enzyme helping DNA to unwind is essential for the transcription and translation of DNA. Therefore helicase must have emerged together with the "analytic linguistic mode" as an analog of written language (DNA) decomposing codons to triplets of letters. This would been a crucial step in evolution comparable to the emergence of written language based on letters. Also the counterpart of RNA polymerase and separate RNA nucleotides for transcription should have emerged if not already present.

   An alternative option would involve "tDNA" as the analog of tRNA and the emergence of helicase and polymerases later as the transition from holistic to analytic mode took place.

   The minimal picture would be emergence of a subset of DNA codons corresponding to RNAs associated with pre-tRNA and the emergence of the analogs of helicase and DNA and RNA polymerases as the roles of amino-acid and RNA codon in tRNA were changed.

5. How DNA could have emerged from RNA? The chemical change would have been essentially the replacement of ribose with de-oxiribose to get DNA from RNA and U$\rightarrow$ T. Single O-H in ribose was replaced with H. O forms hydrogen bonds with water and this had to change the hydrogen bonding characteristics of RNA.

   If the change of $h_{eff} = n \times h_0$ was involved, could it have led to stabilization of DNA? Did cell membrane emerge and allow to achieve this? I have proposed [L38] (see `http://tinyurl.com/yalny39x`) that the emergence of cell membrane meant the emergence of new representation of dark genetic code based on dark nuclei with larger value of h_{eff}.

   Remark: One has $h = 6 \times h_0$ in the most plausible scenario [L23, L42] (see `http://tinyurl.com/goruuzm` and `http://tinyurl.com/y9jxyjns`).

The communication between dark and ordinary variants of biomolecules involves resonance mechanism and would also involve genetic code represented as 3-chords, music of light, and it is interesting to see whether this model provides additional insights.

1. The proposal is that 3-chords assignable to nucleotides as music of light with allowed 64 chords defining what I have called bio-harmony is essential for the resonance [L43, L46, L42](see `http://tinyurl.com/ydhxen4g`, `http://tinyurl.com/yd5t82gq`, and `http://tinyurl.com/y9jxyjns`). The 3 frequencies must be identical in the resonance: this is like turning 3 knobs in radio. This 3-fold resonance would correspond to the analytic mode. The second mode could be holistic in the sense that it would involve only the sum only the sum of the 3 frequencies modulo octave equivalence assigning a melody to a sequence of 3-chords.

2. The proposal is that amino-acids having no triplet decomposition are holistic and couple to the sum of 3 frequencies assignable to tRNA and mRNA in this manner. Also the RNAs in tRNA could couple to mRNA in this manner. One could perhaps say that tRNA, mRNA and amino-acids codons sing whereas DNA provides the accompaniment proceeding as 3-chords. The couplings of DNA nucleotides to RNA nucleotides would rely on the frequencies assignable to nucleotides.

3. If the sum of any 3 frequencies associated with mRNA codons is not the same except when the codons code for the same amino-acids, the representation of 3-chords with the sum of the notes is faithful. The frequencies to DNA and RNA nucleotides cannot be however independent of codons since the codons differing only by a permutation of letters would

correspond to the same frequency and therefore code for the same amino-acid. Hence the information about the entire codon would be needed also in transcription and translation and could be provided either by dark DNA strand associated with DNA strand or by the interactions between the nucleotides of the DNA codon.

4. The DNA codon itself would know that it is associated with dark codon and the frequencies assignable to nucleotides could be determined by the dark DNA codon. It would be enough that the frequency of the letter depends on its position in the codon so that there would be 3 frequencies for every letter: 12 frequencies altogether.

   What puts bells ringing is that this the number of notes in 12-note scale for which the model of bio-harmony [L12, L43] (see `http://tinyurl.com/yad4tqwl` and `http://tinyurl.com/ydhxen4g`) based on the fusion of icosahedral (12 vertices and 20 triangular faces) and tetrahedral geometries by gluing icosahedron and tetrahedron along one face, provides a model as Hamiltonian cycle and produces genetic code as a by-product. Different Hamiltonian cycles define different harmonies identified as correlates for molecular moods.

   Does each DNA nucleotide respond to 3 different frequencies coding for its position in the codon and do the 4 nucleotides give rise to the 12 notes of 12-note scale? There are many choices for the triplets but a good guess is that the intervals between the notes of triplet are same and that fourth note added to the triplet would be the first one to realize octave equivalence. This gives uniquely $CEG\sharp$, $C\sharp FA$,$DF\sharp B\flat$, and $DG\sharp B$ as the triplets assignable to the nucleotides. The emergence of 12-note scale in this manner would be a new element in the model of bio-harmony.

   There are 4!=24 options for the correspondence between $\{A, T, C, G\}$ as the first letter and $\{C, C\sharp, D, D\sharp\}$. One can reduce this number by a simple argument.

   (a) Letters and their conjugates form pyrimidine-purine pairs T, A and C, G. The square of conjugation is identity transformation. The replacement of note with note defining at distance of half-octave satisfies this condition (half-octave - tritonus - was a cursed interval in ancient music and the sound of ambulance realizes it). Conjugation could correspond to a transformation of 3-chords defined as

   $$CEG\sharp \leftrightarrow DF\sharp B\flat \ , \quad C\sharp FA \leftrightarrow D\sharp GB \ .$$

   (b) One could have

   $$\{T, C\} \leftrightarrow \{CEG\sharp, C\sharp FA\} \ , \quad \{A, G\} \leftrightarrow \{DF\sharp B\flat, D\sharp GB\} \ ,$$
   $$\text{or}$$
   $$\{T, C\} \leftrightarrow \{DF\sharp B\flat, D\sharp GB\} \ , \quad \{A, G\} \leftrightarrow \{CEG\sharp, C\sharp FA\} \ .$$

   .

   (c) One can permute T and C and A and G in these correspondences. This leaves 8 alternative options. Fixing the order of the image of (T, C) to say $(C, C\sharp)$ fixes the order of the image of (A, G) to $(D, D\sharp)$ by the half-octave conjugation. This leaves 4 choices. Given the bio-harmony and having chosen one of these 4 options one could therefore check what given DNA sequence sounds as a sequence of 3-chords [L12].

   That the position the frequency associated with the nucleotide depends on its position in the codon would also reflect the biochemistry of the codon and this kind of dependence would be natural. In particular, different frequencies associated with the first and third codon would reflect the parity breaking defining orientation for DNA.

11.4 Improved reckless speculation about higher level variants of dark genetic code

In an earlier article I represented what I called reckless speculations about higher level variants of genetic code (see [L38] for the updated version of the original article). The speculations turned out

to be not only reckless but to contain besides an unrealistic working hypothesis for p-adic length scale of dark DNA also a numerical error in the estimate of dark nuclear excitation energy scale leading to a wrong track.

The wrong working hypothesis was the assumption that ordinary DNA, RNA, etc correspond to same p-adic length scale as their dark variants. Simple argument shows that the dark scales must result via radial scaling of the typically linear structures such as DNA, RNA, etc and also 2-D structures such as membranes and microtubules giving rise to 2-D lattice like realizations of genetic code generalizing the ordinary 1-D realizations.

Also new improved picture conforms with the vision that dark realizations of genetic code at various p-adic length scales serve as controllers of the ordinary biochemistry, which is kind of shadow dynamics. Replication, certainly one of the most mysterious feats of living matter, would reduce to the replication at the level of dark DNA in various p-adic length scales involved. This would be a huge simplification.

A hierarchy of dark nuclear physics with hierarchy of $n = h_{eff}/h_0 = n$ coming as certain powers of two so that the corresponding length scales correspond to p-adic length scales is an attractive idea. I have speculated with this idea already earlier. A hierarchy of dark nuclear physics with hierarchy of $n = h_{eff}/h = n$ coming as certain powers of two so that the corresponding length scales correspond to p-adic length scales is an attractive idea. I have speculated with this idea already earlier [K27].

11.4.1 Ideas

Consider first the general ideas.

1. The assumption of prime values for k in $L(k)$ would pose extremely tight constraints on the allowed p-adic length scales and values of h_{eff}/h_0. One would have $k \in \{127, 131, 137, 139, 149\}$ and $k \in \{151, 157, 163, 167\}$ and $k \in \{173, ..\}$ at least at the level of dark matter. So predictive an idea deserves to be killed, if not anything else.

   A further motivation for these speculations is that the Gaussian Mersenne primes $M_{G,k=}(1+i)^k - 1$ for $k \in \{151, 157, 163, 167\}$ define p-adic length scale $L(k) \propto 2^{k/2}$ between 10 nm assignable to the neuronal membrane and 2.5 μm assignable to cell nucleus: so many Gaussian Mersenne in so short length scale range is a number theoretical miracle.

2. Cell membrane consisting of two lipid layers (see `http://tinyurl.com/h9a2hsq`) is a binary structure as also DNA double strand. DNAs replicate as would do also RNAs during RNA era. Also cells and therefore also cell membranes replicate so that the analogy might make sense. Since processes like translation and transcription do not occur, cell membrane might serve as 2-D as analog of RNA: the counterpart of RNA era might prevail at these levels. Neuronal membrane might correspond to 2-D analog of DNA.

   So: could various 2-D structures such as nuclear membrane, cell membrane, neuronal membrane, and microtubuli correspond to a new level in the hierarchy of dark codes for which genes and their dark variants would be 2-D rather than 1-D structures? One would have 2-D lattices of codons. Could there be entire hierarchy of them assignable to certain p-adic length scales? As 2-D realizations could be paired with their dark variants so that one could speak of dark variants of various membrane like structures. This applies also to microtubuli.

   The idea that dark variants of DNA, RNA, and AAs are their radially scaled up variants generalizes also. The processes like replication of cell could be induced by a much simpler replication of 2-D dark DNA. This kind of pairing hierarchy could be behind miraculous looking replication of entire organisms. p-Adic fractality and hierarchy of dark DNAs could lurk behind the curtains.

3. The structures of ordinary bio-matter and also their dark variants assumed to control them are characterized by p-adic length scales. How these p-adic length scales could relate? The natural idea inspired by scaling invariance is that the dark variants of 1-D linear structure and 2-D structures formed from ordinary bio-matter are obtained by radial scaling consistent with p-adic length scale hypothesis, and guaranteeing that the distances between building bricks are scaled to the size scales of dark variants of DNA and other basic molecules. This

rule makes sense also for the 2-D structures. For instance, it would scale up the p-adic length scale $L(143)$ characterizing lipid to $L(149)$ assignable to single dark RNA strand or $L(151)$ assignable to dark double DNA strand.

4. One can argue that cell membrane - in particular neuronal membrane - is highly dynamical unlike RNA. In ZEO however dynamical evolutions of space-time surfaces as preferred extremals - correlates for behaviors - replace 3-D static patterns as basic entities so that the emergence of cell membrane might mean dark genetic code for dynamical patterns analogous to deterministic computer programs defining predetermined dynamical patterns. In central nervous system nerve pulse patterns coded by dark RNA could provide similar coding of behavioral patterns.

5. I have claimed in earlier publications that the lipid double layer defining cell membrane has thickness $L_e(151) = 10$ nm: actually the thickness is $L_e(149) = 5$ nm for ordinary cells and 8-10 nm - roughly $L_e(151)$ - only for neuronal membranes. Therefore the emergence of neuronal membranes could be seen as an evolutionary step in p-adic and thus number theoretic sense. Needless to say, this little difference might be absolutely crucial for undestanding why neurons are at higher evolutionary level than ordinary cells. It would be nice if this difference could correspond to an increase of $h_{eff}/h_0 = n$ and p-adic length scale of ordinary and dark membrane like structure by a factor 2.

   There is double cell membrane associated with mitochondria. The thickness of the two double membranes is about 7 nm so that they might correspond to $k = 149$. The double membrane would have roughly the thickness 22 nm. If this structure is a functionally coherent structure it would corresponds to $L_e(153)$ and could be controlled by its dark counterpart.

6. I have proposed that the flux tubes connecting the dark DNA sequences above lipid layer to those associated with DNA could make possible to realize topological quantum computation [K17, K53] in terms of braiding induced by the 2-D liquid flow induced by nerve pulse patterns at nuclear membrane. Flux tubes might be associated with cytoskeleton and define an analog of central nervous system at the level of cell. A rough estimate for the numbers of codons for human DNA of length about 1 m and the number of codons allowed by the surface of the nuclear membrane are of order 10^9 so that the proposal might make sense.

   This proposal generalizes and has many alternative forms. For instance, microtubules inside axons could be connected by flux tubes to the surface of axons.

   One could also consider braidings between ordinary and dark levels, say braiding of flux tubes connecting lipid layers of neuronal membrane to 2-D analog of dark DNA. This braiding would code quantum computer programs and be part of coding of nerve pulse patterns inducing 2-D flow of lipids to memories represented as braidings. Quite generally, the braidings could be very naturally between ordinary and dark variants of structures considered.

11.4.2 Could cell membrane and neuronal membrane realize genetic codons as 2-D structures?

In the sequel I discuss in more quantitative level the idea that cell membrane and neuronal membrane realize analogs of genes as 2-D structures.

The p-adic length scales associated with the dark variants of 2-D structures?

Consider next the p-adic length scales associated with the structures considered.

1. The thickness of ordinary cell membrane corresponds roughly to $L_e(149) = 5$ nm whereas the coiling associated with the cell membrane corresponds to $L_e(151)$. Also neurons correspond to $L_e(151)$. Could $k = 149$ *resp.* $k = 151$ define levels of ordinary cell *resp.* neuron in the hierarchy of dark nuclear physics?

2. Cell membrane consists of lipid bilayer. The lipid layer has three parts (see `http://tinyurl.com/h9a2hsq`).

- The totally hydrated layer nearest to water is hydrophilic head group, which in the case of phospholipids contains negatively charged phosphate. This phosphate layer has thickness $.7 - 1.0$ nm.
- Below it is a partially hydrated layer of thickness .3 nm, which corresponds to $L(141)$: this of course puts bells ringing!
- Hydrophobic lipid tail layer below it is dehydrated. The thickness of single lipid layer is 1.25-1.75 nm and would correspond to the p-adic length scale $L_e(145) = 1.2$ nm. $k = 145$ is not prime.

3. The phosphate layer analogous to phosphate-ribose backbone and the thickness $L(141)$ of partially hydrated layer suggests that it corresponds to EZ created in Pollack effect so that there would be parallel dark RNA sequence along axon (possibly helical as for microtubules). In the case of cell membrane would have lattice like system formed from dark protons, and maybe even dark neutrons (as an analog for the neutron halo in some nuclei).

4. If the recent biology is the analog of RNA era for $k = 149$ codes, their manifestations could be seen as analogs of RNAs and the number of different lipids associated with the cell membrane could give some idea about their number. Cell membrane could perhaps be seen as a 2-D analog of RNA polymer. Cell division implying membrane replication would be induced by dark RNA replication. Even the analogs of tRNA and AAs but not proteins might be present if one takes the analogy very seriously. Could one identify pairs of lipids and some molecules analogous to proteins appearing in cell division?

What kind of general conditions can one pose on the dark variants of DNA, RNA, and AAs?

1. Dark variant of 2-D variants of DNA, RNA, or AAs realizing the hierarchy of dark codes should control their analogues or possibly some other molecules coded by them. The coupling would be by resonance. This suggest the hierarchy of codes uses as building bricks simpler structures by starting from 1-D structures and building from them more complex structures. Hence the natural hypothesis is that the 2-D variants of proteins consisting of a 2-D lattice like structure formed from proteins is in question.

2. The geometric aspect of membrane dynamics would be determined by basic dynamics of TGD determined by action, which is a generalization of charged point-like particle coupling to Maxwell field by replacing the particle orbit with 4-D surfaces. This allows as special case minimal surfaces such as deformations of cosmic strings giving magnetic flux tubes. Cell membranes should correspond to extremals for which coupling to Kähler force is non-trivial as it indeed is by membrane potential. This because static closed surfaces, in particular spherical layers, are not possible as minimal surfaces. Remarkably, these extremals are not analogs of external particles (geodesic lines) but correspond to interaction regions. This conforms with the fact that cell membrane is a self-organization pattern requiring a continual feed of metabolic energy.

   The 2-D dark variants of DNA, RNA, and AAs would be involved mostly with the control the electro-chemistry of membrane like structures. Of course their geometrodynamics would induce also morphogenesis of ordinary bio-matter.

   Also enzymes and ribozymes would have dark variants controlling their behavior. Folded protein represents an interesting example about possibly 3-dimensional graph like structure in which the protein forms an analog of Hamilton's cycle going through all points of the graph defined as a lattice with nearest neighbors connected by edges without self-intersections. This hypothesis is rather powerful since for Hamiltonian cycle do not necessarily exist for an arbitrary graph.

3. In the case of cell membrane membrane proteins are the natural candidate for the building bricks. They indeed have an active role and serve as both channels and pumps and in the case of the neural membrane this role is especially important. Membrane proteins are identified in TGD framework as generalized Josephson junctions. In the case of cell membranes mebrane proteins having length of about 5 nm (5 AAs) or 10 nm (10 AAs) going through the membrane

are an excellent candidate for the basic building brick. One could see the basic structure either as 2-D structure built from membrane proteins or 3-D structure build from AAs. Membrane proteins would form kind of generalized protein as a 2-D lattice of proteins and accompanied by their dark variants or of 2-D dark variants of RNA or DNA coding for them and identifiable as radial scalings of these proteins to $k = 149$ or $k = 151$.

The model for topological quantum computation [K17] suggesting that DNA codons of are connected to lipids of cell membrane could be modified so that that dark DNA, RNA, or AAs associated with membrane proteins are connected to them by flux tubes which can get braided. This would allow the quantum control of the 2-D protein like structure and make it effectively single quantum coherent Josephson junction as suggested in the quantum model for nerve pulse [K44].

The original proposal was that that there might exist an analog of genetic code for lipids. The number of different lipids is however too high to allow any simple correspondence. Lipids have also rather passive role in the dynamics of the cell membrane: their serve as signal pathways, provide metabolic energy, and serve as signal pathways (see `http://tinyurl.com/z7d7osm`). The proposal however deserves to be explained.

1. Both sides of the lipid bilayer of cell membrane could pair with 2-D lattice of dark RNA whose size scale would be obtained by radial scaling giving rise to what might be called dark cell membrane. In the case of neuronal membrane the dark lattice would consist of pairs of dark DNA codon and its conjugate. In the case of axon one could have the analog of dark DNA strand extended to a cylinder containing bundles of these strands at its surface. Lipid layers would be 2-D analogs of 1-D DNA strands in this case.

2. Lipids would be analogs of ordinary RNA codons and dark RNA codons would code for them: this would predict 64 different lipids in cell membrane. Single dark RNA would correspond to the size scale of single lipid given by $L(143) = 2L(141) = .625$ nm. The dark nuclear physics would correspond to $k = 149$. The number N of parallel dark RNA strands would be roughly the circumference of the axonal lipid layer divided by the size of single lipid about $L(143) = .625$ nm given by $N \sim 2\pi \times L_e(167)/L_e(143) = \pi \times 2^{24} \sim 5 \times 10^6$.

Thermodynamical constraints

Could this totally irresponsible speculation about p-adic hierarchy of dark nuclear physics and genetic codes survive thermodynamical constraints?

1. The condition that metabolic energy quantum is not below thermal energy at physiological temperatures poses constrains on the model. I have considered several identifications of the the metabolic energy quantum. These identification need not be mutually exlusive.

   - One interpretation is as 1-D zero point kinetic energy of proton at tubular space-time sheet of atomic size with transversal length scale $L(137)$. This energy is invariant under scalings induce by increase of h_{eff} since h_{eff}^2/L^2 is not changed.
   - Second identification of metabolic quanta would be as energies assignable to hydrogen bond and its dark variants.
   - Third identification of the metabolic energy quantum would be as scaled variant of $E_b(k) = 2^{(k-107)/2}E_b$ of typical dark nuclear binding energy $E_b =\sim 1$ MeV. The value would be about .5 eV for $k = 149$ and .25 eV for $k = 151$.

2. Note that the action potential assignable to $k = 151$ neuronal membrane is around .05 eV (the membrane potential for some photoreceptors is .03 eV). In TGD Universe the cell membrane can be seen as Josephson junction decomposing in an improved resolution to membrane proteins acting as Josephson junctions [K41, K42]. Josephson energy of Cooper pair is twice this - that is $E_J = 0.1$ eV slightly above the maximum $E_{max} = 3T = .09$ eV of the thermal distribution at physiological temperature.

3. As far Josephson radiation are considered, for $k = 151$ membrane would be a quantum critical system. Quantum criticality could give rise to instability making possible the generation of nerve pulses. During nerve pulse the dark protons at the dark space-time sheet would return to the neuronal membrane and destroy the ionic equilibrium. Also the temperature criticality of consciousness manifesting itself as the generation of hallucinations during fever could be understood. For $k = 151$ the situation would be overcritical and will be discussed separately.

The Josephson energy of Cooper pair is scaled down to $E_J = .1$ eV near to $E_{max} = .09$ eV. This is slightly above the thermal energy but one could still argue that Josephson radiation cannot carry information. Or could Nature have found the means to overcome this potential problem? The notion of generalized Josephson junction central in TGD inspired theory of EEG as communications from brain to MB [K44, K15] could save the situation.

1. For the generalized Josephson junction the energy of quantum of Josephson radiation is $E = E_J + \Delta E_c$, where ΔE_c is the difference of cyclotron energies at the two sides of the membrane. E_c is proportional to $h_{eff} = n \times h$ and large enough value of n guarantees that E_c is above $E_{max} \simeq 3T$ irrespective of the value of the membrane potential. The variations of the membrane potential modulate Josephson frequency, and are proposed to provide a coding of sensory data defined by nerve pulse patterns communicated to MB.

2. $h_{eff} = h_{gr} = GMm/v_0$ hypothesis [K76, K75] guarantees the spectrum of cyclotron energies is universal and does not depend on the mass m of the charged particle being in the range of visible and UV energies of photons (this allows to deduce information about the values of mass M and velocity parameter $v_0 < c$): bio-photons would be produced in energy conserving phase transitions transforming dark photons to ordinary ones [K65, K66].

3. If MB itself (a structure which has size scale of Earth at EEG frequencies around 10 Hz) has low enough temperature, this would allow to overcome the limitations caused by the thermal masking of the ordinary Josephson radiation so that the frequency modulations by nerve pulse patterns could code for the sensory data. $h_{eff} = h_{gr} = GMm/v_0$ hypothesis indeed allows very large values of h_{eff} for which ordinary cyclotron energies proportional to h_{eff} would be ridiculously small for the ordinary value of h.

What about the situation for massive particles like proton? Now Maxwell-Boltzmann (Gaussian) distribution is a good approximation and for effectively D-dimensional system the value of distribution is reduced by $1/e$ at thermal energy $E_{cr} = DT/2$. One could argue that above this energy thermal masking can be avoided. For $D = 1$ at magnetic flux tubes this would give $E_{cr} = T/2 = E_{max}/6$. At $T_{phys} = .03$ eV one would have $E_{cr} = 0.15$ eV. Metabolic energy quantum would be above E_{cr} for $k = 151$. Even $k = 153$ possibly assignable to mitochondrial double membrane can be considered but represents an upper bound at physiological temperatures.

Remark: In TGD view about information processing in brain [L28] active linear neuron groups relate to verbal cognition and 2-D neuronal groups relate to the geometric cognition associated with the decomposition of perceptive field to objects. At cellular level DNA and cell membrane could perhaps be seen as counterparts for these structures. In TGD framework neuronal membrane is proposed to be a constructor of sensory representations communicated to the magnetic body (MB) using generalized Josephson radiation whereas motor control by MB has been assumed to take place via DNA [K23].

11.4.3 DNA packing problem and p-adic length scales

DNA manages to pack huge amount of DNA to single cell nucleus. For instance, human DNA as length of about 1 meter. This is achieved by a hierarchical coiling structure involving 3 levels with highest level identifiable as chromatides and the lowest level defined by nucleosomes (see `http://tinyurl.com/yat5cm4y`) wound around histon isomers linked together by straight portions of DNA. One can find a detailed representation of the 4-levelled packing of DNA (see `http://tinyurl.com/ybxv6w4v`).

There are 4 levels involved. Could they relate to the Gaussian miracle primes $k = 151, 157, 163, 167$? The general proposal is that the products of powers of small primes define the scale hierarchy. There

is evidence that at least the powers of 2 and 3 define p-adic length scales, which would correspond also to dark scales. The simple guess is that the dark scales are identical to the ordinary p-adic scales.

- The diameter of the nucleosome is 11 nm $= 1.1L(151)$, which suggests $k = 151$. Chromatosome consists of histone H_1 plus nucleosome.
- Nucleosomes coil to form a fiber of diameter $d = 30$ nm. This scale is $3L(151)$.
- At the next level loops of average length 300 nm $= 30L(151) \sim 32L(151)$. This level is only intermediate level in packing.
- These loops compress and fold to 250 nm $=25L(151) \simeq 3 \times L(157)$, $L(157) = 8L(151)$ wide fiber. Thus third harmonic of also the miracle length scale $L(157)$ would be involved.
- This fiber compresses a tight coil of radius 700 nm $= 70L(151) \simeq 64L(151) = L(163) = 640$ nm giving rise to the chromatid fiber of chromosome. $k = 163$ is the third miracle length scale.
- Chromosomes have width 1400 nm which corresponds to the scale $L(165)$.

The 3 levels $k = 131, 157, 163$ seem to be realized although not in the simplest manner. Nuclear membrane would correspond to $L(k = 167) = 2.5$ μm. For $n = h_{eff}/h_0$ these levels would correspond to the values n of form $n = 2^r 3^s$.

Consider next nucleosome.

1. DNA wraps of around histone octamers forming a cubical structure consisting of 8 smaller cubes (octamers). There are 2×4 histones forming two identical layers. The 4 histones H_{2A}, H_{2B}, H_3, H_4 of given layer are not identical. There is also histone H_1 attached to the entire structure. The incoming DNA double strand enters to the upper end of H_1 and leaves from its lower end. H_1 is related to the secondary coiling. The wrapping gives rise nucleosomes as helices with two turns and containing about 146 base pairs making 48 codons plus 2 base pairs.
2. According to the standard model of nucleosome double DNA strand wraps around the analog of a spool formed from an octamer consisting of two identical units above each other consisting of 4 different histones. The incoming DNA strand enters the upper 4-histone unit and winds once around it and then does the same for the lower unit before leaving the nucleosome.

One can construct a rough TGD inspired model for this structure (not completely realistic) to get a concrete idea about what is involved.

1. The size scale of the cube like structure is $L(151) = 10$ nm so that single histone corresponds to a cube with side roughly about $L(149) = 5$ nm. One can estimate the total length L of the wire from the equation $z = xR\phi/\pi$, $R \sim L(149)$, $\phi \in [0, 4\pi]$, as $L = \sqrt{1 + \pi^{-2}} 4\pi R$. For $R \sim L(149)$ and $h = L(151)$ this gives $L \sim 66$ nm, There are roughly 146 DNA base pairs and 48 whole codons ($144 = 3 \times 48$ base pairs) and each codon has length about 1 nm. This gives total length of 48 nm. The reduction of radius R by factor $r = 48/66 = 3/4$ to $R = 3L(149)/4$ would give a correct value of L

   According to the representation for the hierarchy of packings (see `http://tinyurl.com/ybxv6w4v`), the diameter of the structure is $d = 1.1L(151)$ rather than small and the height of the structure is smaller in the illustration. This width is however not consistent with the helix structure for any value of the height.
2. If the double DNA strand is accompanied by a dark double strand of radius $L(149)$, the situation is like having a band of width $L(151)$ going around the spool. The dark double strand covers an area, which is 4/3 times the spool area. The horizontal thickness of the entire dark structure is about $d_D = (7/4)L(151)$. If the radius of DNA double strand is $r = L(151)$ the area covered by the double strand is roughly twice the area of the spool. This suggests that one should identify the p-adic length scale of DNA double strand as its diameter about $L(151)$ rather than its radius.

Remarks:

1. While trying to understand nucleosomes in TGD framework, I encountered an interesting side result related to Hamiltonian face paths and Hamiltonian cycles on octahedron, which to my best understanding must correspond to Hamiltonian paths and cycles on cube. The octahedral face paths can be identified as closed paths connecting the middle points of the centers of a cube. The 8 histones define a decomposition of the entire cube to 8 sub-cubes. The idea was that that Hamiltonian face cycles in these cubes could give up to tight packing of 6 codons. The number of the Hamiltonian paths for cube is 64 (see `http://tinyurl.com/ybqw6zpt`) and the number of cycles is 6! Single genetic codon would dictate the choice of the Hamiltonian path on cue! Although the idea did not work (the length of, it led to ask whether the Hamiltonian cycles on octahedron or their duals at cube might have some biological relevance.

2. A further interesting finding is that the sequence of 8 quints defines a piece of 12-note scale proceeding by quints as steps between nearest neighbor vertices (using octave equivalence) in the icosahedral model of harmony [L12, L50] based on 12-note scale could be interpreted as cubic Hamiltonian cycle giving rise to the notes $F, C, G, D, A, E, H, F\sharp$. This gives the notes of C major scale with 7 notes plus tritonus $F\sharp$ defining half-octave as 8:th note. One could also identify the cycles as consisting of the notes of 8-note scale along cycle in the usual order $C, D, E, F, G, A, H, F\sharp$ based on standard notion of nearness for which neighboring vertices correspond to neighboring notes of the scale. Allowed 3-chords would correspond to triplets containing no neighboring notes. The Hamiltonian cycle for cube is unique apart from isometries as also for tetrahedron and and dodecahedron.

11.4.4 Microtubules as quantum critical systems

Also microtubules (see `http://tinyurl.com/y8km9vve`) are 2-D structures having a strong resemblance with the lipid layers of cell membrane. Could a higher level representation of genetic code similar to the one proposed for cell membranes make sense for them. Also now one can imagine that the microtubular surface is accompanied by its dark variant realizing 2-D dark genes, dark RNA, or dark proteins with scaled up size. The p-adic prime should correspond to $k > 151$ so that higher level realization of genetic code would be in question. In the case of axons a possible identification for the dark scale would be as the radius of the axonal membrane.

1. Microtubules are hollow cylinders with outer *resp.* inner diameter equal to 24 *resp.* 12 nm (the scales differ by factor 2) so that their thickness is 12 nm is same as the inner radius and would correspond to $L(151) = 10$ nm. They decompose to 13 parallel helical filaments consisting of 13 tubulin proteins having size scale of order $L_e(151)$.

2. Tubulins are dimers of α and β tubulin and the pairs are oriented along the helical filament. One can estimate the size of α and β tubulin by diving the circumference of 24 nm of the microtubule with the number of filaments, which is 13. This gives for the size scale of tubulin the estimate $R_{tub} \sim 12$ nm not far from $L(151)$. This supports the view that p-adic length scale $L(151)$.

   The size scale of the transversal volume associated with lipid is roughly .62 nm that is $L(143) = 2L(141)$ so that they could correspond to $k \in \{141, 143\}$, presumably $k = 141$. Therefore one could see microtubules as scaled up variants of cell membrane with scaling factor $2^{(151-141)/2} = 2^5 = 32$. Similar scaling would take place for the value of $n = h_{eff}/h$ giving $n = 2^{23}$ so that microtubules would represent a higher level of evolution identified as increase of n. Microtubules have indeed emerged after cell membrane.

3. It has been proposed that the α and β conformations of tubulin give rise to bit or even qubit. If this were the case, single helical filament rotating one full turn would have 2^{13} states and carry 13 bits of information. 13 independent filaments would have $2^{26} \simeq 64 \times 10^6$ states and carry 26 bits of information. One could also think of codon as sequence of 13 filaments with the states of filaments representing 2^{13} letters of the code.

4. Microtubular surface has rather high charge density and is polarized: the almost stationary end has negative local charge density roughly equal to that of DNA whereas the growing end has lower surface charge density. One manner to control the charge of the tubulin dimer is in terms of the charge states of GDP and GTP by ionization of the phosphates. Maximal negative charge for tubulin dimer would be 5 units.

   Microtubules are highly dynamical objects with inherent instability and have varying length: one might say that microtubules are quantum critical objects. Quantum criticality and thus instability might relate to the fact that the metabolic energy quantum is very near to thermal energy at room temperature.

   The dynamics for the length of microtubule could be induced from the dynamics of EZ involving the flow of protons between microtubule and its magnetic body defined by dark DNA. The gradient in charge density would make possible positive net charge density at the growing end of the microtubule.

   In ZEO it looks reasonable to argue that the dynamical patters are coded by a generalization of genetic code just as computer programs code for deterministic dynamical patterns.

5. What could the dark code behind the dynamics be? The α- and β tubulins of tubulin dimer involve GTP (see `http://tinyurl.com/ybtjluaf`) *resp.* GDP (see `http://tinyurl.com/y8uok7kq`). In the case of DNA one has XMP, $X = A, T, C, G$. The analogs of dark RNA sequences would contain mere G and the information coded by the tubulin would be determined by the conformation of the tubulin dimer giving 1-bit code. This looks somewhat disappointing.

   If the charge states of the phosphates of GDP and GTP can vary and all charge combinations for phosphates are possible, one has 2^3 charge states for GTP and 2^2 charge states for GDP. Together with the bit associated with the tubulin conformation this would give 2^6 states and realize 6 bits of the ordinary genetic code! One would have 2-D realization of the genetic code analogous to that proposed for the lipid layer with the state of tubulin analogous to RNA codon.

   This coding together with thermal criticality would make microtubule a dynamical object since the deviation of the tubulin charge from -1 units would spoil charge local charge neutrality of tubulin-dark RNA pair.

I have proposed that flux tubes connecting tubulins to the lipids of the axonal lipid layer could give rise to topological quantum computation [K17, K17]. The size scale of lipid is about $L_e(141)$ and that of tubulin about $L_e(151) = 32L_e(141)$, and the the radius of axonal membrane is by two orders of magnitude larger than microtubular surface. Hence this proposal does not look realistic unless one assumes that sub-structures of cell membrane with size scale of order $L_e(167)/L_e(151) = 2^8$ larger than tubulin size represented as space-time sheets with cell nucleus size $L(167)$ have flux tube connections to tubulins.

This kind of map would give rise to a kind of abstraction about what happens at the level of axonal membrane integrating out un-necessary details. This abstraction is natural since microtubules would indeed correspond to a higher level of cognitive hierarchy. Roughly $N = 2^{16}$ lipids would contribute to the information received by single tubulin. Could nerve pulse patterns can induce braiding of the flux tubes in this scale?

Part III

NUMBER THEORETICAL MODELS FOR GENETIC CODE

Chapter 12

Could Genetic Code Be Understood Number Theoretically?

12.1 Introduction

I have developed several models for genetic code with motivation coming from the belief that there might be some deeper number theoretical structure involved. The model based on Combinatorial Hierarchy was discussed in the chapter "Genes and Memes". In this chapter two further models are developed. The chapter begins with a discussion of a model relying on exact A-G symmetry and almost exact T-C symmetry of the genetic code with respect to the third nucleotide. The idea is that genetic code has emerged in some sense as a product of 1-code and 2-code via symmetry breaking. This symmetry breaking is also a central element of both the second model discussed in this chapter and the number theoretic model developed in the next chapter. Second idea is that there is some kind of variational principle mathematically analogous to the second law of thermodynamics involved.

Unfortunately, the physical model developed for the pre-biotic evolution of the genetic code does not fully support the proposed symmetry breaking scenario. The 2-code in the physical model trivial in the sense that it is induced by RNA conjugation for RNA doublets whereas 1-code is deducible directly from wobble rules and is non-deterministic. Symmetry breaking of the physical model has a beautiful interpretation in terms of fundamental physics but the realization of the symmetry breaking is not quite what has been assumed in these three models and also in the model based on Combinatorial Hierarchy discussed in the chapter "Genes and Memes". Despite this the models deserve to be represented.

Since the number theoretic model is the basic topic of this chapter, it is perhaps in order to describe the basic observations leading to the model. The number of DNA triplets is 64. This inspires the idea that DNA sequence could be interpreted as an expansion of an integer using 64 as the base. Hence given DNA triplet would represent some integer in {0,1....,63} (sequences of I Ching symbols give a beautiful representation of numbers in 64 base).

The observation which puts bells ringing is that the number of primes smaller than 64 is 18. Together with 0, and 1 this makes 20: the number of amino-acids!

12.1.1 Questions

The finding just described stimulates a whole series of questions.

Do amino-acids correspond to integers in the set $S = \{primes < 64\} \cup \{0, 1\}$. Does amino-acid sequence have an interpretation as a representation as a sequence of integers consisting of 0, 1 and products of primes $p = 2, ..., 61$? Does the amino-acid representing 0 have an interpretation as kind of period separating from each other structural units analogous to genes representing integers in the sequence so that we would quite literally consists of sequences of integers? Do 0 and 1 have

some special biological properties, say the property of being biologically inert both at the level of DNA and amino-acids?

Does genetic code mediate a map from integers 0,...,63 to set S such that 0 and 1 are mapped to 0 and 1? If so then three integers $2 \leq n \leq 63$ must correspond to stopping sign codons rather than primes. What stopping sign codon property means at the level of integers? How the map from integers 2,...,61 to the primes $p = 2, ..., 61$ is determined?

12.1.2 The Chain Of Arguments Leading To A Number Theoretical Model For The Genetic Code

The following chain of arguments induced to large part by concrete numerical experimentation leads to a model providing a partial answer to many of these questions.

1. The partitions of any positive integer n can be interpreted in terms of number theoretical many boson states. The partitions for which a given integer appears at most once have interpretation in terms of fermion states. These states could be identified as bosonic and fermionic states of Super Virasoro representation with given conformal weight n or even better, with the states of conformal weight n created by U(1) Kac Moody generators so that basically a breaking of Kac Moody symmetry would be in question.

2. The generalization of Shannon entropy by replacing logarithms of probabilities with the logarithms of p-adic norms of probabilities allows to have systems with negative entropy and thus positive negentropy. The natural requirement is that n corresponds to such prime $p \leq 61$ that the negentropy assigned to n is maximal in some number theoretic thermodynamics. The resulting correspondence $n \to p(n)$ would naturally determine the genetic code.

3. One can assign to the bosonic and fermionic partitions a number theoretic thermodynamics defined by a Hamiltonian. Purely bosonic and fermionic thermodynamics are defined by corresponding partition functions Z_B and Z_F whereas supersymmetric option is defined by the product $Z_B \times Z_F$.

4. The simplest option is that Hamiltonian depends only on the number r of the integers in the partition. The dynamics would be in a well defined sense local and would not depend on the sizes of summands at all. The thermodynamical states would be degenerate with degeneracy factors given by total numbers $d_I(n, r)$ of partitions of type $I = B, F$. The invariants known as rank and crank define alternative candidates for basic building blocks of Hamiltonian.

5. Ordinary exponential thermodynamics based on, say $e^{-H/T} = q_0^{r-1}$, q_0 a rational number, produces typically unrealistic genetic codes for which most integers are mapped to small primes $p \leq 11$ and many primes are not coded at all. The idea that realistic code could result at some critical temperature fails also.

6. Quantum criticality and fractality of TGD Universe inspire the idea that the criticality is an inherent property of Hamiltonian rather than only thermodynamical state. Hence Hamiltonian can depend only weakly on the character of the partition so that all partitions contribute with almost equal weights to the partition function.

   Fractality is achieved if Boltzmann factors are given by $e^{-H/T} = (r + r_0)^{n_0}$ so that $H(r) = log(r + r_0)$ serves as Hamiltonian and n_0 corresponds to the inverse temperature. The supersymmetric variant of this Hamiltonian yields the most realistic candidates for the genetic code and one might hope that a number theoretically small perturbation not changing the divisors $p \leq 61$ of partition function but affecting the probabilities could give correct degeneracies.

   Numerical experimentation suggests however that this might not be the case and that simple analytic form of Hamiltonian is too much to hope for. A simple argument however shows that $e^{-H/T} = f(r)$ could be in quantum critical case be deduced from the genetic code by fixing the 62 values of $f(r)$ so that the desired 62 correspondences $n \to p(n)$ result. The idea about almost universality of the genetic code would be replaced with the idea that quantum criticality allows to engineer almost arbitrary genetic code. In this case the model becomes predictive if the condition that $S_{tot} = \sum_n S_{p(n)}(n)$ is minimized (negentropy maximization)

with the constraint that each prime is coded and one could consider the possibility that $f(n)$ and $n \to p(n)$ is determined by this condition.

7. Genetic code has an almost unbroken symmetry in the sense that DNA triplets for which last nucleotide is A or G code for same amino-acid. For T and C this symmetry is slightly broken. This implies that the number of DNAs coding given amino-acid is almost always even. A very general number theoretic counterpart for this symmetry as a symmetry of partition function in the set 59 integers containing other than stopping codons. This symmetry must have fixed point and this is enough to explain why there is only single amino-acid coded by odd number DNAs besides singlets.

A natural guess is that the map of codons to integers is given as a small deformation of the map induced by the map of DNA codons to integers induced by the identification of nucleotides with 4-digits 0,1,2, 3 (this identification depends on whether first, second, or third nucleotide is in question). This map predicts approximate $p(n) = p(n+1)$ symmetry having also a number theoretical justification. One can deduce codon-integer and amino-acid-prime correspondences and at (at least) two Boltzmann weight distributions $f(n)$ consistent with the genetic code and Negentropy Maximization Principle constrained by the degeneracies of the genetic code.

12.1.3 What Is The Physical Counterpart Of The Number Theoretical Thermodynamics?

The partitions of any positive integer n can be interpreted in terms of number theoretical many boson states. The partitions for which a given integer appears at most once have interpretation in terms of fermion states. The states could be identified as bosonic and fermionic states of Super Virasoro representation with given conformal weight n or even better, with the states of conformal weight n created by U(1) Kac Moody generators so that basically a breaking of Kac Moody symmetry would be in question.

The obvious question concerns about the identification of the system in question. For instance, could it be associated with the light-like boundaries of magnetic flux quanta which are key actors in TGD based model of topological quantum computation [K55] ? If so, then each DNA triplet would correspond to a portion of magnetic flux quantum characterized by a conformal weight n determined by the DNA triplet in question. If there is single flux quantum parallel to the DNA strand, the value of n would be constant only along the portion of length corresponding to single DNA triplet. This non-conservation of conformal weight along light-like boundary is quite possible due to the breaking of strict classical non-determinism in TGD Universe having interpretation as a space-time correlate of quantum non-determinism.

With this identification one might perhaps interpret the integer determined by a given gene as a code for a topological quantum computer program using 64-base instead of 2-base. Since the boundaries of the magnetic flux tubes associated with DNA double strands are light-like, they can be interpreted either as states or as dynamical evolutions. Therefore the light-like boundary of the flux tube associated with DNA strand could be interpreted either as a code of a quantum computer program or as a running quantum computer program [K55].

The appendix of the book gives a summary about basic concepts of TGD with illustrations. There are concept maps about topics related to the contents of the chapter prepared using CMAP realized as html files. Links to all CMAP files can be found at `http://tgdtheory.fi/cmaphtml.html` [L10]. Pdf representation of same files serving as a kind of glossary can be found at `http://tgdtheory.fi/tgdglossary.pdf` [L11].

12.2 The First Model For The Evolution Of The Genetic Code

The exact A-G symmetry and almost exact T-C symmetry of the memetic codons with respect to third nucleotide suggest that genetic code factorizes in a good approximation to a product of codes associated with DNA doublets and singlets. This suggests factorization also at the level of pre-amino-acids. Perhaps DNAs triplets have resulted as a symbiosis of singlets and doublets

whereas amino-acids might have been developed via a symbiosis of 2 molecules coded by 4 DNA singlets and 10 molecules coded by 16 DNA doublets.

In this section a formal model for the evolution of the genetic code based on the approximate factorization of the genetic code into a product code formed by doublet and singlet codes is discussed. Also physical model for the evolution of the genetic code is briefly discussed. Product code as such predicts degeneracies approximately but fails at the level of detailed predictions for DNA-amino-acid correspondences. A "volume preserving" flow in discrete DNA space is needed to produce realistic DNA-amino-acid correspondences. This flow has the general tendency to cluster amino-acids to connected vertical stripes inside the 4-columns appearing as elements of the 4×4 code table, whose elements are labeled by the first two bases of DNA triplet. One can invent an information maximization principle providing a quantitative formulation for this tendency. The physical model for the evolution modifies the vision about RNA world [I113, I142].

12.2.1 Does Amino-Acid Structure Reflect The Product Structure Of The Code?

The exact A-G symmetry and the almost exact T-C symmetry of our genetic code supports approximate 2×10 structure such that 16 DNA doublets and 4 DNA singlets code for 10 *resp.* 2 "pre-amino-acids" which combine to form the real amino-acids. The 3×7 decomposition of the number 21 of amino-acids plus stopping sign suggests 3×7 decomposition of the genetic code. This decomposition is however not favored by the symmetries of the genetic code and will not be discussed in the sequel.

The coding of amino-acids involves tRNA binding with amino-acids and this means that the structure of amino-acids need not reflect the product structure of the genetic code and it might be that only the structure of tRNA reflects the product structure. The study of the amino-acid geometric structure does not reveal any obvious structural 3×7-ness or 2×10-ness. One can however wonder whether this kind of structures might be present at more abstract level and present only in the interactions of tRNA and amino-acids. As will be found, pre-amino-acids correspond most naturally to RNA sequences so that the product decomposition is realized trivially.

12.2.2 Number Theoretical Model For The Genetic Code

The study of the genetic code allows to deduce the process leading to the breaking of the product symmetry and T-C symmetry.

Approximate reduction to a product code

The dependence of the amino-acid coded by DNA on the third codon of DNA triplet is weak. This inspires the guess that triplet code might have evolved as a fusion of doublet code and singlet codes.

This should be reflected in its structure. The decomposition $20 = 2 \times 10$ for real amino-acids suggest that singlet code maps four bases to 2 "pre-amino-acids" such that A and G resp. T and C are mapped to same pre-amino-acid, and 16 doublets to 10 "pre-amino-acids". The exact A-G symmetry and almost exact T-C symmetry of our genetic code support this interpretation.

Product code hypothesis is very strong since the degeneracies of the product code are products of the degeneracies for the composite codes so that the number n_{AB} of DNA triplets coding a given amino-acid having the product form "AB", to be referred as the degeneracy of the amino-acid, is given by the product

$$n_{AB} = n_A \times n_B$$

of the degeneracies of the "pre-amino-acids" A and B. Here A and B can refer to $(A, B) = (3, 7)$ or $(A, B) = (2, 10)$ respectively.

The number $N_{AB}(n)$ of amino-acids with given degeneracy n is given by the formula

$$N_{12}(n) = \sum_{n_1 \times n_2 = n} N_1(n_1) N_2(n_2) \ ,$$

Table 12.1: The numbers $N(n)$ of amino-acids coded by n DNAs for unperturbed 2×10 product code and for the real genetic code for 2×10 option.

n	1	2	3	4	6
N(prod)	0	12	0	4	4
N(real)	2	9	2	5	3

where $N_1(n_1)$ resp. $N_2(n_2)$ is the number of pre-amino-acids with the degeneracy n_1 resp. n_2.

For 2×10 case singlet sector allows only single candidate for the code since the genetic code has exact A-G symmetry and almost exact T-C symmetry with respect to the last base. Thus A and G code for the first pre-amino-acid and T and C the second one. A breaking of the T-C symmetry is needed to obtain realistic code.

Our genetic code as result of symmetry breaking for 2×10 product code

As found, there are two cases to be considered: 3×7 T-C asymmetric and 2×10 T-C symmetric product code. The approximate T-C symmetry favors strongly 2×10 option and 3×7 will be considered only briefly in a separate subsection. On basis of degeneracies alone it is not possible to distinguish between these codes and 3×7 code was in fact the first guess for the product code.

In case of 2×10 code the decomposition of 16 DNA doublets giving almost the degeneracies of our genetic code is (3322 111 111).

$$(2 \oplus 2) \times (3 \oplus 3 \oplus 2 \oplus 2 \oplus 6 \times 1)$$

This gives

It is important to notice that the multiplets appear as doubled pairs corresponding to A-G and T-C symmetries. One generalized amino-acid (which cannot correspond to stopping sign) is lacking and must result by a symmetry breaking in which one amino-acid in the code table is transformed to a new one not existing there. Alternatively three amino-acids are transformed to stopping signs.

It is easy to find the deformation yielding correct degeneracies by removing DNAs from the DNA-boxes defined by various values of degeneracies to other boxes and adding them to other boxes. The rule is simple: taking m DNAs from a box containing n DNAs creates a box with $n - m$ DNAs and annihilates one n-box:

$$N(n) \to N(n) - 1 \ , \quad and \ N(n-m) \to N(n-m) + 1 \ .$$

If one adds k of these DNAs to r-box one has

$$N(r) \to N(r) - 1 \ , \ \ N(r+k) \to N(r+k) + 1 \ .$$

The operation which is not allowed is taking the entire content of a DNA box defined by amino-acid and adding it to other boxes since this would mean that the amino-acid in question would not be coded by any DNA. Thus the number of boxes can only grow in this process.

Realistic degeneracies are obtained by a rather simple operation.

1. Take from one 6-plet two amino-acid and move the first of them to 2-plet to get $N(6) = 3$, $N(4) = 5$, $N(3) = 1 < 2$, $N(2) = 11 > 9$ and move the second one to hitherto non-existing singlet to get $N(1) = 1$.

2. Move one DNA from some doublet to second doublet to get triplet and singlet to get $N(1) = 2$, $N(2) = 9$ and $N(3) = 2$.

This operation gives correct degeneracies only and it turns out that correct symmetry structure requires additional operations.

Failures of the product structure and the symmetry breaking as volume preserving flow in DNA space

A slightly broken product structure allows to understand the degeneracies of our genetic code relatively easily. It however leads also to wrong predictions at the level of DNA-amino-acid correspondence.

1. Exact product structure predicts that all 4-columns XYU, $U = A, G, T, C$ appearing as elements of the code table labelled by first and second bases of DNA triplet should have similar amino-acid structure. For 2×10 code the prediction is that all 4-columns should have $AABB$ structure and this prediction breaks down only for $AAAA$ type 4-columns.

2. For 2×10 code a given amino-acid should be coded either by DNA pairs of form (XYA, XYG) or of form (XYC, XYT). This is not the case. A given amino-acid tends to appear as connected vertical stripes inside the elements of the 4×4 table (4-columns). For instance, all 4-columns of form $AAAA$ (A=leu, val, ser, pro, thr, ala, arg, gly) and 3-column ile break the prediction of the product code.

3. In the case of 2×10 2n-plet formed by (XYA, XYG)-pairs is accompanied always by an 2n-plet formed by (XYT, XYC) pairs. By studying the degeneracies of the code one can get idea about how good these predictions are.

It seems that the breaking of the product symmetry tends to form connected vertical clusters of amino-acids inside a given element of the 4×4 code table but that one cannot regard stripes longer than 4 elements as connected structures. The 2×10 structure is favored by approximate T-C symmetry, and one can imagine that relatively simple flow in DNA space could yield the desired condensation of the amino-acids to form connected vertical stripes. The most general flow is just a permutation of DNAs and obviously preserves the degeneracies of various amino-acids. There are 64! different permutations but A-G and T-C symmetries reduce their number to 32!.

The idea about discrete volume preserving flow in DNA space can be made more precise. A-G and T-C gauge symmetries suggest the presence of a discrete symplectic structure. Perhaps one could regard 16×4 DNAs as 16 points of 4-dimensional discrete symplectic space so that the canonical symmetries of this space (volume preserving flows) acting now as permutations would be responsible for the exact A-G gauge invariance and approximate T-C gauge invariance. This brings in mind the canonical symmetries of CP_2 acting as $U(1)$ gauge transformations and acting as almost gauge symmetries of the Kähler action.

A natural guess is that the DNAs coding same amino-acid tend to be located at the same column of the 4×4 code table before the breaking of the product symmetry. If this is the case then only vertical flows need to be considered and A-G and T-C symmetries imply that their number is $8!^4$ corresponding to the four columns of the table.

Table 6c) summarizes our genetic code. It is convenient to denote the rows consisting of A-G resp. T-C doublets by X_1 and X_2. For instance, A_1 corresponds to the highest row phe-phe, ser-ser, tr-tyr, cys-cys and G_2 to the row leu-leu, pro-pro, gln-gln, arg-arg.

1. The simplest hypothesis is 2×10 option is realized and that the flow permutes entire rows of the code table consisting of A-G and T-C doublets. From **Table 12.2** it is clear that there is a G-C symmetry with respect to the first nucleotide broken only in the third row. This kind of primordial self-conjugacy symmetry would not be totally surprising since first and third nucleotides are in a somewhat similar position.

2. There are 3 6-plets leu, ser, and arg, and it is easy to see that one cannot transform them to the required form in which all 6-plets are on A-G or T-C row alone using this kind of transformation. For instance, one could require that leu doublets correspond to T-C doublets before the symmetry breaking. This is achieved by permuting the G_1 row with the C_2 row. Since A_2 contains also ser-doublet, also ser must correspond to T-C type 6-plet, and since arg is contained by G_2 row, also arg must correspond to T-C type 6-plet. Thus there would be 4 T-C type 6-plets but the product code gives only 2 of them.

3. The only manner to proceed is to allow mixing of suitable 6-plet of A-G type and 4-plet of T-C type in the sense that A-G doublet from 6 is moved to T-C doublet inside 4-plet and

Table 12.2: Code table before the flow inducing the breaking of the product symmetry

	A	G	T	C	
A	phe	ser	tyr	cys	A
	phe	ser	tyr	cys	G
	leu	thr	asn	thr	T
	leu	thr	asn	thr	C
G	val	ala	glu	gly	T
	val	ala	glu	gly	C
	leu	pro	gln	arg	T
	leu	pro	gln	arg	C
T	ile	ser	stop	ser	A
	ile	ser	stop	ser	G
	met	thr	lys	arg	T
	met	thr	lys	arg	C
C	val	ala	asp	gly	A
	val	ala	asp	gly	G
	leu	pro	his	arg	A
	leu	pro	his	arg	G

T-C doublet in 4-plet is moved to A-G doublet inside 6-plet. The exchange of AG_2 (ser doublet) and TG_1 (trh-doublet) represents this kind of permutation.

The tables below summarize the three stages of the construction.

At the last stage the T-C symmetry breaking giving rise to bla-trp and ile-met doublets occurs.

1. thr 6-plet is transformed to 4-plet by replacing thr-thr in AC_2 by bla-trp. trp is the missing amino-acid.

2. TA_2 met-doublet is transformed to ile-met so that the realistic genetic code results.

One might argue that symmetry breaking permutations $G_1 - C_2$ and $AG_2 - TG_1$ should permute amino-acids with a similar chemical character. A similar constraint applies to T-C symmetry breaking. By studying the chemical structure of the amino-acids, one finds that this is satisfied to a high degree.

1. The permutations val-leu and ala-pro exchange amino-acids with non-polar (hydrophobic) side groups. The permutations glu-his and gly-arg exchange polar (hydrophilic) amino-acid with a polar amino-acid which is also basic. Ser and thr are both non-polar amino-acids.

2. Ile and met are both non-polar so that ile$\rightarrow$ met replacement satisfies the condition.

3. The objection is that the side group for trp is non-polar but polar for thr. Interestingly, the code table decomposes to two connected regions corresponding to non-polar/polar side groups at the left/right such that the non-polar trp located inside the polar region is the only black sheep whereas thr naturally belongs to the polar region (see **Fig. ??**). As will be found trp is also otherwise singular case.

The information maximization principle determining the "volume preserving flow"

The interaction between the DNA singlets and doublets is the physical explanation for the breaking of the product symmetry. This interaction involves two parts: the flow and T-C symmetry breaking. The flow is analogous to the formation of connected vertical stripes of amino-acids in DNA space: kind of condensation process in which different phases represented by amino-acids tend to condense

Table 12.3: The code table after the action of the flow inducing the breaking of product symmetry

	A	G	T	C	
A	phe	ser	tyr	cys	A
	phe	ser	tyr	cys	G
	leu	ser	stop	thr	T
	leu	ser	stop	thr	C
G	leu	pro	his	arg	A
	leu	pro	his	arg	G
	leu	pro	gln	arg	T
	leu	pro	gln	arg	C
T	ile	thr	asn	ser	A
	ile	thr	asn	ser	G
	met	thr	lys	arg	T
	met	thr	lys	arg	C
C	val	ala	asp	gly	A
	val	ala	asp	gly	G
	val	ala	glu	gly	T
	val	ala	glu	gly	C

Table 12.4: The code table after the T-C symmetry breaking

	A	G	T	C	
A	phe	ser	tyr	cys	A
	phe	ser	tyr	cys	G
	leu	ser	stop	stop	T
	leu	ser	stop	trp	C
G	leu	pro	his	arg	A
	leu	pro	his	arg	G
	leu	pro	gln	arg	T
	leu	pro	gln	arg	C
T	ile	thr	asn	ser	A
	ile	thr	asn	ser	G
	ile	thr	lys	arg	T
	met	thr	lys	arg	C
C	val	ala	asp	gly	A
	val	ala	asp	gly	G
	val	ala	glu	gly	T
	val	ala	glu	gly	C

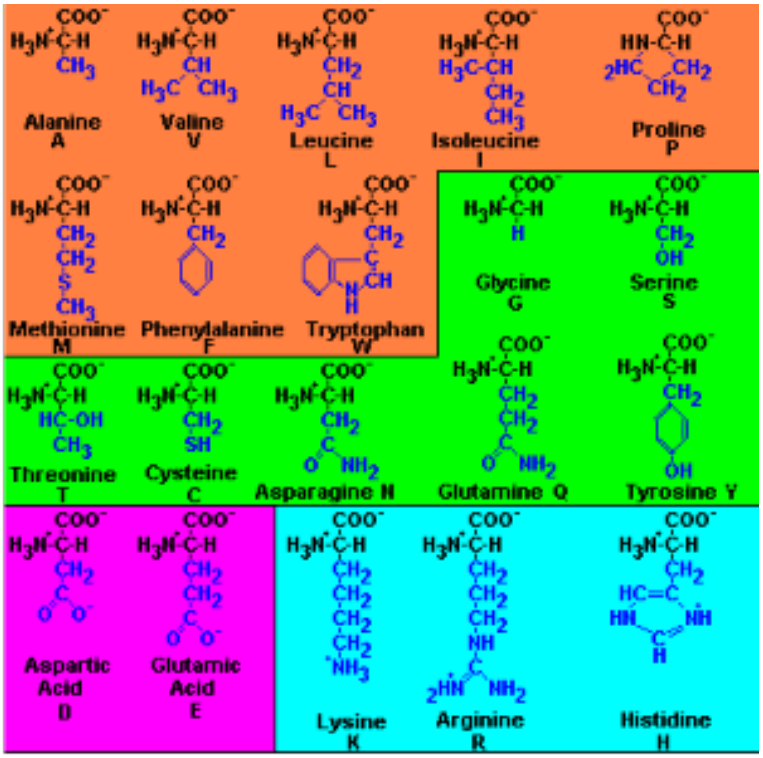

Figure 12.1: The chemical structure of amino-acids. The first group (ala, ...) corresponds to non-polar amino-acid side groups, the remaining amino-acids to polar side groups. The two lowest groups correspond to acidic (asp, glu) and basic side groups.

to form regions consisting of at most 4-units of type XYU, $U = A, G, T, C$. Obviously this means continuity and thus also symmetry analogous to that emerging when (amino-acid) gases condense to a liquid state: the breaking of the product symmetry is the price paid for this additional symmetry. It turns out to be possible to formulate a variational principle consistent with the proposed flow in the direction of the columns of the code table and defining the dynamics of the condensation.

What this means that one can assign an information measure to the code table such that the volume preserving flow in question maximizes this information measure.

1. Information measure is assumed to be local in the sense that it decomposes into a sum of information measures associated with the elements C_{AB}, $A, B \in \{A, G, T, C\}$, of the 4×4 code table (elements are 4-element columns). In the physical analogy this means that the condensed droplets of various amino-acids can have at most the size of single 4-element column.

2. Consider the element C_{AB}. Let the multiplet associated with the amino-acid a_k contain $n(k, AB)$ amino-acids and let $i(k, AB)$ tell the number of the disjoint parts to which the amino-acids a_k in the 4-plet AB split. The number of these disjoint multiplets can be $0, 1, 2$. Let the i: th region contain $n(k, AB, i)$ amino-acids a_k. The meaning of the equations

$$\sum_{i=1}^{i(k,AB)} n(a_k, AB, i) = n_k(AB) \quad ,$$

$$\sum_{AB} n_k(AB) = n_k \quad ,$$

$$\sum_k n_k = 64$$

is obvious.

Assign to the i: th connected region containing $n(k,i,AB)$ identical amino-acids a_k probability

$$p(k,i,AB) = \frac{n(k,i,AB)}{64} \ ,$$

to the element AB the total probability

$$p(k,AB) = \sum_{i=1}^{i(k,A,B)} p(k,i,AB) \ ,$$

and to the entire table the probability

$$p_k = \sum_{AB} p(k,AB) = \frac{n(k,AB)}{64} \ .$$

The sum of the probabilities associated with various amino-acids satisfies

$$\sum_k p_k = 1 \ .$$

The information measure associated with amino-acid a_k element AB is defined as

$$I(k,AB) = \sum_{i=1}^{i(k,A,B)} p(k,i,AB) \times log[p(k,i,AB)] \ ,$$

Note that this number is non-positive always. The total information associated with the amino-acid a_k in code table is defined as

$$I(k) = \sum_{AB} I(k,AB) \ .$$

The total information of the code table is defined as the sum of the information measures associated with various amino-acids:

$$I = \sum_k I(k) \ .$$

This information measure is maximized (which means the minimization of the absolute value of the measure since one can speak of the minimization of entropy) by the vertical flow satisfying the previous constraints, and thus satisfying the constraints that the numbers a_k of various amino-acids are fixed and $A \leftrightarrow G$ and $T \leftrightarrow C$ symmetries are respected. There is a direct analogy with thermodynamical equilibrium with fixed particle numbers and symmetry. The equilibrium is characterized by the chemical potentials associated with the amino-acids. There is no temperature type parameter now.

The variational principle indeed favors the formation of vertically connected regions consisting of $n = 2, 3$ or 4 amino-acids. By construction the variational principle does not tell anything about larger regions. In particular, it is more favorable for 4 amino-acids in a given column (say ser in the second column of the table) to be contained by single element than by 2 elements since the information measure would be $-1/16log(1/16)$ for two disjoint doublets and $-1/16log(1/8)$ for singlet 4-plet in same element and thus smaller in absolute value. In the similar manner the AAAB decomposition of singlet element instead of say AABA is favored.

The deviations from the standard code as tests for the basic symmetries of the model

The deviations of the genetic codes from the standard code [I47] provide a testing ground for the postulated symmetries of the genetic code and might also help to deduce the alien codes.

The deviations from universality of the Start codon (coding for met) and stop codons are very rare. With two exceptions all known deviations from the standard code are located in the first and fourth columns of the code table. For the first exceptional case the codon is ATC in the third column and codes for both stopping sign and pyrrolysine, which is an exotic amino-acid. It is somewhat a matter of taste whether one should say that the universality of the third

column is broken or not since, depending on context, ATC codes stopping sign or pyrrolysine. Second exceptional case corresponds to the use of two stop codons to code amino-acids and this necessarily breaks the universality of the third column in T-C 2-subcolumns. No violations of the predicted A-G symmetry and the universality of the second column of the code table are known.

The deviations from the standard code [I47] provide valuable hints when one tries to deduce information about the alien codes.

1. Consider first the mitochondrial genes.
   i) Mitochondrial codon ACT from animals and micro–organisms (but not from plants) codes trp instead of stopping sign.
   ii) Most animal mitochondria use TAT to code met instead of ile.
   iii) Yeast mitochondria use GAX codons to code for thr instead of leu.

2. The violations of the universality are very rare for nuclear genes. A few unicellular eukaryotes have been found that use one or two of three stop codons to code amino-acids instead. The use of two stop codons to code amino-acids necessarily violates the universality of the third column but need not break the universality for the imbedding of amino-acid space to DNA space.

3. There are also two non-standard amino-acids: selenocysteine and pyrrolysine.

   (a) Selenocysteine is encoded by ACT (fourth column) coding stopping sign normally. Interestingly, ACT codes also stopping sign and the translation machinery is somehow able to discriminate when selenocysteine is coded instead of stop. This codon usage has been found in certain Archaea, eubacteria, and animals. This deviation means that the number of amino-acids is 21 or 20 depending on context. This conforms with the view that number 21 indeed has a deep number theoretical meaning and that one can regard stopping sign formally as amino-acid.

   (b) In one gene found in a member of the Archaea, exotic amino-acid pyrrolysine is coded by ATC, which corresponds to the lower stopping sign in the code table. This case represents the only deviation from universality of the third column of the code table but even in this case also stopping sign is coded. How the translation machinery knows whether to code pyrrolysine or to stop translation is not yet known. TGD would suggest that electromagnetic signalling mechanisms ("topological light rays") might be involved.

12.3 Basic Ideas And Concepts Underlying Second Model Of Genetic Code

In the following the basic ideas and concepts are summarized.

12.3.1 Genetic Code From The Maximization Of Number Theoretic Information?

One of the earlier ideas about genetic code was that genetic code maximizes some kind of information measure [K19, K12, K13]. In that context ordinary entropy was used. The discovery of number theoretic variants of Shannon entropy based on p-adic norm allows however a modified approach.

12.3.2 Genetic Code From A Minimization Of A Number Theoretic Shannon Entropy

The idea about entropy minimization determining genetic generalizes to the idea that the map $n \to p(n)$ from integers representing DNA to primes representing amino-acids maximizes some kind of information measure.

Identification of ensembles

There is a natural candidate for the ensemble. This ensemble is defined by the partitions of n to sums of integers identified in terms of many-boson states. Each partition of an integer would correspond to a physical state. For Virasoro representations encountered in conformal field theories this is indeed the case. One can also consider partitions subject to some additional conditions. For instance, one could require that same integer appears at most once or that only odd integers appear in the partition (these options are in fact equivalent).

These two ensembles correspond to bosonic and fermionic systems and states in question correspond to the bosonic and fermionic states of given conformal weight n in Super Virasoro reprsentation. Supersymmetric alternative would be based on the product of bosonic and fermionic partitition functions so that entropy would be the sum of the bosonic and fermionic contributions. In the sequel all these options will be studied and supersymmetric option turns out to be the most promising one.

In the bosonic case the partition numbers are conveniently calculated by using the recurrence relation [A6]

$$d_B(n,r) = P(n,r) = P(n-1,r-1) + P(n-r,r) \ , \ P(n,1) = 1 \ . \tag{12.3.1}$$

In the fermionic case the numbers $Q(n,k)$ of partitions of n to a sum of integers such that same integer does not appear twice characterize simplest models. These numbers are obtained from the formula [A6]

$$d_F(n,r) = Q(n,r) = P(n - \left(\begin{array}{c} r \\ 2 \end{array} \right), r) \quad . \tag{12.3.2}$$

These formulas allow a highly effective numerical treatment when Boltzmann weights depend on r only.

Identification of information measures

There is also a good guess for the information measure as the p-adic entropy S_p obtained by replacing the argument logarithm of a rational valued probability p_k appearing in Shannon entropy with the logarithm of its p-adic norm $|p_k|_p$. If the probabilities of partitions are same and given by $1/d_I(n)$, $I = B, F$, where $d_I(n)$ is the total number of partitions, one would have

$$S_{I,p}(n) = -\sum_1^{d_I(n)} \frac{1}{d_I(n)} log(|\frac{1}{d_I(n)}|_p) = -log(|\frac{1}{d_I(n)}|_p) \ , \ I = B, F \ . \tag{12.3.3}$$

The simplest model obviously corresponds to a high temperature limit in thermodynamics. $S_{I,p}(n)$ can be expressed also in a form which is a convenient starting point for finite temperature thermodynamics with Hamiltonian given by the number r of integers in the partition.

$$\begin{aligned} S_{I,p}(n) &= -\sum_{r=1}^{n} p_I(n,r) log(|\frac{1}{d_I(n)}|_p) \ , \\ p_I(n,r) &= \frac{d_I(n,r)}{d_I(n)} \ , \ d_I(n) = \sum_{r=1}^{n} d_I(n,r) \ , \ I = B, F \ . \end{aligned} \tag{12.3.4}$$

$p_I(n,r)$ is the total probability that partition has r summands.

What makes number theoretical thermodynamics so fascinating is that p-adic entropies can be negative so that they can become genuine information measures. Indeed, if $d_I(n)$ is divisible by p the p-adic norm of $d_I(n)$ can become smaller than one and its contribution to the entropy is negative. Hence the maximization of $S_{I,p}$ as a function of p assigning to n a unique prime $p(n)$

is natural in the case of genetic code. Furthermore, if $S_{I,p}(n)$ zero or positive, n does not carry information and is an excellent candidate for the stopping sign codon.

It is possible to deduce the correspondence $n \to p(n)$ by using simple number theoretical arguments. If the number $d_I(n)$ of partitions is divisible by p, n might be mapped to p since the logarithm of $1/d_I(n)$ receives a large negative contribution tending to make the number theoretic entropy negative. It is easy to see that the largest power of prime appearing in $d_I(n)$ determines $p(n)$ in the case that $d_I(n)$ is divisible by some primes $p \leq 61$. At high temperature limit any prime $p \leq 61$ yields the same value of $S_{I,p}(n)$.

12.3.3 High Temperature Limit For Bosonic, Fermionic, And Supersymmetric Thermodynamics

The tables below represent the bosonic and fermionic partition numbers and the prediction of high temperature limit of number theoretical thermodynamics in the bosonic, fermionic, and supersymmetric cases.

High temperature limit does not predict a realistic genetic code.

1. The decompositions of $d(n)$ to primes contain all primes < 64 except 37 and 61. 23 is not allowed by the rule determining the value $p(n)$. In fermionic case $d(n)$ is divisible by 61 for $n = 24$ and by 37 for $n = 28, 20, 47, 62$.

2. For $n = 13$ and $n = 36$ for which $d(n)$ is prime larger than 61 so that it is not possible to assign any unique prime to them ($n = 13$ seems to deserve its bad reputation!), p-adic entropy and thus also information vanishes. A possible interpretation is that these two zero information integers correspond to stopping sign codons. In the general case integers coding $p = 2$ are good candidates for stopping codons since minimization of entropy favors $p = 2$ when the partition function fails to be divisible by any prime $p \leq 61$.

3. The primes p smaller than 13, in particular $p = 11$, which would be coded by as many as 19 DNAs, are strongly over-represented. The over-representation of small integers might reflect the three congruences $p(4+5d) \mod 5 = 0$, $d(5+7r) \mod 7 = 0$, and $d(6+11r) \mod 11 = 0$ found by Ramanujan for which quite recently a proof and generalization has been found [A28].

4. For both fermionic and supersymmetric partition functions primes 41 and 43 fail to be coded and there is strong over-abundance of $p = 2$. An amusing numerical coincidence is that $d_F(20) = 64$ holds true.

Table 12.5: Table represents the partition numbers $d_B(n)$ and $d_F(n)$ as well as the primes $p_B(n)$, $p_F(n)$, $p_{BF}(n)$ resulting from the minimization of the p-adic entropy $S_{I,p}(n)$, $I = B, F, BF$ as a function of n for $n < 30$.

n	$d_B(n)$	$p_B(n)$	$d_F(n)$	$p_F(n)$	$p_{BF}(n)$
0	1	1	1	0	0
1	1	1	1	1	1
2	2	2	1	1	2
3	3	3	2	2	3
4	5	5	2	2	5
5	7	7	3	3	7
6	11	11	4	2	11
7	3×5	5	5	5	5
8	2×11	11	6	3	11
9	$2 \times 3 \times 5$	5	8	2	2
10	$2 \times 3 \times 7$	7	10	5	3
11	$2^3 \times 7$	2	12	2	2
12	7×11	11	15	5	11
13	101 (prime)	?	18	3	3
14	$3^3 \times 5$	3	22	11	3
15	$2^4 \times 11$	2	27	3	3
16	$3 \times 7 \times 11$	11	32	2	2
17	$3^3 \times 11$	3	38	19	3
18	$5 \times 7 \times 11$	11	46	23	23
19	$2 \times 5 \times 7^2$	7	54	3	7
20	$3 \times 11 \times 19$	19	64	2	2
21	$2^3 \times 3^2 \times 11$	11	76	2	2
22	$2 \times 3 \times 167$	3	89(prime)	?	3
23	5×251	5	104	13	13
24	$3^2 \times 5^2 \times 7$	5	122	61	61
25	$2 \times 11 \times 89$	11	142	11	11
26	$2^2 \times 3 \times 7 \times 29$	29	165	29	29
27	$2 \times 5 \times 7 \times 43$	43	192	2	2
28	$2 \times 11 \times 13^2$	13	222	37	13
29	$5 \times 11 \times 83$	11	256	2	2

12.4 Could Finite Temperature Number Theoretic Thermodynamics Reproduce The Genetic Code?

The number theoretical ansatz in its simplest form fails. It is however possible to modify the measure associated with the partitions, which can be regarded as $T \to \infty$ limit of thermodynamics. Some kind of conserved quantity playing the role of Hamiltonian and distinguishing between different partitions should be introduced.

p-Adic thermodynamics implies that the counterpart of Boltzmann exponent $exp(-H/T)$ should be rational. One manner to guarantee this is to assume Boltzmann weight has the form q_0^{-H/T_r} for some rational number q_0 assuming that H/T_r is integer valued. A stronger condition is that q_0 is integer. With natural conventions both Hamiltonian and the inverse of the reduced temperature T_r are integer valued. For $T_r = 1/k$ the counterpart of the ordinary temperature would be $T = k/log(q_0)$. Thus q_0 would partially characterize the number theoretical temperature of DNA-amino-acid system and varying temperature would allow the possibility of several codes. The genetic code indeed involves small variations [K19, K13]. The Hamiltonian should depend on the number r of integers in the partition and possibly n, perhaps also on more refined properties of the partition.

The finite temperature need not as such be enough to guarantee a reasonable genetic code. On purely statistical grounds one expects that small primes appear very frequently as divisors of integer valued reduced partition function and over- abundance of small primes is expected. Detailed calculations in low temperature phase confirm this prediction.

Physical intuition suggests that there could exists something analogous to a critical temperature in the sense that large long range fluctuations for ordinary criticality correspond to large degeneracies for large primes. The challenge would be to find this critical phase expected to be located somewhere between high temperature phase and low temperature phases with $(r_0 > 1, s_0 = 1)$ and thus characterized by $r_0 > s_0 > 1$. The attempts to realize this program have not led to a success, and it seems that it is not only particular thermodynamical state of the system which should be critical, but the very Hamiltonian defining the number theoretical thermodynamics as the quantum criticality of TGD Universe indeed suggests.

12.4.1 How To Choose The Hamiltonian?

Hamiltonian as a function of the number of summands in the partition?

The most symmetric positive definite Hamiltonian one can imagine is $H(n, r) = H(r) = r$ thermodynamically equivalent with $H(r) = r - 1$. The independence of the Hamiltonian on n conforms with the idea that the dynamics is local in the sense that only the number r of integers in the partition matters and that the value n of the individual integer is irrelevant. Dynamics would be same for all values of n and in this sense universal.

A possible interpretation for $H(r)$ is in terms of the breaking of conformal symmetry allowing to distinguish between states characterized by the same eigenvalue n of the Virasoro generator L_0 and generated by the products $\prod_k L_{n_k}$ of Virasoro generators. This Hamiltonian is certainly the most natural starting point because it possesses maximal symmetries and is also computationally tractable.

For the corresponding thermodynamics temperature corresponds to a rational $q = r/s > 1$ and Boltzmann weights are given by the exponents q^r. It turns out difficult to find realistic looking genetic codes for this thermodynamics. Unless q is near unity only lowest values of r contribute and the general tendency is that the spectral power concentrates at small primes ≤ 11. This can be understood from the fact that small primes are the most probable divisors of random integers. The only hope seems to be that there exists a critical temperature at which large long range fluctuations correspond to large degeneracies for large primes.

The most general thermodynamics allows arbitrary function $exp(H/T) = f(r, T)$ of r having positive integers as values. An especially natural choice is $f(r) = (r + r_0)^n$ corresponding to Hamiltonian $H = log(r + r_0)$ and temperature $T = 1/n$ so that one has

$$exp(-H/T) \quad = \quad (r + r_0)^{n_0} \quad , \quad n_0 = \pm 1, \pm 2, ... \quad , \quad r_0 = 0, 1, 2, ... \quad . \tag{12.4.1}$$

Table 12.6: Table represents the partition numbers $d_B(n)$ and $d_F(n)$ as well as the primes $p_B(n)$, $p_F(n)$, $p_{BF}(n)$ resulting from the minimization of the p-adic entropy $S_{I,p}(n)$, $I = B, F, BF$ as a function of n for $30 \leq n \leq 65$. Note that for bosonic case $p = 37$ and 61 are not coded whereas for supersymmetric case $p = 41$ and 43 are not coded.

n	$d_B(n)$	$p_B(n)$	$d_F(n)$	$p_F(n)$	$p_{BF}(n)$
30	$2^2 \times 3 \times 467$	2	296	2	37
31	$2 \times 11 \times 311$	11	340	17	17
32	$3 \times 11^2 \times 23$	11	390	13	11
33	$3^2 \times 7^2 \times 23$	7	448	2	7
34	$2 \times 5 \times 1231$	3	512	2	2
35	$3 \times 11^2 \times 41$	11	585	13	11
36	17977(prime(	?	668	2	2
37	$7 \times 11 \times 281$	11	760	19	19
38	$5 \times 11^2 \times 43$	11	864	2	11
39	$3^4 \times 5 \times 7 \times 11$	3	982	2	3
40	$2 \times 3 \times 7^2 \times 127$	7	1113	53	7
41	$3 \times 7 \times 11 \times 193$	11	1260	3	7
42	$2 \times 11 \times 2417$	11	1426	31	31
43	$3^4 \times 11 \times 71$	3	1610	23	7
44	$5^2 \times 31 \times 97$	31	1816	2	31
45	$2 \times 41 \times 1087$	41	2048	2	2
46	$2 \times 3 \times 73 \times 241$	3	2304	2	2
47	$2 \times 7^2 \times 19 \times 67$	7	2590	37	7
48	$3 \times 7 \times 7013$	7	2910	5	3
49	$5^2 \times 11 \times 631$	5	3264	2	2
50	$2 \times 11 \times 9283$	11	3658	59	59
51	$3 \times 11^2 \times 661$	11	4097	17	11
52	$3 \times 7 \times 11 \times 23 \times 53$	53	4582	29	53
53	$3^2 \times 7 \times 5237$	3	5120	2	2
54	$5 \times 7 \times 11 \times 17 \times 59$	59	5718	3	59
55	$2^2 \times 7 \times 71 \times 227$	7	6378	3	2
56	$11 \times 47 \times 1019$	47	7108	47	47
57	$2 \times 3 \times 102359$	3	7917	29	29
58	$2^2 \times 5 \times 11 \times 3251$	11	8808	2	2
59	$2^2 \times 5 \times 11 \times 19 \times 199$	19	9792	2	2
60	$17 \times 139 \times 409$	17	10880	2	17
61	$3 \times 5 \times 7 \times 11 \times 971$	11	12076	2	11
62	$2^2 \times 11 \times 13 \times 2273$	13	13394	37	37
63	$3 \times 113 \times 4441$	3	14848	2	2
64	$2 \times 5 \times 11 \times 71 \times 223$	11	16444	11	11
65	2×1006279	2	18200	5	5

Table 12.7: The numbers $N(n)$ of amino-acids coded by n DNAs.

n	1	2	3	4	6
N	2	9	2	5	3

so that a second integer valued parameter creeps in. Note that the thermodynamics is invariant under the scalings $(r + r_0) \to \lambda \times (r + r_0)$.

For $n \geq 0$ the formula for $S_p(n)$ is computationally very attractive but $n_0 > 0$ corresponds to negative temperatures or negative values of $H(r)$. It is of course not clear whether the sign of temperature is really important since the number of states is finite. The general vision that rational valued entanglement coefficients correspond to negative entropy and are associated with bound states would suggest that H has interpretation as the analog of negative of binding energy and is therefore negative.

For $n_0 < 0$ the numerical calculations are somewhat intricate due to the emergence of factorials up to 63! in the calculation of p-adic norms of partition coefficients. The factors $1/(r + r_0)^{n_0}$ tend to divide from the partition function prime factors $r_0 + 1$ away and this means that for small values of r_0 the primes $pr_0 + 1 \leq 61$ rarely divide it. Hence an entropic phase is in question for $r_0 < 61$ and numerical calculations demonstrate that only few $p > 2$ are coded. One might hope that the situation changes for $r_0 > 61$ and should resemble that for $n_0 > 0$. Numerical calculations show that this is not the case. The outcome is a complete spontaneous magnetization in the sense that only $p = 2$ is coded. This can be understood from the fact that entropy is minimum for $p = 2$. The safe conclusion seems to be that $n_0 > 0$ phase is the only option possibly reproducing the genetic code for a properly chosen Hamiltonian.

The polynomial rather than exponential thermodynamics would conform with the quantum criticality and fractality of TGD Universe. The nice feature of the logarithmic Hamiltonian is that it describes inherently critical system since the thermodynamical weights are slowly varying functions of r and therefore thermal fluctuations are large. Therefore there are hopes of achieving criticality, perhaps for all values of n for $n_0 > 0$.

These optimistic expectations turn out to be correct. Numerical calculations for $n_0 > 0$ bosonic case demonstrate that the concentration of spectrum to small primes is not anymore present, all primes can be coded in some cases, and qualitatively reasonable looking genetic codes are obtained with degeneracies smaller than 8. The next improvement is super-symmetry which leads to more realistic candidates for genetic code with small parameter values. It is quite possible that the requirement that the realistic genetic code results exactly fixes the Hamiltonian completely and that some kind of symmetry breaking is required to get the correct code.

Hamiltonian as a function of the rank of the partition?

There are also more complex candidates for the Hamiltonian if one allows Hamiltonian to have different values for partitions having the same value of r. Already Dyson introduced the notion of rank of a partition of type (n, r) as the difference

$$R(n, r, n_{max}) \quad = \quad n_{max} - r \ , \tag{12.4.2}$$

where n_{max} is the largest integer appearing in the partition [A28].

Rank divides the partitions into equal sized classes and the number of them obviously appears as a factor in $d(n)$. The notion of rank allows to prove the congruences $d(4+5d) \ mod \ 5 = 0$ and $d(5 + 7r) \ mod \ 7 = 0$ discovered by Ramanujan but fails for $d(6 + 11r) \ mod \ 11 = 0$ as found by Dyson [A19]. Dyson speculated the existence of a more complex invariant which he christened crank.

Rank is not positive definite as the study of simplest examples demonstrates. A simple manner to get a non-negative Hamiltonian is based on the so called group number defined as rank modulo $n + 1$:

$$G(n, r, n_{max}) \quad = \quad R(n, r, n_{max}) \ mod \ n + 1 \ , \tag{12.4.3}$$

and having values only in the set $\{0, ..., n\}$. The modulo arithmetics has the effect of producing double degeneracy of partitions with same group number. The numbers $N(p)$ coding given prime satisfy $N(p) \geq 2$ for the real genetic code and this might be due to the modular arithmetics (the exponential thermodynamics based on rank predicts typically $N(p) = 1$ or 0 for $p > 11$).

Hence one could consider the Boltzmann weights

$$\begin{aligned} exp(-H/T) &= q^{kH(n,r,n_{max})} \ , \\ kH(n,r,n_{max}) &= G(n,r,n_{max}) \ . \end{aligned} \tag{12.4.4}$$

For this option partitions $(r, n_2...n_r)$ are favored for positive temperatures since $R = 0$ in this case and at low temperature limit the finding of genetic code reduces to the identification of the largest prime power factors of the number of partitions of n of type $(r, n_2...n_r)$. Note that ground state degeneracy results whereas for $H = r$ the ground state is singly degenerate at low temperature limit. The study of small values of n shows that this thermodynamics is not very interesting since the number of partitions of this kind is rather small. For large primes this would mean that they cannot be coded.

The inherently critical option corresponds to

$$exp(-H/T) = (G(n,r,n_{max}) + g_0)^k \ , \tag{12.4.5}$$

with integer valued temperature k. For $g_0 = 0$ the partitions of type $(r, n_2...n_r)$ would have zero thermodynamical weights for $k > 0$ and infinite conformal weight for $k < 0$.

Hamiltonian as the function of the crank of the partition?

Quite recently Mahlburg [A28] represented an ingenious proof of a theorem generalizing the famous regularities of partitions discovered by Ramanujan and followers (for a popular representation of what is involved see the article [A19]). The proof is based on the identification of the invariant anticipated by Dyson.

The reason why a function of crank is a promising candidate for Hamiltonian is following.

A partial explanation for why primes $p \leq 11$ are so abundant at infinite temperature limit is that $d(n)$ is divisible by $5, 7, 11$ for $n = 4 + 5k$, $n = 5 + 7k$, and $n = 6 + k11$ respectively so that these primes are strong competitors in negentropy maximization race for a large number of values of n (19 for $p = 5$, 8 for $p = 7$, 5 for $p = 11$).

Crank, denote it by C, decomposes the partitions to subsets for which numbers of elements are divisible by $5, 7$ *resp.* 11 in these three cases. The expression for $S_p(n)$ in the case of polynomial thermodynamics can be written as

$$\begin{aligned} S_p(n) &= \sum_i N(n,i) C^k(i) log(|\frac{C^k(i)}{Z(n)}|_p) \ , \\ Z(n) &= \sum_i N(n,i) C^k(i) \ , \end{aligned} \tag{12.4.6}$$

It is clear that 5, 7, 11 appearing as divisors in both $N(n,i)$ and $Z(n)$ cancel each other and there is no large contribution to negentropy from these primes. This contribution is actually tamed also for other Hamiltonians defining polynomial dynamics.

12.4.2 Could Supersymmetric $N_0 > 0$ Polynomial Thermodynamics Determine The Genetic Code?

The numerical experimentation excludes exponential thermodynamics whereas exponential thermodynamics produces qualitatively reasonable looking genetic codes for $n_0 > 0$ whereas for $n_0 < 0$ most of the spectral power is concentrated at $p = 2$. For small values of n_0 and r_0 purely bosonic thermodynamics fails to reproduce codes satisfying the necessary conditions $D(p) > 0$ and $D(p) < 7$ satisfied by the real genetic code. Super symmetric variant with $S_p(n) = S_{B,p}(n) + S_{F,p}(n)$ however yields several codes satisfying this condition when Hamiltonian is taken to be $exp(H/T) = (r + r_0)^{n_0}$, r the number of summands in the partition.

Basic conditions

The basic conditions on the degeneracies are following:

1. 3 values of n should correspond to stopping codons due to their non-positive or negative entropy. Non-positive entropy is certainly the logical option since the notion of zero information codon does not seem to be reasonable. Numerical computations demonstrate that negative entropies are rather rare whereas $S_p(n) = 0$ occurs rather often. The reason is that if partition function is not divisible by any $p \leq 61$ then the smallest prime $p \leq 61$ not dividing any of the numerators of Boltzmann weights minimizes information and gives $S_p(n) = 0$. These observations suggest that $S_p(n) \leq 0$ condition should be used as a criterion for stopping codon property.

2. The degeneracies $D(p)$ satisfy $D(p) > 1$ if one has $(0,1) \to (0,1)$ so that 0 and 1 correspond to the two amino-acids coded by single DNA.

3. Complete hit means that the numbers $N(k)$ of DNAs coding $D = k \in \{2,3,4,5,6\}$ real amino-acids (as distinguished from stopping sign) should be $(9,1,5,0,3)$. This condition combined with the condition $N(stop) = 3$ allows an automatic search of candidates for codes.

Results

For polynomial thermodynamics the range $n_0 \in \{1,5\}, r_0 \in \{0,5\}$ is scanned. For exponential thermodynamics the range studied is $r_0 \in \{1,5\}, s_0 \in \{1,5\}$. B, F, and BF variants are studied applying the two alternative criteria for the stopping codon and requiring that exactly 3 stopping codons result.

1. $S \leq 0$ as a criterion for the stopping codon

a) Polynomial thermodynamics.

i) Numerical experimentation shows that the number of stopping codons increases rapidly with the values of (n_0, r_0) for polynomial thermodynamics so that only small parameter values seem to be worth of considering.

ii) For cases B and F no solutions are found. BF allows single solution. This code corresponds to $(n_0, r_0) = (2,4)$ having degeneracies

$$(D(2), D(3), ..., D(61)) = (4,4,9,3,7,6,2,2,1,1,4,1,3,1,2,2,3,4) \ .$$

The numbers of DNAs associated with the degeneracies (1, 2, 3, 4, 5, 6) are

$$(N(1), N(2), N(3), N(4), N(5), N(6)) = (6,4,3,3,0,1)$$

to be compared with the degeneracies

$$(2,9,1,5,0,3)$$

of the real code. If 3 DNAs from 9-plet ($p = 5$) and 1 DNA from 7-plet ($p = 11$) are shifted to 4 1-plets, and 1 DNA from 3-plet is shifted to 3-plet, correct degeneracies result. A modification of r_0 by adding the product of primes $p \leq 61$ with $p \notin \{5,11\}$ would affect the degeneracies associated with 5 and 11.

b) Exponential thermodynamics.

There are no solutions for F and BF. B gives solution $(r_0, s_0) = (5,3)$ with degeneracies

$$(9,1,3,1,5,2,3,2,4,4,4,2,3,2,2,3,1,8) \ .$$

From this solution it is possible to construct the real genetic code by shifting 3 codons from 9-plet to 3 1-plets, one codon from 3-plet to a second 3-plet, and 2 codons from 8-plet to 5-plet and 3-plet.

2. $S < 0$ as a criterion for the stopping codon

1. Polynomial thermodynamics.
   For F and BF no solutions are found. B gives single solution $(n_0, r_0) = (3, 1)$. The degeneracies are $(3, 2, 11, 6, 3, 1, 5, 1, 5, 6, 4, 1, 2, 1, 1, 2, 2, 3)$ and quite far from those of the real genetic code.

2. Exponential thermodynamics.
   No solutions are found.

The conclusion is that BF for $S_p < 0$ criterion for stopping codon is the most realistic one and might produce by a small deformation the real genetic code.

12.4.3 Could Small Perturbations Of Hamiltonian Cure The Situation?

The troubling outcome of calculations is that no realistic code is found for the simplest Hamiltonian. The obvious guess is that one should study small perturbations of the Hamiltonian. There are two kinds of small perturbations. The perturbations of the first kind are small in the real sense but can induce dramatic changes of the genetic code by affecting the p-adic norms of $Z(n)$. The perturbations of the second kind are small in the number theoretical sense but as a rule affect strongly the values of the real probabilities.

Small perturbations in the real sense

The perturbations which are small in the real sense would simply modify $f(r)$ by few units. They would however dramatically affect the p-adic norms of $Z(n)$ and induce thorough changes in the genetic code. In order to proceed in a rational manner some additional assumptions are necessary and therefore this approach will be left in the next subsection where the maximization of the total negentropy of the genetic code is introduced as a variational principle allowing to fix the Hamiltonian as a small perturbation reducing the values of $f(r) = r$ of the Boltzmann weight. It seems that this approach is the more promising one.

Number theoretically small perturbations

The small values of n_0 and r_0 plus unsuccessful searches for $n_0 > 5$ encourage to ask whether the real code result from the semi-realistic codes via a small perturbation of Hamiltonian changing only the partition function Z in number theoretical sense.

The simplest situation is achieved if perturbations do not distinguish between partitions with the same value of r. The number theoretical generalization for the notion of symmetry of action principle suggests that perturbations should leave invariant the prime power factors p^k of Z for $p \leq 61$ but affect them for $p > 61$. This would affect only the probabilities of individual partitions and the positive contributions to $S_p(n)$ coming from the numerators of Boltzmann weights. This might be enough to affect the situation in the case that two primes p_1 and p_2 have nearly the same value of $S_p(n)$ in the original situation. What would be needed that three singly (and thus rarely) coded primes would become doubly coded by this kind of fine tuning.

More precisely, the Boltzmann weight associated with r transforms in $H(r) \to H(r)+\Delta H(r)$ as $B(r) = exp(-H(r)/T) \to B(r) \times (1 + \Delta H(r)/T)$. From this it is clear that the p-adic norm of the contribution of r to the partition function is unaffected if $H(r)$ is divisible by a sufficiently high powers of all primes $2 \leq p \leq 61$: this by the way defines what the notion of small perturbation means number theoretically. Obviously this kind of symmetries exist and since large powers of p in $\Delta H(r)$ modify dramatically the probabilities $p(n, r)$, it is indeed possible to affect the degeneracies associated with various amino-acids.

The simplest perturbation corresponds to the addition of a sufficiently high power of the product $P = \prod_{p \leq 61} p$ to r_0: $r_0 \to r_0 + P^k$. The p-adic norms appearing as arguments of logarithms would remain invariant. Boltzmann weights would be identical in an excellent approximation as for infinite temperature limit so that the probabilities $p(n, r)$ would reduce to $p(n, r) \simeq d(n, r)/d(n)$. The model would result via the replacement of $p(n, r) \to d(n, r)/d(n)$ from the original model.

It turns out that this replacement does not solve the problem in the range $(n_0 \in \{1, 5\}, r_0 \in \{0, 5\}$: no codes with 3 stopping sign codons are found. One cannot of course exclude the possibility that larger values of n_0 and r_0 might provide a solution.

A more general trial would assume that the perturbation modifies the p-adic norms of Boltzmann weights but leaves the norms of partition function invariant.

Should one break the symmetry between partitions with same r?

A more radical modification results if the perturbation distinguishes between partitions with different values of r. It is however not clear whether integer valued perturbation can be small in number theoretic sense. Rank and crank distinguish between partitions with same r.

The most radical option is to replace r with a new invariant. If rank and crank define the entire Hamiltonian, they divide partitions into equivalence classes by combining partitions with different values of r to single equivalence class so that the situation changes dramatically. The knowledge about the numbers of partitions in corresponding equivalence classes plus values of these invariants would make it easy to check whether either of them could reproduce the real genetic code.

12.4.4 Could One Fix Hamiltonian $H(R)$ From Negentropy Maximization?

Numerical calculations suggests that number theoretically small modifications might not be the correct manner to find a correct genetic code: the codes having the correct number of stopping codons and coding for all primes differ simply too much from the real code. Even if such a code could be found one can argue that it is only a skillful exercise in the modular arithmetics. Numerical difficulties are also obvious since powers of the product $P = 2 \times 3.... \times 61$ must be added to $f(r)$.

For the perturbations of $f(r) = r$ which are small in the real sense numerical control is not lost but with physicist's intuition in the number theory the modifications of the genetic code are completely unpredictable. The reduction of $f(r)$ by a single unit for single sufficiently small value of r could change the whole biology! In order to study them one should have additional principle allowing to get grasp of the problem.

The great principles of physics are variational principles and Negentropy Maximization Principle is the basic principle in TGD inspired theory of consciousness [K32]. Quantum criticality predicts a Universe able to engineer itself and this suggests that the Hamiltonian $H(r)$ determining the genetic code could be a result of "genetic engineering" maximizing the total negentropy of the genetic code.

Could one engineer $H(r)$ from the real genetic code in the case of polynomial thermodynamics?

The most general hypothesis would be that the 62 values of $f(r) = exp(-H(r)/T)$ are completely free positive integers and look whether it is possible to find a Hamiltonian reproducing the genetic code. The naive idea is that since the number of integers $f(r)$ is the same as the values of n, a judicious choice of $f(r)$ could allow to assign to a given n arbitrary $p(n)$ or make it a stopping sign codon. If each r is shifted by the same sufficiently large power of $P = \prod_{p \leq 61} p$, the probabilities for partitions are in an excellent approximation identical in the case of polynomial thermodynamics so that the situation would reduce to a mere modular arithmetics.

One could start from $n = 2$ and proceed by increasing n and determining the value of $f(r = n)$ at n: th step from the requirement that the desired value of p results. What seems obvious is that the value of the partition function $Z(n) = \sum_{r=1}^{n} d(n,r)f(r)$ can be fixed to have an arbitrary prescribed value and thus also the $k_p(Z(n))$ giving the negative contribution to the entropy can be fixed to a desired value. This leaves still some freedom to arrange the value of $k_p(d(n,n)f(n)) = k_p(f(n))$ making possible fine tuning in the n: th numerator contributing to the entropy. The entropies $S_p(n+1)$ and $S_p(n)$ would be related by the condition

$$\begin{aligned}\frac{S_p(n+1)-S_p(n)}{log(p)} &= -k_p(Z(n+1))+k_p(Z(n)) \\ &+ \sum_{r=1}^{n}\left[d(n+1,r)-d(n,r)\right]k_p(f(r))+k_p(f(n+1)) \ .\end{aligned} \tag{12.4.7}$$

The modular arithmetics is of course different from real analysis and the situation might not be so simple as it looks. On the other hand, if this picture is correct, one might interpret the freedom to construct the genetic code almost at will as the fruit of quantum criticality making possible genetic engineering.

Maximization of the total negentropy of the genetic code as a manner to fix the Hamiltonian

The basic objection to this approach is that it is not predictable. It is however possible to introduce a natural variational principle. The maximization of the total negentropy $N_{tot} = -\sum_n S_{p(n)}(n)$ of the genetic code subject to the constraint that all primes are coded and there are 3 stopping codons would in principle allow to fix the function $f(r)$ uniquely.

The maximization of the total negentropy allows to conclude that large (small) prime powers correspond to large (small) DNA multiplets. For instance, if only first powers of p appear, 9 doublets would correspond to $p = 2, ..., 23$, triplet to $p = 29$, five 4-plets to $p = 31, ..., 47$, and 3 6-plets to $p = 53, 59, 61$. Furthermore, since the value of $Z(n)$ increases with n, and thus also the probability that it has large prime power factors, one expects that large values of n should correspond to large values of p. Hence the orderings of multiplet sizes, primes powers p^k appearing as factors of $Z(n)$, and integers n should correlate strongly.

Is there then any bound on the exponents of powers p^k appearing in $Z(n) = \sum_r d(n,r)f(r)$? If not, then the variational principle does not work. For instance, one might think that ones has

$$f(n+1) = \sum_{r=1}^{n} d(n+1,r) + mp^k \ ,$$

where k is an arbitrarily large power of p so that $Z(n+1) = mp^k$ holds true and gives an unbounded contribution to $k_p(Z(n+1))$. Only $p(n+1, n+1)$ would differ significantly from zero and would be near 1 but this does not give any restriction. It would seem that there must exist some natural bound on the values of $f(r)$ to stabilize the variational principle.

The most natural option is modulo n+1 arithmetics based on the assumption that Boltzmann factors depend on both n and r and one has $f(n,r) \leq n$ at level n. Boltzmann factors would formally restrict the partition of any integer $m > n$ to partitions of n. This would make the problem numerically more tractable. With this assumption the model for $f(r) = r$ would correspond to the maximum value of $Z(n)$. There would be $61! \sim 5 \times 10^(83)$ alternatives to be scanned but reasonable assumptions should reduce considerably this number.

One can imagine two kinds of additional assumptions.

1. If the genetic code has resulted as a product of singlet and doublet codes then one could argue that also $n = 4$ and $n = 16$ should maximize their total negentropy and code for all primes $p < n$ as real or stopping codons.

2. A much stronger additional assumption that a genetic code coding all primes $p \leq n$ results for every value of n does not work since it implies that highest primes are coded only once.

Consider the situation for the smallest values of n in the bosonic case. For $n = 2$ $f(r) = r$ implies $Z(2) = 3$ giving $p(2) = 3$ favored by local negentropy maximization and $S(2) = -log(3)$. $f(2) = 1$ would give $p(2) = 2$ and $S(2) = -log(2)$. For $n = 3$ to $f(r) = r$ would give $Z(3) = 6$ giving $p(2) = p(3) = 3$ and $S(3) = -log(3) + log(2)/3$ and $S_{tot} = -2log(3) + log(2)/3$. This corresponds to the maximum of total negentropy for 4-code. The code is consistent with the proposal that $2n$ and $2n+1$ code for the same amino-acid for $n < 61$ explaining the fact that almost all amino-acids

are coded by an even number of codons. The absence of stop codon does not allow this code as a genuine singlet code. For $(f(1), f(2), f(3)) = (1, 2, 2)$ with $(Z(2), Z(3)) = (3, 5)$ one would have $n(2) = 3$ and $n = 3$ would represent stopping codon.

For larger values of n a convenient starting point would be $f(n) = n$ and direct checking of values $f(n) = n - k$ for not too large values of k to find a value of Z corresponding to a large prime power. This would give a precise content to what a small perturbation of the Hamiltonian $H(r) = log(r)$ in real sense means in practice. Perturbation would be small only in sense of real analysis and number theoretic effects would be rather dramatic for perturbations at small values of r. Also the notion of a small perturbation of a given genetic code makes also sense. If $f(r)$ is changed only for the values of r near to $r = 63$, only the degeneracies of the amino-acids coded by largest integers and thus having largest degeneracies are affected.

Bosonic Hamiltonian maximizing negentropy subject to constraints coming from the real genetic code

The direct computational search of genetic codes maximizing the total negentropy without any assumptions about genetic code besides non-degeneracy requires a considerable computational power. It is much easier to search for $n \to p(n)$ assignments maximizing the negentropy subject to the constraint that the assignment is consistent with the genetic code.

The reason is that one can imagine a very simple method giving hopes of finding an assignment $n \to f(n)$, $1 \leq f(n) \leq n$ consistent with the genetic code. The basic observation is the variation of $f(n)$ in the allowed range allows always to achieve the condition $Z(n)\ mod\ p = 0$ for $p \leq n$. This gives reasonable hopes that the nearest prime $p \leq n$ maximizes $Z(n)$. Of course, it can happen that some prime $p > n$ divides $Z(n)$ or some large power of small prime divides $Z(n)$. The optimistic guess for the assignment is simple to construct by starting from $n = 63$ and by proceeding downwards in this manner. One might argue that the ansatz is too conservative. With some good luck it might be possible to assign 6-plets to quite many large primes since the probability $P(n, p)$ to find a value of $f(n)$ guaranteeing $Z(n)\ mod\ p = 0$ for p slightly larger than n is $P(n, p) = n/p$ and near to one. The assignment of 2-plets and stopping to small primes also helps to maximize the total negentropy.

Computational testing of various ansätze based on guesses for stopping codons required to correspond to as small integers as possible is rather straightforward when one starts from a simple guess deduced by the strategy above and described in table 4 below. The strategy is following.

1. It is easy to deduce the map $n \to p(n)$ for $n \leq 13$. For larger values of n prime divisors larger than that implied by the ansatz produce trouble so that the natural strategy is to look whether stopping codons could correspond to integers above $n = 14$ and near to it.

2. The larger the values n of integers corresponding to stopping codons are, the larger the numbers of values $f(n(stop))$ satisfying the criterion for the stopping codon are. The criterion is the indivisibility of $Z(n(stop))$ by any $p \leq 61$ so that prime values of $Z(n(stop))$ certainly satisfy the constraint for $n(stop) > 7$. This increases the hopes that the constraints from the real code can be satisfied. The smallest values of $n(stop)$ for which the constraints can be satisfied for all values of n are $n(stop) \in \{14, 15, 17\}$. The computation proceeds simply by checking whether any combination of candidates for these three stopping codons satisfies is consistent with the genetic code.

In the sequel considerations are restricted to the bosonic partition function but the generalization to the supersymmetric case is straightforward. **Table 12.8** represents the ansatz which served as a starting point for the calculations.

Maps $n \to p(n)$ consistent with the real code can be found by a numerical experimentation starting from the simple guess summarized by Table 4 above and changing the assignments in a obvious manner in the case that some relatively small n yields a large prime factor. In this manner for instance $p = 61$ multiplet can be completed to a 6-plet. The table below represents such a map. From the table it is clear that $p(n) = p(n + 1)$ symmetry is only slightly broken and can be understood as a direct consequence of the mechanism assigning to given n the desired prime $p \sim n$.

Table 12.8: The $n \to p(n)$ correspondence whose deformation produces an $n \to f(n)$ correspondence consistent with the real genetic code.

n in range	is coded to	multiplet
63-61	61	3
60-59	59	2_1
58-53	53	6_1
52-47	47	6_2
46-43	43	4_1
42-41	41	2_2
40-37	37	4_2
36-31	31	6_3
30-29	29	2_3
28-25	23	4_3
24-21	19	4_4
$\{20-18, 16\}$	17	4_5
17		*stop*
15-14		*stop*
13-12	12	2_4
11-10	11	2_5
9-8	7	2_6
7-6	2	2_7
5-4	5	2_8
3-2	3	2_9

Table 12.9: The $n \to p(n)$ correspondence maximizing the total negentropy with a constraint for multiplicities coming from the real genetic code.

n in set	is coded to p	multiplet
$\{63-60, 52, 27\}$	61	6_1
$\{59, 57\}$	59	2_1
$\{58, 56-53, 51\}$	53	6_2
$\{50, 49, 31\}$	47	3
$\{48-44, 33\}$	43	6_3
$\{43, 28, 26, 24\}$	23	4_1
42-41	41	2_2
40-37	37	4_2
36-32	31	4_3
30-29	29	2_3
25-21	19	4_4
$\{20, 19, 18, 16\}$	17	4_5
$\{17, 15, 14\}$		$stop_3$
13-12	13	2_4
11-10	11	2_5
9-8	7	2_6
7-6	2	2_7
5-4	5	2_8
3-2	3	2_9

The Boltzmann weights for the $n \to p(n)$ correspondence represented in the table are given in the array below.

n	1	2	3	4	5	6	7	8	9	10	11	12
$f(n)$	1	2	3	2	2	2	1	4	6	5	1	12
n	13	14	15	16	17	18	19	20	21	22	23	24
$f(n)$	7	12	12	3	16	4	13	19	9	18	21	18
n	25	26	27	28	29	30	31	32	33	34	35	36
$f(n)$	22	11	6	1	6	23	19	17	15	22	34	5
n	37	38	39	40	41	42	43	44	45	46	47	48
$f(n)$	11	32	32	25	41	28	10	37	35	25	11	39
n	49	50	51	52	53	54	55	56	57	58	59	60
$f(n)$	1	11	24	22	2	5	47	39	9	25	1	48
n	61	62	63									
$f(n)$	21	15	20									

12.4.5 Could The Symmetries Of The Genetic Code Constrain Number TheoreticalThermodynamics?

The number theoretic approach alone leaves completely open the correspondence between DNA triplets and integers n and only the comparison of a code predicting correctly the degeneracies of various amino-acids with the real genetic code allows to deduce information about this correspondence. For instance, 0, 1 DNAs and amino-acids can be identified immediately.

The model for prebiotic evolution [**?**, K19] relies on the fact that the genetic code has an almost exact symmetry: the third nucleotide of the codon has symmetry under A-G exchange and slightly broken symmetry under T-C exchange and an interesting possibility is that this symmetry could be understood at the number theoretical level. Certainly it cannot be a property of the map mapping DNA triplets to integers alone.

What exact A-G symmetry and almost exact T-C symmetry could mean number theoretically?

The most natural interpretation for A-G and T-C symmetries of last nucleotide of codon is that the third 4-digit of the DNA triplet interpreted as a number in the set $\{0, 63\}$ represented in 4-base do not matter much. The symmetry for T-C is slightly broken and this gives 64-20 code instead of $64 \to N \leq 16$ code. Real mathematics would suggest that these 4-digit corresponds to zeroth power of 4 whereas 2-adic arithmetics suggests that it corresponds to the second power of 4.

The characteristic feature of the genetic code is that the degeneracies come in pairs which can be understood in terms of A-G symmetry. There are 3 6-plets, 5 4-plets, 9 2-plets and 1 3-plet of amino-acids and one 3-plet of stopping codons besides the 2 singlets assignable to 0 and 1. That almost all multiplets contain even number of DNAs reflects the additional approximate T-C symmetry.

Even degeneracies must correspond to an approximate symmetry of the partition function. This kind of symmetry could be produced by hand by expressing the partition function as a product of partition functions $Z(n)$ and $Z(f(n))$, where $n \to f(n)$ represents the symmetry but numerical experimentation shows that this does not work. The reason is that for a given n the primes associated with n and $f(n)$ compete and product partition function selects winners from these pairs reducing the degeneracies of the losers so that spectral power tends to get peaked. Hence the product model works only if the symmetry is already there in the sense that the largest prime power factor for $Z(n)$ and $Z(f(n))$ correspond to same prime p.

Suppose that 3 codons correspond to stopping codons. Suppose that there exist a symmetry $n \to f(n)$, not necessary reflection, acting on remaining codons with the property that the largest prime power dividing $Z(n)$ and $Z(f(n)$ corresponds to the same p. Since the number of these codons is odd, the map $n \to f(n)$ must have a fixed point. Obviously the degeneracies are even for primes coded by non-fixed points and odd for those coded by fixed points and the structure of genetic code is consistent with this prediction.

Table 12.10: Genetic code.

	A	G	T	C	
A	phe	ser	tyr	cys	A
	phe	ser	tyr	cys	G
	leu	ser	stop	stop	T
	leu	ser	stop	trp	C
G	leu	pro	his	arg	A
	leu	pro	his	arg	G
	leu	pro	gln	arg	T
	leu	pro	gln	arg	C
T	ile	thr	asn	ser	A
	ile	thr	asn	ser	G
	ile	thr	lys	arg	T
	met	thr	lys	arg	C
C	val	ala	asp	gly	A
	val	ala	asp	gly	G
	val	ala	glu	gly	T
	val	ala	glu	gly	C

Quite generally, for the reduction of the code to a maximal subset of integers $2 \leq n \leq 63$ not containing $f(n)$ for any n, one would have 11 singlets, 5 2-plets, and 3 3-plets in the set of even integers, or briefly

$$29 = 10 \times \mathbf{1} \oplus 5 \times \mathbf{2} \oplus 3 \times \mathbf{3} \ .$$

The fixed point $n = f(n)$ would code the amino-acid (ile) coded by 3 DNAs.

A reasonable candidate for the symmetry is suggested by the preceding construction reproducing the degeneracies of the genetic code correctly and predicting that n and $n+1$ tend to code the same amino-acid.

A further input is the information provided by the deviations from the universality of the genetic coded to be discussed later. The deviations from the universality typically involve stopping codons and in the proposed construction it is easy to perform small modifications of the code for values of n near 63. Hence it is natural to test the stronger assumption $2n$ and $2n+1$ code for the same p for $2 \leq n < 60$ and that $n = 61, 62, 63$ act as stopping codons so that $n = 60$ would correspond to the fixed point coding for ile.

An objection against this hypothesis is that a lot of negentropy is lost if large integers are forced to act as stopping codons. Also the successful construction of the genetic code table starting from the A-G and T-C symmetries of the code table leads to the assignment of the stopping codons to relatively small integers. In this construction the assignment of stopping codons to large values of n codons would also make more difficult to assign large multiplets to large primes.

How close is the correlation between the map from DNA triplets to integers and the map $n \to p(n)$?

The number theoretical model alone does not fix the map between DNA triplets and integers although it poses constraints on this correspondence. A-G symmetry and almost T-C symmetry of the code table however suggest a labelling of the codons which in good approximation could determine *codon* $\to n$ map.

1. A-G and T-C symmetries suggests that the numbering of genetic codons using 4-base representations, that is as sequences of integer triplets (n_1, n_2, n_3), $0 \leq n_i \leq 3$ in 4-base such that each integer labels the four bases. The correspondence can be different for the different members of the triplet. The natural correspondence would be such that (n_1, n_2, n_3) interpreted as 4-digit representation of n gives the map in a reasonable approximation.

Table 12.11: Genetic code with the proposed correspondences between DNA triplets with integers n and amino-acids with primes $p(n)$. For instance, $ala(50, 47)$ tells that CGA is mapped to $n = 50$ and ala corresponds to the prime $p = 47$.

	A	G	T	C	
A	phe (46, 43)	ser(62, 61)	tyr(16, 17)	cys(31, 29)	A
	phe(47, 43)	ser(63, 61)	tyr (17, 17)	cys(32, 29)	G
	leu (44, 41)	ser (61, 61)	stop (14)	stop(30)	T
	leu (45, 41)	ser(62, 61)	stop(15)	trp(0/1)	C
G	leu(42, 41)	pro(58, 59)	his(12, 13)	arg(28, 23)	A
	leu (43, 41)	pro(59, 59)	his(13, 13)	arg(29, 23)	G
	leu(40, 41)	pro(56, 59)	gln(10, 11)	arg(26, 23)	T
	leu (41, 41)	pro(57, 59)	gln(11, 11)	arg(27, 23)	C
T	ile (38, 37)	thr(54, 53)	asn(8, 7))	ser(24, 61)	A
	ile(39, 37)	thr(55, 53)	asn (9, 7)	ser(25, 61)	G
	ile (37, 37)	thr(52, 53)	lys (6, 2)	arg(22, 23)	T
	met (1/0)	thr(53, 53)	lys (7, 2)	arg(23, 23)	C
C	val(35, 31)	ala(50, 47)	asp(4, 5)	gly(20, 19)	A
	val(36, 31)	ala(51, 47)	asp(5, 5)	gly(21, 19)	G
	val(33, 31)	ala(48, 47)	glu(2, 3)	gly(18, 19)	T
	val (34, 31)	ala(49, 47)	glu(3, 3)	gly(19, 19)	C

2. The correspondence $(T, C, A, G) \leftrightarrow (0, 1, 2, 3)$ for the third nucleotide turns out to be most realistic one from the point of view of $n \to p(n)$ correspondence. A-G and T-C symmetries suggests that n_3 is mapped almost as such to the third 4-digit of n apart from symmetry breaking due to the complications caused by the insertion of 0 and 1 to the code table.

3. The previous example for the genetic code suggests that $n = 14, 15$ correspond to stopping codons. Negentropy Maximization Principle favors doublets for small integers. Since the third column of the code table contains only doublets, it should correspond to small integers. These constraints are satisfied under two conditions. First, n_1 labels the rows of the table with the correspondence $(T, C, A, G) \leftrightarrow (0, 1, 2, 3)$ along the rows of the table so that first and second and third and fourth columns are permuted. Secondly, n_2 must label the entries formed by 4-sub columns of the table and one must have $(C, T, G, A) \leftrightarrow (0, 1, 2, 3)$ for so that n_2 increases from bottom to top.

4. The two stopping codons ATT and ATC would would correspond to $n = 14, 15$ as in the example discussed above. Stopping codon ACT would correspond to $n = 30$ ($n = 17$ in the example). Encouragingly, ser corresponds to $\{63, 62, 61, 60, 22, 23)\}$ coding very naturally $p = 61$. Also in the example discussed 61 belongs to 6-plet.

5. The correspondence between codons (n_1, n_2, n_3) and integers n cannot be given exactly by the representation of n in 4-base since 0 and 1 do not correspond to ACC coding trp (0 or 1) but would correspond to $(1, 3, 3) = 31$. TAC coding met (1 or 0) would correspond to $(2, 1, 3) = 39$. The map from codons to integers with minimal symmetry breaking is obtained from the 4-digit coding of n by shifting 0 and 1 to the positions of 31 and 39. For $n(codon) < 29$ this induces the map $n = n(codon) + 2$. For $41 > n(codon) > 29$ the map is $n = n(codon) + 1$, and for $n(codon) > 41$ the map is $n = n(codon)$. Table 7. lists the resulting number theoretic code in the bosonic case and its correspondence with DNA triplets and amino-acids for this option. It is clear that the risky assignments $n \to p(n)$ are associated with ser and pro.

1. Numerical testing in the bosonic case

It is straightforward to test the proposed $n(codon) \to n$ map by numerical computations. They are done for both bosonic and supersymmetric case. In the bosonic case correspondence

Table 12.12: $n \to p(n)$ correspondence allowing two different Boltzmann weights $f_1(n)$ and $f_2(n)$ consistent with the real genetic code obtained by a small modification of the correspondence $n \to p(n)$ implied by the map $n(codon) \to n$ discussed above. This correspondence is also shown in the table for comparison purposes.

n	1	2	3	4	5	6	7	8	9	10	11	12	13
model	0	3	3	5	5	2	2	7	7	11	11	13	13
real	0	3	3	5	5	2	2	7	7	11	11	13	13
$f_1(n)$	1	2	3	2	2	2	1	4	6	5	1	12	7
$f_2(n)$	1	2	3	2	2	2	1	4	6	5	1	12	7
n	14	15	16	17	18	19	20	21	22	23	24	25	26
model	0	0	17	17	19	19	19	19	23	23	61	61	23
real	0	0	17	17	19	19	19	19	23	23	61	61	23
$f_1(n)$	4	8	6	10	12	12	3	5	12	11	15	17	7
$f_2(n)$	4	12	2	6	12	12	7	5	16	11	15	17	7
n	27	28	29	30	31	32	33	34	35	36	37	38	39
model	23	23	0	29	29	23	31	31	31	31	37	37	43
real	23	23	0	29	29	23	31	31	31	31	37	37	37
$f_1(n)$	7	6	21	28	20	27	33	33	21	21	15	36	30
$f_2(n)$	3	6	21	24	24	31	33	33	17	17	15	32	26
n	40	41	42	43	44	45	46	47	48	49	50	51	52
model	37	41	41	41	41	41	41	43	47	47	47	47	53
real	41	41	41	41	41	41	43	43	47	47	47	47	53
$f_1(n)$	13	6	18	23	12	27	28	44	24	33	14	23	52
$f_2(n)$	9	10	18	23	12	31	32	5	20	29	6	23	10
n	53	54	55	56	57	58	59	60	61	62	63		
model	53	53	53	59	61	59	59	59	61	61	61		
real	53	53	53	61	59	59	59	59	61	61	61		
$f_1(n)$	29	26	25	56	10	49	9	10	4	27	49		
$f_2(n)$	5	48	45	41	14	56	15	27	8	35	22		

cannot be realized as such. $n = 29$ corresponding to 6^{th} arg is the source of problems and by a trial and error one ends up with a slightly modified $p \to n(p)$ correspondence allowing two solutions for Boltzmann weights $f(n)$ represented in Table 8 below. The requirement that the small deviations from the standard code are realizable as small deviations of $f(n)$ without affective genetic code leaves only $f_1(n)$ into consideration (as will be found in the next section).

2. Numerical testing in the supersymmetric case

One might hope that the replacement of the bosonic partition function with the supersymmetric one might allow an exact realization of the simplest $n(codon) \to n$ correspondence. The multiplication of Z_B by Z_F does not destroy any divisors already present so that the effect might be small. It however turns out that the proposed ansatz fails already at $n = 10$ since Z_F equals to prime $p = 23$ giving higher negentropy than $p = 11$-factor of Z_B. One can try to continue by a modification of the ansatz but the troubles continue and are basically due to the large prime power factor of Z_F. Hence it seems that bosonic ansatz is the only realistic one. Fermionic ansatz is certainly non-realistic since the number of non-vanishing elements of $d_F(n, r)$ is as small as 10 even for $n = 63$.

12.5 Confrontation Of The Model With Experimental Facts

The proposed model of genetic code means that we would rather literally consist of sequences of numbers with DNA representing sequences in base 64 and amino-acid sequences represented as products of primes $2 \leq p \leq 61$ and separated by zeros. What this predicts depends on how literally

we take this interpretation.

12.5.1 Basic Facts About Amino-Acids

Amino-acids can be classified into three groups.
i) The first class contains 8 hydrophobic non-polar amino-acids with non-polar neutral side-chain. They are leu (6), ala (4), val (4), pro (4), ile (3), phe (2), met (1), trp (1) (numbers in parenthesis tell the number of DNAs coding the amino-acid in question).
ii) Second class consists of 7 hydrophilic polar amino-acids with polar neutral side-chain: ser (6), gly (4), thr (4), cys (2), asp (2), gln (2), tyr(2).
iii) The third class consists of polar hydrophilic acidic amino-acids with charged side chain: asp (2), glu (2) and hydrophilic basic amino-acids arg (6), lys (2), his (2): 5 altogether.

As already noticed, met and trp representing 0 and 1 should belong to the group of non-polar neutral amino-acids and indeed do so. Also the amino-acid representing a fixed point of symmetry $n \to f(n)$ (ile) (if such a symmetry indeed exists) would belong to this group. It is worth of noticing that each group contains single amino-acid coded by 6 DNAs.

12.5.2 Could The Biological Characteristics Of An Amino-Acid Sequence Be Independent On The Order Of Amino-Acids?

The representation of an integer as a product of primes does not depend on the order of factors. Unless the amino-acid sequence does not inherit the natural order of DNA triplets somehow, the biological properties of portions of amino-acid sequences separated by zeros would be invariant under the permutations of amino-acids: the permutation of amino-acids would be analogous to a permutation of bosons. The prediction is extremely strong and certainly testable and might have been observed long ago if indeed true. Professional biologist could probably immediately kill this option.

12.5.3 Are The Amino-Acids And DNAs Representing 0 And 1 Somehow Different?

The amino-acid representing 0 would most naturally separate different structural and/or functional units and both 0 and 1 could represent a biologically inert amino-acid. Also other interpretation might of course be imagined. The amino-acids representing 0 and 1 would be met coded by TAC and trp coded by ACC, not necessarily in this order.

Do met and trp then have some special properties distinguishing them as 1 and 0?

1. Consider first chemical structure. Both are neutral and non-polar amino-acids, which can be regarded as a basic prerequisite for biological inertness. Met is the only amino-acid containing $CH_2 - S - CH_3$ side chain (cys contains $CH_2 - S - H$ side chain and there are no other amino-acids containing sulphur). Trp in turn is the only amino-acid containing two cyclic chains.

   This kind of arguments must be however taken with a big grain of salt as the following argument shows. Proline differs from all other amino-acids in that the neutral group $H_3N^+ - COO^- - C - H$ group is replaced by a charged $H_2N - COO^- - C - H$ group and is therefore a reasonable looking candidate for 0: pro is however coded by 4 DNAs which would correspond to 2 n and $n + 2$ DNAs with $2 \leq n \leq 31$.

2. At the level of biological function there is indeed a deep difference. The DNA triplet coding for met acts almost universally (for deviations see [I47]) as a starting codon which conforms with the identification of met as an amino-acid representing either 0 or 1 (literally the first amino-acid!) and having no other biological significance than telling where in a more complex structure consisting of amino-acid sequences a structural basic element coded by single gene begins.

12.5.4 The Deviations From The Standard Code As Tests For The Number Theoretic Model

One can take two different attitudes concerning the deviations from the universality of the code.

Since the deviations occur in mitochondrial genomes and in nuclear genomes of some unicellular eukaryotes, one could argue that in these cases the code need not have achieved full negentropy maximization and that NMP model does not apply. Even if NMP applies, one can argue that the maps $n(codon) \to n$, $n \to f(n)$, and even $n \to p(n)$ correspondence can differ dramatically from that for the nuclear genome.

Second attitude would be that these codes correspond to different local maxima of total negentropy and that the codes correspond to small perturbations of nuclear $n(codon) \to n$, $n \to f(n)$ correspondences.

The deviations from the standard genetic code [I47] allow to test between these options, in particular the genetic variant of Negentropy Maximization Principle predicting that small perturbations of $f(n)$ inducing small perturbations of genetic code can affect only large values of n. Numerical experimentation suggest that small perturbations of $n(codon) \to n$, $n \to f(n)$ correspondences are not in question.

Violations of universality for nuclear genes are consistent with the number theoretical model

The violations of the universality [I47] are very rare for nuclear genes. A few unicellular eukaryotes have been found that use one or two of three stop codons to code amino-acids instead. The use of two stop codons to code amino-acids necessarily violates the universality of the third column of the code table.

These violations would be consistent with the hypothesis that the two stopping codons ATA and ATG correspond to large values of n (most naturally 62 and 63) but do not force this model. For the codes represented in **Table 12.13** however ATA and ATG however correspond to $n = 14, 15$ so that the modification of the code occurs at rather small values of n and the modifications of $f(n)$ at these values radiate their effect to all higher values of $f(n)$ via the coupling $Z(n) = \sum_{r=1}^{n} d(n,r)f(r)$ and this effect is large in number theoretical sense. Hence small perturbations of $n \to f(n)$ and $n(codon) \to n$ correspondences might not be enough and even $n \to p(n)$ correspondence might need a modification. A detailed numerical computation is required to check whether the model can reproduced the modified codes with some assignment $f(n)$ of Boltzmann weights.

The mitochondrial deviations related to codons representing 0, 1, and stopping sign

For the mitochondrial genes the situation is more complex. There are several kinds of deviations and first kind of deviations related to codons representing 0, 1, and stopping sign.

1. Deviations

Consider first the exceptions associated with stopping codons and codons representing usually 0 and 1 in the proposed model.

1. Mitochondrial codon ACT from animals and micro–organisms (but not from plants) codes trp instead of stopping sign. The problem is that trp corresponds to singly coded amino-acid and should represent either 0 or 1.

2. Most animal mitochondria use TAT in the first column of the code table to code met instead of ile coded usually 3 times. Also this is troublesome since met should correspond to $n = 0$ and be coded only once.

Since both trp and met correspond to 0 and 1 in either order in the model, the question what it means that DNA not representing 0 or 1 codes for 0 or 1. The working hypothesis is that met codes for $p = 1$ whereas trp codes for 0 acting as a codon separating two functional units of amino-acid sequence and being in this sense almost equivalent with stopping codon.

1. Does the notion of $p = 1$ codon make sense?

Table 12.13: $n \to p(n)$ correspondence allowing three different Boltzmann weights $f_{1i}(n)$ and 4 different Boltzmann weights $f_{2i}(n)$ as perturbations of $f_1(n)$ and $f_2(n)$. $f_{11} = f_1$ and $f_{21} = f_2$ implies that these "perturbations" are unique and correspond to $p(37) = 13$ instead of $p(37) = 37$. The table lists only the rows for which deviation from $f_1(n)$ and $f_2(n)$ occurs.

n	27	28	29	30	31	32	33	34	35	36	37	38	39
p(n)	23	23	0	29	29	23	31	31	31	31	13	37	43
$f_{11}(n)$	7	6	21	28	20	27	33	33	21	21	21	30	24
$f_{12}(n)$	7	6	21	28	20	27	33	33	21	21	22	29	23
$f_{13}(n)$	7	6	21	28	20	27	33	33	21	21	30	21	15
$f_{21}(n)$	3	6	21	24	24	31	33	33	17	17	9	38	32
$f_{22}(n)$	3	6	21	24	24	31	33	33	17	17	10	37	31
$f_{23}(n)$	3	6	21	24	24	31	33	33	17	17	21	26	20
$f_{24}(n)$	3	6	21	24	24	31	33	33	17	17	22	25	19
n	40	41	42	43	44	45	46	47	48	49	50	51	52
p(n)	37	41	41	41	41	41	41	43	47	47	47	47	53
$f_{11}(n)$	13	6	24	23	18	27	28	44	24	27	14	23	46
$f_{12}(n)$	13	6	25	23	19	27	28	44	24	26	14	23	45
$f_{13}(n)$	13	6	33	23	27	27	28	44	24	18	14	23	37
$f_{21}(n)$	9	10	12	23	6	31	32	5	20	35	6	23	16
$f_{22}(n)$	9	10	13	23	7	31	32	5	20	34	6	23	15
$f_{23}(n)$	9	10	24	23	18	31	32	5	20	23	6	23	4
$f_{24}(n)$	9	10	25	23	19	31	32	5	20	22	6	23	3
n	53	54	55	56	57	58	59	60	61	62	63		
$p(n)$	53	53	53	59	61	59	59	59	61	61	61		
$f_{11}(n)$	29	26	25	56	10	49	15	10	4	27	55		
$f_{12}(n)$	29	26	25	56	10	49	16	10	4	27	56		
$f_{13}(n)$	29	26	25	56	10	49	24	10	4	27	3		
$f_{21}(n)$	5	48	45	41	14	56	9	27	8	35	16		
$f_{22}(n)$	5	48	45	41	14	56	10	27	8	35	17		
$f_{23}(n)$	5	48	45	41	14	56	21	27	8	35	28		
$f_{24}(n)$	5	48	45	41	14	56	22	27	8	35	29		

The condition $S_{p(n)}(n) = 0$ is the most general manner to define effective $p = 1$ codon whereas stopping codon would has positive entropy. This requires that for effective $p = 1$ codons $Z(n)$ is divisible by $p(n)$ and gives a negative contribution to $S_{p(n)}(n)$ but despite this $S_{p(n)}$ is vanishing or positive.

Perhaps it is not a accident that the triply coded ile corresponds to the exceptional multiplet with odd degeneracy. As proposed, single odd degeneracy could be understood if the partition function has an approximate symmetry $n \to f(n)$ such that the DNA coding the third ile corresponds to a fixed point of this symmetry. The fixed point codon would code for 1 in the sense proposed rather than for ile.

In the proposed model $p = 37$ corresponds to ile and the ile transforming to met in yeast mitochondria is coded by $n = 37$. Numerical search demonstrates that $p(37) = 13$ instead of $p(37) = 37$ provides 3 modifications of $f_1(n)$ and 4 modifications of $f_2(n)$ for which $p = 1$ condition is satisfied. The solutions $f_{11}(n)$ and $f_{21}(n)$ are identical with $f_1(n)$ and $f_2(n)$. Obviously this solution is unique.

3. What coding of $p = 0$ could mean?

What it means that $n > 0$ codes instead of stopping sign for 0 is more difficult to interpret unless 0 indeed effectively represents an amino-acid (trp) separating functionally independent units of amino-acid sequence effectively coded by separate genes and stopping sign in this sense. One

Table 12.14: $n \to p(n)$ correspondence allowing single distribution $f(n)$ of Boltzmann weights consistent with the genetic code of yeast mitochondria obtained by a small modification of the correspondence $n \to p(n)$ implied by the map $n(codon) \to n$ discussed above. The $n \to f(n)$ correspondence results as a modification of $n \to f_2(n)$ for nuclear genetic code so that this option is favored by universality. Only the rows of $n \to p(n)$ and $n \to f(n)$ correspondences differing from those for the nuclear code are given in the table. The correspondences for nuclear genetic code are also shown in the table for comparison purposes.

n	1	2	3	4	5	6	7	8	9	10	11	12	13
nuclear	0	3	3	5	5	2	2	7	7	11	11	13	13
$f_2(n)$	1	2	3	2	2	2	1	4	6	5	1	12	7
n	14	15	16	17	18	19	20	21	22	23	24	25	26
nuclear	0	0	17	17	19	19	19	19	23	23	61	61	23
$f_2(n)$	4	12	2	6	12	12	7	5	16	11	15	17	7
n	27	28	29	30	31	32	33	34	35	36	37	38	39
nuclear	23	23	0	29	29	23	31	31	31	31	37	37	43
$f_2(n)$	3	6	21	24	24	31	33	33	17	17	15	32	26
n	40	41	42	43	44	45	46	47	48	49	50	51	52
nuclear	37	41	41	41	41	41	41	43	47	47	47	47	53
yeast	53	53	41	53	53	43	43	41	47	47	47	47	53
$f_2(n)$	9	10	18	23	12	31	32	5	20	29	6	23	10
$f(n)$	13	2	18	22	10	3	36	42	14	29	4	20	7
n	53	54	55	56	57	58	59	60	61	62	63		
nuclear	53	53	53	59	61	59	59	59	61	61	61		
yeast	41	59	41	61	41	59	59	59	61	61	61		
$f_2(n)$	5	48	45	41	14	56	15	27	8	35	22		
$f(n)$	53	53	53	59	61	59	59	59	61	61	61		

might think that code has evolved like a computer program via modularization so that in the advanced form of the code DNA sequences code only for the basic building amino-acid sequences rather than their composites separated by exotic amino-acids. Other deviations are consistent with the genetic variant of Negentropy Maximization Principle.

The anomalous behavior of yeast mitochondria

Yeast mitochondria use GAX codons in the first column to code for thr (coded by 4 codons usually) instead of leu (coded by 6 codons usually). For the $n \to p(n)$ correspondences motivated by the mapping $n(codon) \to n$, the deviation would mean that the integers $n = 40 - 43$ code for $p = 53$ (thr) besides n in the range 52-55. A rough modular arithmetics based estimate for the probability that this occurs for single codon is roughly n/p for $n < p$ so that the total probability for this to occur would be $P = 40 \times 41 \times 42 \times 43/53^4 \simeq .38$. It turns out that $n = (40, 41, 42, 43)$ fails to code for $p = 53$. Thus mitochondrial code and nuclear code for yeast should have slightly different $n(codon) \to n$ correspondence. The modification

$$\begin{aligned} p(40, 41, 42, 43, 44, 45, 46, 47) = &\quad (41, 41, 41, 41, 41, 41, 43, 43) \\ \to &\quad (53, 53, 41, 53, 53, 43, 43, 41) \end{aligned}$$

is consistent with negentropy maximization. This means that the permutations $(42 \leftrightarrow 44)$ and $(45 \leftrightarrow 47)$ distinguish the map $n(codon) \to n$ from that for the nuclear code. The modification is given in **Table 12.14**.

The deviations associated with exotic amino-acids and stopping sign codons

There are also two non-standard amino-acids: selenocysteine and pyrrolysine.

1. Selenocysteine is encoded by ACT (fourth column) coding stopping sign normally. Interestingly, ACT codes also stopping sign and the translation machinery is somehow able to discriminate when selenocysteine is coded instead of stop. This codon usage has been found in certain Archaea, eubacteria, and animals. This deviation means that the number of amino-acids is 21 or 20 depending on context.

2. In one gene found in a member of the Archaea, exotic amino-acid pyrrolysine is coded by ATC, which corresponds to the lower stopping sign in the code table. This case represents the only deviation from universality of the third column of the code table but even in this case also stopping sign is coded. How the translation machinery knows whether to code pyrrolysine or to stop translation is not yet known.

   These deviations are consistent with the number theoretical models discussed in [**?**, K19] for which number 21 indeed has a deep number theoretical meaning and assuming that stopping sign can be regarded formally as an amino-acid. In the recent model a reasonable looking interpretation of the exotic amino-acids is as variants of stopping sign in some sense. For instance, the resulting amino-acid sequences could consist of separate functional units separated by selenocysteine/pyrrolysine.

To sum, all deviations challenging the number theoretic model discussed in this chapter are associated with mitochondrial genome only and involve stopping sign codons, codons representing 0 and 1 and exotic amino-acids.

12.5.5 Model For The Evolution Of The Genetic Code And The Deduction Of $N \to P(N)$ Map From The Structure Of tRNA

In [K19] a detailed model for the evolution of the genetic code is developed. The hypothesis is that recent DNA-amino-acid code evolved from a code mapping RNA triplets to RNA triplets with the mediation of pre-RNA catching RNA molecules from environment and bringing them to the growing RNA sequence. Amino-acids served originally as catalyzers of the reaction but at some stage began attach to the growing RNA sequence after which RNA sequence become un-necessary and only amino-acid sequence remained.

In the recent framework tRNA would represent the mapping of integers represented by RNA as sequences in 64 base to RNAs representing sequences of primes. Genetic coded literally mapped RNA representing integer $0 \leq n \leq 63$ to an RNA representing the prime $p(n)$. The map $n \to p(n)$ could be determined up to a permutation of the 18 primes $2 \leq p \leq 61$ and permutations of integers mapped to same p (not larger than 6) from the structure of the recent tRNA since tRNA molecules could still contain RNA pairs representing $n(p) - p$ pairs. That mRNA-RNA correspondence at the level of tRNA would represent $n \to p(n)$ correspondence means that there is no need to ponder the problem how to assign to a given amino-acid the corresponding prime p: tRNA-amino-acid correspondence would be determined by biochemistry.

12.5.6 Genetic Code As A Product Of Singlet And Doublet Codes?

The model of the genetic code applies to any number n of DNAs and maps the numbers $n = 0, 1...n-1$ to $\{0,1\} \cup \{primes\ p \leq n-1\}$. In [K19] a model for the genetic code resulting via a symmetry breaking from the product of codes associated with 16 DNA doublets and 4 DNA singlets was considered. At the level of DNAs the product code is very natural and the almost symmetries of the genetic code with respect to the last codon support the idea.

The product structure at the level of amino-acids is however not at all manifest and seems to be absent. This is what the number theoretical model predicts. The primes associated with the product of singlet and doublet codes have no natural composition into products of primes associated with singlet and doublet codes. Nor is the number of these primes product of numbers of primes associated with singlet and doublet codes.

12.6 Exponential Thermodynamics Does Not Work

In the following various unsuccessful attempts to understand genetic code in terms of exponential thermodynamics using Hamiltonian $H(r) = r$ are summarized.

12.6.1 What Can One Conclude About P-Adic Temperature Associated With The Genetic Code In The Case Of Exponential Thermodynamics?

Ordinary thermodynamics suggests that also in the case of exponential thermodynamics temperature should be non-negative. This would boil down to basic requirement $q_0 = r_0/s_0 > 1$ characterizing the genetic temperature. This condition has been however dropped in computations since it is not mathematically necessary in the case of finite state system.

The work with exponential thermodynamics is restricted to the bosonic case. As already found, the fermionic high temperature limit is extremely unrealistic. One important requirement is that also the primes 37 and 61 can appear as divisors in the generalization of $d(n)$ to be discussed. For the remaining primes the most conservative, and probably unrealistic, assumption would be that the arguments of the logarithms appearing in S_p are unaffected so that only the reduction of large r contributions would reduce the degeneracies of over-represented primes. It seems that for small over-represented primes the norms of logarithms must be affected.

The requirement that all entropies $S_{p(n)}(n)$ associated are negative poses strong conditions on q_0, and this might not be possible for all n. The entropic or zero entropy integers could correspond to stopping sign codons.

1. Conditions on q_0

Writing $q_0 = r_0/s_0 > 1$ one can express S_p and assuming $H = r - 1$ and $T_r = 1$ in terms of integers alone:

$$\begin{aligned} S_p(n) &= \sum_{r=1}^{n} p(n,r)(\frac{r_0}{s_0})^{-r+1} log(|\frac{r_0^{n-r+1}s_0^{r-1}}{\hat{d}(n)}|_p) \ , \\ \hat{d}(n) &= \sum_{r=1}^{n} \hat{d}(n,r) \ , \\ \hat{d}(n,r) &= r_0^{n-r+1}s_0^{r-1}d(n,r) \ . \end{aligned} \tag{12.6.1}$$

The use of different representation for $p(n,r)$ and the argument of logarithm is especially convenient in the numerical calculation of entropy since modular arithmetics can be applied to deduce the argument of logarithm.

To make the representation more fluent, introduce the set $\mathcal{Q}_R$ as subset of primes $p \in \mathcal{P} = \{2, 3, ..., 61\}$ by excluding primes in the set $\mathcal{R} \subset \mathcal{P}$. It turns out that $\mathcal{Q} = P \setminus \mathcal{R}$ condition is too restrictive and hence the subscript $_R$ is added to the definition. The minimal choice for $\mathcal{R}$ is $\mathcal{R}_{min} = \{37, 61\}$ but also 23 is a reasoanable candidate for an element of $\mathcal{R}$. More explicitly,

$$\mathcal{Q}_{max} = \mathcal{P} \setminus \mathcal{R}_{min} = \{2, 3, 5, 7, 11, 23, 17, 19, 23, 29, 31, 41, 43, 47, 53, 59\} \ .$$

Define also integer X_Q as the product of primes in $\mathcal{Q}$:

$$X = \prod_{p_k \in \mathcal{Q}} p_k \ . \tag{12.6.2}$$

Consider now the conditions on q_0 in more detail.

1. Every prime $2 \leq p \leq 61$ must divide $\hat{d}(n)$ for some values of $n(p)$ in order that the prime in question has integers n mapped to it. This has two implications. First, the arguments of the logarithms appearing in the entropy should remain invariant for all primes in $\mathcal{Q}$ to guarantee that no prime is lost. Secondly, for each prime $q \in \{23, 31, 61\}$ there should exist n_q such that $\hat{d}(n)$ is divided by q and q corresponds to the largest prime power of prime in $\hat{d}(n)$.

2. Stopping sign codons correspond to zero information integers n not containing $p \leq 61$ in their decomposition to primes. Assume that $n = 13$ and 36 remain such primes so that $\hat{d}(13)$ and $\hat{d}(36)$ remain indivisible by $p \leq 61$. Also a third similar integer must emerge in finite temperature thermodynamics.

2. Conditions for primes in $\mathcal{Q}$

Consider now these conditions for primes in $\mathcal{Q}$.

1. The p-adic norms of $\hat{d}(n,r)$ and $\hat{d}(n)$ are same as those of $d(n,r)$ and $d(n)$ if the conditions

$$r_0 \ mod \ p = 1 \ , \quad s_0 \ mod \ p = 1 \tag{12.6.3}$$

hold true. This guarantees that logarithms appearing in S_p are unaffected.

2. These conditions could hold for all primes in $\mathcal{Q}$ and can be satisfied by the ansatz:

$$\begin{aligned} r_0 &= 1 + R_0 X \ , \ s_0 = 1 + S_0 X \ , \\ X &= \prod_{p_k \in \mathcal{Q}} p_k \ . \end{aligned} \tag{12.6.4}$$

Note that one must have $R_0/S_0 > 1$ in order to have a positive temperature T.

3. The condition $\mathcal{Q}_R = \mathcal{P} \setminus \mathcal{R}$ is un-necessarily restrictive. One can also consider the situation in which one drops some over-represented small primes from X. The dropping of say $p = 7$ and $p = 11$ could make possible the representability of 23 appearing as a factor in $d(32) = 3 \times 11^2 \times 23$ and $d(33) = 3^2 \times 7^2 \times 23$. In fact, the dropping of all small primes $p \leq 11$ might cure at single stroke the over-representability problem. They are probably not lost totally since they have a considerable probability to appear as factors in $\hat{d}(n)$.

3. Conditions for primes in $\mathcal{R}$

Consider next the situation for a prime $q \in \mathcal{R}$, say $\mathcal{R}_{min} = \{37, 61\}$. The task is to deduce conditions on the integers (R_0, S_0).

1. There must exist at least one n_q such that $\hat{d}(n_q)$ is divisible by q:

$$\begin{aligned} \hat{d}(n_q) &= \ mod \ q = 0 \ , \ q \in \mathcal{R} \ , \\ \hat{d}(n_q) &= \sum_{r=1}^{n_q} \hat{d}(n_q, r) \ , \\ \hat{d}(n_q, r) &= (1 + R_0 X)^{n_q - r + 1} (1 + S_0 X)^{r-1} d(n_q, r) \ , \\ X &= \prod_{p_k \in S} p_k \ . \end{aligned} \tag{12.6.5}$$

S_0 and R_0 satisfying these conditions for some n_q can be found by a direct numerical search.

2. For each n_q there must exist at least one r_q satisfying the condition

$$\hat{d}_{n_q r_q} \; mod \; q \neq 0 \;\; , \;\; q \in \mathcal{R} \;\; . \tag{12.6.6}$$

These conditions are very general and allow many solutions (R_0, S_0).

i) For $\mathcal{R}_{min} = \{37, 61\}$ and $\mathcal{Q}_{max} = \mathcal{Q}_{R_{min}}$ one can use the conditions $X_Q = X_{min} \; mod \; 37 = 7$ and $X_{min} \; mod \; 61 = 1$ to reduce conditions to a numerically more tractable form

$$\begin{aligned} \sum_{r=1}^{n_{37}} (1+7R_0)^{n_{37}-r+1}(1+7S_0)^{r-1} d(n_{37}, r) \; mod \; 37 &= 0 \;\; , \\ \sum_{r=1}^{n_{61}} (1+R_0)^{n_{61}-r+1}(1+S_0)^{r-1} d(n_{61}, r) \; mod \; 61 &= 0 \;\; . \end{aligned} \tag{12.6.7}$$

ii) If one drops the over-represented small primes $p \leq 11$ from X one obtains $X_Q = X_{min} \; mod \; 37 = 27$ and $X_{min} \; mod \; 61 = 40$. In this case conditions are obtained from previous ones by the replacement $(7, 1) \to (27, 40)$.

iii) For $\mathcal{R} = \{23, 37, 61\}$ one would have $X_R \; mod \; 23 = 10$, $X \; mod \; 37 = 22$ and $X \; mod \; 61 = 2$ and one would have the conditions

$$\begin{aligned} \sum_{r=1}^{n_{23}} (1+10R_0)^{n_{37}-r+1}(1+10S_0)^{r-1} d(n_{37}, r) \; mod \; 23 &= 0 \;\; , \\ \sum_{r=1}^{n_{37}} (1+22R_0)^{n_{37}-r+1}(1+22S_0)^{r-1} d(n_{37}, r) \; mod \; 37 &= 0 \;\; , \\ \sum_{r=1}^{n_{61}} (1+2R_0)^{n_{61}-r+1}(1+2S_0)^{r-1} d(n_{61}, r) \; mod \; 61 &= 0 \;\; . \end{aligned} \tag{12.6.8}$$

12.6.2 Low Temperature Limit Of Exponential Thermodynamics

The case $s_0 = 1$ ($S_0 = 0$) corresponds to integer valued q_0 and to the low temperature limit of number theoretical thermodynamics characterized by R_0 alone. In this case only $r = 1$ partition contributes significantly to $S_p(n)$ and one expects that the genetic code is determined by the decomposition of the probability $p(r = 1) = r_0^n / \hat{d}(n)$ to prime factors. The positive contribution to information comes from $\hat{d}(n)$ so that in practice this is of primary interest.

The deduction of primes minimizing $S_p(n)$ can be done conveniently by separating the calculation of the exponents of the p-adic norms from the calculation of probabilities. The calculation of the probabilities from their basic formulas is convenient due to the rapid convergence of the exponents $(1 + R_0 X)^{-r+1}$ $r = 1$ term indeed gives an excellent approximation to $S_p(n)$ so that the decomposition of $\hat{d}(n)$ to primes determines $p(n)$ completely unless $d(n, r)$ compensates for the exponential decrease. This might of course mean that the assumption $S_0 = 1$ is not realistic. The study of the low temperature limit in detail can however provide valuable information about a more realistic model.

The overall idea is simple.

1. The primes in $\mathcal{R}_{min} = \{37, 61\}$ must divide $\hat{d}(n)$ for some values of n and these give conditions on R_0.

2. Sum of the over-represented small primes $n \leq 11$ can be dropped from Q and thus from X_Q to see whether $\hat{d}(n)$ is not anymore divisible by these primes so often.

The computational algorithm for finding candidates for realistic genetic codes uses the fact that the number N of DNA triplets coding given amino-acid is never large than 6 for the real genetic code.

1. Form an array of plausible looking choices of X labelling the models to be studied.
2. Calculate the allowed values of R_0 for a given model X and arrange them to a vector.
3. Calculate the components of the vector $p(n)$ for allowed values of R_0 for given X one by one. Keep count of the number of occurrence $N_n(i) = N(p(i))$ of prime $p(i)$ $i = 1, , ..18$ for given (X, R_0) as n increases. If the number $max\{N_i, i = 1, .., 18\}$ exceeds 6, stop the further scanning of n values as useless and start to test the next value of R_0.

Preliminary calculations suggest that the predictions of low temperature thermodynamics do not differ in an essential manner from those of high temperature thermodynamics. The problem is still posed by the over abundance of small primes. The reason is that in the decomposition of integer small primes are most abundant whereas large primes are rare. The probability that small prime p divide random integer is $P = 1/p$. $p = 11$ seems to be the boundary between under-represented primes and over-represented primes. Typically about 40 integers code for primes $p \leq 11$.

12.6.3 How To Find The Critical Temperature In Exponential Thermodynamics?

The challenge is to understand whether and how $S_0 > 0$ could cure the situation and whether there exists something analogous to a critical temperature in the sense that large long range fluctuations for ordinary criticality correspond to large degeneracies for large primes. From the point of view the association of a number theoretical critical temperature to genetic code would be rather natural since in TGD framework living systems indeed are quantum critical systems. and genetic code should be be something completely exceptional.

The following arguments give some glimpse about what criticality might mean.

1. For $r_0 \sim s_0$ near criticality the probabilities $p(n, r) = r_0^{n-r} s_0^r p(n, r)/\hat{d}(n)$ are of same order of magnitude so that all values of r contribute significantly to $S_p(n)$ as in the case of infinite temperature limit. Individual contributions are however relatively small for large values of $\hat{n}$.
2. In the argument of logarithm the small primes appearing as factors of $r_0^{n-r} s_0^(r - 1)p(n, r)$ tend to compensate the small primes dividing $\hat{d}(n) = \sum_r r_0^{n-r} s_0^(r - 1)d(n, r)$ so that only a small number of terms with negative entropy remains and the small value of $p(n, r)$ means that overall contribution is small.

The cautious conclusion is that at criticality r_0 and s_0 should be near to each other. There are however tight constraints. For instance, for $s_0 = 1$ r_0 cannot be divisible by primes $2 \leq p \leq 61$ since in this case the partition functions would not be divisible by any of these primes and corresponding amino-acids would not be coded at all. There one must have $r_0 \geq 67, s_0 \geq 67$ in order to not lose the primes from the partition function.

The preliminary computations with small values of r_0 and s_0 near shows that realistic looking degeneracies result except for $p = 2$ whose degeneracy is of order 40 typically: it seems that the spectral power is shifted from primes $p \leq 11$ to $p = 2$. The very special character of $p = 2$ suggests a possible remedy. Perhaps the integers 0, 1, 2 should be mapped to themselves by genetic code and only odd primes compete in the variational principle. This would however mean that the number of amino-acids coded by single DNA would be 3 rather than the observed 2 consistent $(0, 1) \to (0, 1)$ hypothesis. This option can work only if one maps some other DNAs than 0 (1) to 0 (1). This could make sense only in the case that all primes give $S_p(n) = 0$ for some n. It turns out that the dropping of $p = 2$ only shifts the spectral power to $p = 3$ for checked small values of (r_0, s_0). It seem that if the idea of criticality is not enough unless one has clear idea about what makes (r_0, s_0) critical.

The first TGD inspired model for genetic code was based on the Combinatorial Hierarchy $M(n+1) = M_{M(n)} = 2^{M(n)} - 1$ starting from $M(1) = 2$ and giving Mersenne primes $3, 7, 127, 2^{127} -$

1. $M_7 = 127$ corresponds to genetic code. This inspires the idea that perhaps $(r_0 = M_7, s_0 = 1)$ might be worth of checking. The parameter values $r_0 = 127, s_0 = 1$ indeed yield the first example for which the spectral power for primes $p \leq 11$ is reasonably small and equal to 17. 22 units of spectral power however concentrates on $p = 2^5 - 1 = 31$, the Mersenne prime below M_7! many primes are lacking from the spectrum. In any case, it would seem possible to distribute the spectral power outside the small prime region but it is clear that genetic code would be number theoretically something extremely special of realized in this manner.

For $s_0 > 1$ spectral power again concentrates on $p = 2$. Since M_{127} corresponds to the Mersenne assigned to the memetic code, natural curiousity leads to check what happens in this case. All spectral power concentrates to $p = 2$ in this case: this is nothing but 2-adic spontaneous magnetization! It seems that this phenomenon occurs quite generally for very large values of r_0.

There might be something wrong with the program making the modulo arithmetics. For even values of r_0 partition function should be odd and $p = 2$ would give positive contribution to entropy. The general finding is that $p = 2$ is highly degenerate. This is possible only if the partition function fails to be divisible for primes $2 \leq p \leq 61$ for very many values of n. Even this does not help for $r_0 = 2^n$ since in this case $p > 2$ gives non-positive entropy for all values of n.

12.7 Appendix

The appendix sums up some computational aspects of the model and represents the models for doublet and singlet genetic codes as toy models.

12.7.1 Computational Aspects

Calculation of partition numbers $d(n, r)$

The basic problem in the calculation of partition numbers $p(n, r)$ is the presence of partitions containing same integer several times. This problem can be circumvent by arranging the integers in the partition in decreasing order so that one has $n_1 \geq n_2 ... \geq n_r$. Using this ordering the calculation of partition numbers $d(n, r)$

$$d(n,r) = \sum_{k=1}^{n-r+1} d(n-k, r-1|k) \ , \tag{12.7.1}$$

where $d(n, r|k)$ denotes the number of partitions for which the first number n_1 satisfies $n_1 \leq k$. The formula states that the ordered r-partitions of n decompose as $(k, n_1, ...n_{r-1})$, $k \leq n - r - 1$ such that $r - 1$-partition $(n_1, ..., n_{r-1})$ satisfies $n_1 \leq k$ by the ordering assumption.

What one must calculate are the numbers $d(n - k, r|k)$ and this can be done recursively

$$d(n,r|k) = \sum_{k_1 \leq k} d(n-k_1, r-1|k_1) \ . \tag{12.7.2}$$

The basic data item besides these formulas is $d(1, 1) = 1$. Also $d(n, n) = 1$ and $d(n, 1) = 1$ can be used.

The algorithm becomes time consuming for $n > 50$ and larger partition numbers are conveniently calculated by using the recurrence relation [A6]

$$P(n,k) = P(n-1,k-1) + P(n-k,k) \ . \tag{12.7.3}$$

The numbers $Q(n, k)$ of partitions of n to integers such that same integer does not appear twice are obtained from the formula [A6]

$$Q(n,k) = P(n - \begin{pmatrix} k \\ 2 \end{pmatrix}, k) \ . \tag{12.7.4}$$

Numerical treatment of $n_0 < 0$ polynomial thermodynamics

The numerical treatment of $n_0 < 0$ polynomial thermodynamics is somewhat tricky and deserves a separate discussion. For definiteness the consideration is restricted to $H = log(r + r_0)$ case with $T = 1/n_0$. The generalization to other critical Hamiltonians is trivial.

For $n_0 = -m < 0$ case the entropy has the expression

$$\begin{aligned} S_p(n) &= \sum_{r=1}^{n} p(n,r) \left[mlog(|\frac{(n+r_0)}{r_0!(r+r_0)}|_p) \right] - log(|Z(n)|_p) \\ &= \left[\sum_{i=r_0+2}^{n+r_0} k_p(i) - \sum_r p(n,r) k_p(r+r_0) \right] mlog(p) - log(|Z(n)|_p) \\ Z(n) &= \sum_{r=1}^{n} \left[\frac{(n+r_0)!}{r_0!(r+r_0)} \right]^m d(n,r) \quad . \end{aligned} \tag{12.7.5}$$

Here $k_p(n)$ is defined by the p-adic norm $|n|_p = p^{k_p}$. The integers appearing as coefficients of $d(n,r)$ in Z are very large and this causes numerical difficulties since factorials are represented precisely as integers only up to 21! and mod operation gives zero above this limit.

In order to calculate the p-adic norm of Z one must perform modulo p^k operations for Z by doing it separately for each summand and summing the resulting expressions. The problem is that the modulo p^k operation for the products involved does not reduce it to a small integer when p is large and one is forced to do the sum of large integers.

The solution of the problem is provided by finite field arithmetics. Start with the expression of $Z(n)$ written as

$$Z(n) = \sum_{r=1}^{n} \frac{1}{(r+r_0)^m} d(n,r) \quad . \tag{12.7.6}$$

Since the calculation of p-adic norm involves only repeated modulo p operations to check whether the result vanishes modulo p, and if it does, a subsequent division by p, it suffices to interpret the factors $(1/(r+r_0)^m$ as elements of finite field $G(p,1)$.

1. If the condition $r + r_0 \; mod \; p \neq 0$ holds true, all denominators are non-vanishing. This is the case when $r_0 + 1 \leq p \leq n + r_0$ holds true. In this case it suffices to calculate the inverses $(r+r_0)_p^{-1}$ of $r + r_0$ in $G(p,1)$ and replace $Z(n)$ with

$$\hat{Z}(n) = \sum_{r=1}^{n} \left[(r+r_0)_p^{-1} \right]^m d(n,r) \quad . \tag{12.7.7}$$

   The resulting expression is free of overflow problems and its p-adic norm can be calculated without difficulties.

2. When the condition $r + r_0 \; mod \; p \neq 0$ fails to be satisfied poles appear at $r = r_k = kp - r_0$, $k_{min} = [(1 + r_0)/p] + 1 \leq k \leq k_{max} = [(n + r_0)/p]$, where $[x]$ denotes nearest integer smaller than x. Note that the problem is not encountered for $r_0 > 60$. The trick is to express Z in the form

$$
\begin{aligned}
Z(n) &= \frac{1}{X} \times \hat{Z}(n) \ , \\
\hat{Z}(n) &= \sum_{r \neq kp - r_0} X \times \left[(r + r_0)_p^{-1}\right]^m \times d(n, r) \\
&+ \sum_{k=k_{min}}^{k_{max}} X_k \times d(n, kp - r_0) \ , \\
X &= \prod_k (r_k + r_0)^m = \prod_{i=k_{min}}^{k_{max}} (ip)^m = \left(\prod_{i=k_{min}}^{k_{max}} i \right)^m p^{m(k_{max} - k_{min})} \ , \\
X_k &= \frac{X}{(r_k + r_0)^m} = \left(\frac{\prod_{i=k_{min}}^{k_{max}} i}{k} \right)^m \times p^{m(k_{max} - k_{min} - 1)} \ . \qquad (12.7.8)
\end{aligned}
$$

This expression involves only relatively small integers and overflow problems are avoided. $k_p(X)$ can be expressed in the form

$$
k_p(X) = m \left[\sum_{k_{min}}^{k_{max}} k_p(k) - k_{max} + k_{min} \right] \ . \qquad (12.7.9)
$$

To sum up, the expression for $S_p(n)$ reduces in $(n_0 = -m < 0, r_0)$ case to the form

$$
\begin{aligned}
\frac{S_p(n)}{log(p)} &= \left[\sum_{i=r_0+2}^{n+r_0} k_p(i) + \sum_{k_{min}}^{k_{max}} k_p(k) - k_{max} + k_{min} - \sum_{r=1}^{n} p(n, r) k_p(r + r_0) \right] m \\
&- k_p(\hat{Z}(n)) \ , \\
\hat{Z}(n) &= \sum_{r \neq kp - r_0} X \left[(r + r_0)_p^{-1}\right]^m d(n, r) + \sum_{k=k_{min}}^{k_{max}} X_k \times d(n, kp - r_0) \ , \\
X &= \left(\prod_{i=k_{min}}^{k_{max}} i \right)^m p^{m(k_{max} - k_{min})} \ , \\
X_k &= = \left(\frac{\prod_{i=k_{min}}^{k_{max}} i}{k} \right)^m \times p^{m(k_{max} - k_{min} - 1)} \ , \\
k_{min} &= [(1 + r_0)/p] + 1 \ , \ \ k_{max} = [(n + r_0)/p] \ . \qquad (12.7.10)
\end{aligned}
$$

In the nonsingular case 1) $X = 1$ and $X_i = 0$ holds true.

In practice $r \neq r_k$ terms do not contribute to $k(\hat{Z}(n))$ unless all $d(n, kp - r_0)$ happen to be divisible by a large power of p. The highest power of $p \leq 61$ appearing in $d(n, r)$ is 4 for $n \leq 63$. For the sake of generality and safety it is however better to keep also these contributions in the formula.

12.7.2 Number Theoretic Model For Singlet And Doublet Codes As AToy Model

The model of the genetic code applies to any number n of DNAs and maps the numbers $n = 0, 1...n - 1$ to $\{0, 1\} \cup \{primes\ p \leq n - 1\}$. In [K19] a model for the genetic code resulting via a symmetry breaking from the product of codes associated with 16 DNA doublets and 4 DNA singlets was considered. At the level of DNAs the product code is very natural and the almost symmetries of the genetic code with respect to last codon support the idea.

Singlet code

In the case of singlet code the requirement that at least single stopping sign codon exists, implies that either $p = 2$ or $p = 3$ fails to be coded. This would conform with the idea that $n = 3 = -1 \; mod \; 4$ represents automatically stopping sign and 3 amino-acids would be coded. Fermionic entropy vanishes identically with this assumption.

It is perhaps instructive to consider the singlet codes at low temperature limit of exponential thermodynamics for $(r_0 > 1, s_0 = 1)$ to get some grasp of the situation. Singlet code gives $(\hat{d}(1), \hat{d}(2), \hat{d}(3)) = (1, 1 + r_0, 1 + r_0 + r_0^2)$. The probabilities $p(n, r)$ are $p(n, r) = r_0^{n-r}/\hat{d}(n)$ and entropy can be written as

$$S_p(n) \;\; = \;\; -\frac{r_0^m}{1 + r_0 + .. + r_0^n} \sum_{m=1}^{n} log(|\frac{r_0^m}{1 + r_0 + ... + r_0^n}|_p) \;\; . \tag{12.7.11}$$

For $r_0 = 2$ *resp.* $r_0 = 3$ one has $(\hat{d}(1), \hat{d}(2), \hat{d}(3)) = (1, 3, 7)$ and $(\hat{d}(1), \hat{d}(2), \hat{d}(3)) = (1, 4, 13)$. For $r_0 = 2$ the code is $(0, 1, 2, 3) \to (0, 1, 3, stop)$ with $n = 3$ having vanishing entropy and thus naturally acting as stopping codon. $p = 2$ is not coded. For $r_0 = 3$ the code is $(0, 1, 2, 3) \to (0, 1, 2, stop)$. $p = 3$ is not coded.

Allowing $s_0 > 1$ does not allow to circumvent these problems. In this case the formula for entropy reads as

$$S_p(n) \;\; = \;\; -\frac{1}{s_0^n + r_0 s_0^{n-1} .. + r_0^n} \sum_{m=1}^{n} r_0^m s_0^{n-m} log(|\frac{r_0^m s_0^{n-m}}{s_0^n + r_0 s_0^{n-1} .. + r_0^n}|_p) \;\; . \tag{12.7.12}$$

For $(r_0 = 3, s_0 = 2)$ the denominator is not divisible by 2 or 3 so that all codons possess vanishing or negative information. The conclusion is that the mapping of $3 = -1 mod 4$ to stopping codon is the only consistent option.

For polynomial thermodynamics with Boltzmann weights given by $(r + r_0)^{n_0}$ there is a large number of parameter combinations giving single stopping codon which is always $n = 2$.

Doublet codes

Doublet code should map the integers $0, 1..., 14(15)$ to primes $0, 1, 2, 3, 5, 7, 11, 13$. The inspection of the tables 1 and 2 shows that at infinite temperature limit $p = 13$ fails to coded for both B, F, and BF and also $p = 7$ for F. $n = 13$ is not coded to a unique prime for B. The parameter values are restricted to the range $(n_0, r_0) \in (\{1, 5\}, \{0, 5\})$ in the polynomial case and to the range $(r_0, s_0)(\{1, 5\}, \{1, 5\})$ in the exponential case. The findings support the view that polynomial thermodynamics is the only viable approach.

1. Stopping sign codons as codons with $S_p < 0$

For finite temperature thermodynamics the conditions used are that least one stopping codon having by definition $S_p < 0$ exists and all primes $p \leq 13$ must be coded.

1. For finite temperature polynomial thermodynamics the cases F and BF allow no solutions whereas B allows four solutions $((n_0, r_0) = (1, 5), (2, 1),$
$(2, 5), (3, 3))$.

2. For exponential thermodynamics neither, B, F, nor BF allow solutions.

2. Stopping sign codons as $n = 15$ codon or codons with $S_p < 0$

One could argue that since $n = 15$ corresponds to -1 in modulo 16 mathematics, it should code for stopping sign. If so, the situation changes.

Table 12.15: Table represents the partition numbers $d_B(n)$ and $d_F(n)$ as well as the primes $p_B(n)$, $p_F(n)$, $p_{BF}(n)$ resulting from the minimization of the p-adic entropy $S_{I,p}(n)$, $I = B, F, BF$ as a function of n for $n < 16$.

n	$d_B(n)$	$p_B(n)$	$d_F(n)$	$p_F(n)$	$p_{BF}(n)$
0	1	1	1	0	0
1	1	1	1	1	1
2	2	2	1	1	2
3	3	3	2	2	3
4	5	5	2	2	5
5	7	7	3	3	7
6	11	11	4	2	11
7	3×5	5	5	5	5
8	2×11	11	6	3	11
9	$2 \times 3 \times 5$	5	8	2	2
10	$2 \times 3 \times 7$	7	10	5	3
11	$2^3 \times 7$	2	12	2	2
12	7×11	11	15	5	11
13	101 (prime)	?	18	3	3
14	$3^3 \times 5$	3	22	11	3
15	$2^4 \times 11$	2	27	3	3

1. Polynomial thermodynamics.

   In BF case $(n_0, r_0) = (1, 1)$ provides in the range $(n_0, r_0) \in (\{1, 5\}, \{0, 5\})$ the only example of a genetic code for which all primes $p \leq 13$ are coded. One can say that supersymmetric option fixes the code uniquely in this parameter range. F allows no solutions. B allows 4 solutions $((n_0, r_0) = (1, 2), (2, 1), (2, 5), (3, 3))$.

2. Exponential thermodynamics

   Neither B, F, nor BF type thermodynamics allow solutions.

12.8 Galois groups and genes

In an article discussing a TGD inspired model for possible variations of G_{eff} [L48], I ended up with an old idea that subgroups of Galois group could be analogous to conserved genes in that they could be conserved in number theoretic evolution. In small variations such as above variation Galois subgroups as genes would change only a little bit. For instance, the dimension of Galois subgroup would change.

The analogy between subgoups of Galois groups and genes goes also in other direction. I have proposed long time ago that genes (or maybe even DNA codons) could be labelled by $h_{eff}/h = n$. This would mean that genes (or even codons) are labelled by a Galois group of Galois extension (see `http://tinyurl.com/zu5ey96`) of rationals with dimension n defining the number of sheets of space-time surface as covering space. This could give a concrete dynamical and geometric meaning for the notion of gene and it might be possible some day to understand why given gene correlates with particular function. This is of course one of the big problems of biology.

12.8.1 Could DNA sequence define an inclusion hierarchy of Galois extensions?

One should have some kind of procedure giving rise to hierarchies of Galois groups assignable to genes. One would also like to assign to letter, codon and gene and extension of rationals and its Galois group. The natural starting point would be a sequence of so called intermediate Galois extensions E^H leading from rationals or some extension K of rationals to the final extension E.

Galois extension has the property that if a polynomial with coefficients in K has single root in E, also other roots are in E meaning that the polynomial with coefficients K factorizes into a product of linear polynomials. For Galois extensions the defining polynomials are irreducible so that they do not reduce to a product of polynomials.

Any sub-group $H \subset Gal(E/K))$ leaves the intermediate extension E^H invariant in element-wise manner as a sub-field of E (see `http://tinyurl.com/y958drcy`). Any subgroup $H \subset Gal(E/K))$ defines an intermediate extension E^H and subgroup $H_1 \subset H_2 \subset ...$ define a hierarchy of extensions $E^{H_1} > E^{H_2} > E^{H_3}...$ with decreasing dimension. The subgroups H are normal - in other words $Gal(E)$ leaves them invariant and $Gal(E)/H$ is group. The order $|H|$ is the dimension of E as an extension of E^H. This is a highly non-trivial piece of information. The dimension of E factorizes to a product $\prod_i |H_i|$ of dimensions for a sequence of groups H_i.

Could a sequence of DNA letters/codons somehow define a sequence of extensions? Could one assign to a given letter/codon a definite group H_i so that a sequence of letters/codons would correspond a product of some kind for these groups or should one be satisfied only with the assignment of a standard kind of extension to a letter/codon?

Irreducible polynomials define Galois extensions and one should understand what happens to an irreducible polynomial of an extension E^H in a further extension to E. The degree of E^H increases by a factor, which is dimension of E/E^H and also the dimension of H. Is there a standard manner to construct irreducible extensions of this kind?

1. What comes into mathematically uneducated mind of physicist is the functional decomposition $P^{m+n}(x) = P^m(P^n(x))$ of polynomials assignable to sub-units (letters/codons/genes) with coefficients in K for a algebraic counterpart for the product of sub-units. $P^m(P^n(x))$ would be a polynomial of degree $n+m$ in K and polynomial of degree m in E^H and one could assign to a given gene a fixed polynomial obtained as an iterated function composition. Intuitively it seems clear that in the generic case $P^m(P^n(x))$ does not decompose to a product of lower order polynomials. One could use also polynomials assignable to codons or letters as basic units. Also polynomials of genes could be fused in the same manner.

2. If this indeed gives a Galois extension, the dimension m of the intermediate extension should be same as the order of its Galois group. Composition would be non-commutative but associative as the physical picture demands. The longer the gene, the higher the algebraic complexity would be. Could functional decomposition define the rule for who extensions and Galois groups correspond to genes? Very naively, functional decomposition in mathematical sense would correspond to composition of functions in biological sense.

3. This picture would conform with $M^8 - M^4 \times CP_2$ correspondence [L30] in which the construction of space-time surface at level of M^8 reduces to the construction of zero loci of polynomials of octonions, with rational coefficients. DNA letters, codons, and genes would correspond to polynomials of this kind.

12.8.2 Could one say anything about the Galois groups of DNA letters?

A fascinating possibility is that this picture could allow to say something non-trivial about the Galois groups of DNA letters.

1. Since $n = h_{eff}/h$ serves as a kind of quantum IQ, and since molecular structures consisting of large number of particles are very complex, one could argue that n for DNA or its dark variant realized as dark proton sequences can be rather large and depend on the evolutionary level of organism and even the type of cell (neuron viz. soma cell). On the other, hand one could argue that in some sense DNA, which is often thought as information processor, could be analogous to an integrable quantum field theory and be solvable in some sense. Notice also that one can start from a background defined by given extension K of rationals and consider polynomials with coefficients in K. Under some conditions situation could be like that for rationals.

2. The simplest guess would be that the 4 DNA letters correspond to 4 non-trivial finite groups with smaller possible orders: the cyclic groups Z_2, Z_3 with orders 2 and 3 plus 2 finite groups

of order 4 (see the table of finite groups in `http://tinyurl.com/j8d5uyh`). The groups of order 4 are cyclic group $Z_4 = Z_2 \times Z_2$ and Klein group $Z_2 \oplus Z_2$ acting as a symmetry group of rectangle that is not square - its elements have square equal to unit element. All these 4 groups are Abelian. Polynomial equations of degree not larger than 4 can be solved exactly in the sense that one can write their roots in terms of radicals.

3. Could there exist some kind of connection between the number 4 of DNA letters and 4 polynomials of degree less than 5 for whose roots one an write closed expressions in terms of radicals as Galois found? Could it be that the polynomials obtained by a a repeated functional composition of the polynomials of DNA letters have also this solvability property?

   This could be the case! Galois theory states that the roots of polynomial are solvable by radicals if and only if the Galois group is solvable meaning that it can be constructed from abelian groups using Abelian extensions (see `https://en.wikipedia.org/wiki/Solvable_group`).

   Solvability translates to a statement that the group allows so called sub-normal series $1 < G_0 < G_1 ... < G_k$ such that G_{j-1} is normal subgroup of G_j and G_j/G_{j-1} is an abelian group. An equivalent condition is that the derived series $G \rhd G^{(1)} \rhd G^{(2)} \rhd ...$ in which $j+1$:th group is commutator group of G_j ends to trivial group. If one constructs the iterated polynomials by using only the 4 polynomials with Abelian Galois groups, the intuition of physicist suggests that the solvability condition is guaranteed! Wikipedia article also informs that for finite groups solvable group is a group whose composition series has only factors which are cyclic groups of prime order.

   Abelian groups are trivially solvable, nilpotent groups are solvable, p-groups (having order, which is power prime) are solvable and all finite p-groups are nilpotent. Every group with order less than 60 elements is solvable. Fourth order polynomials can have at most S_4 with 24 elements as Galois groups and are thus solvable. Fifth order polynomials can have the smallest non-solvable group, which is alternating group A_5 with 60 elements as Galois group and in this case are not solvable. S_n is not solvable for $n > 4$ and by the finding that S_n as Galois group is favored by its special properties (see `https://arxiv.org/pdf/1511.06446.pdf`).

   A_5 acts as the group icosahedral orientation preserving isometries (rotations). Icosahedron and tetrahedron glued to it along one triangular face play a key role in TGD inspired model of bio-harmony and of genetic code [L12, L50]. The gluing of tetrahedron increases the number of codons from 60 to 64. The gluing of tetrahedron to icosahedron also reduces the order of isometry group to the rotations leaving the common face fixed and makes it solvable: could this explain why the ugly looking gluing of tetrahedron to icosahedron is needed? Could the smallest solvable groups and smallest non-solvable group be crucial for understanding the number theory of the genetic code.

An interesting question inspired by $M^8 - H$-duality [L30] is whether the solvability could be posed on octonionic polynomials as a condition guaranteeing that TGD is integrable theory in number theoretical sense or perhaps following from the conditions posed on the octonionic polynomials. Space-time surfaces in M^8 would correspond to zero loci of real/imaginary parts (in quaternionic sense) for octonionic polynomials obtained from rational polynomials by analytic continuation. Could solvability relate to the condition guaranteeing M^8 duality boiling down to the condition that the tangent spaces of space-time surface are labelled by points of CP_2. This requires that tangent or normal space is associative (quaternionic) and that it contains fixed complex subspace of octonions or perhaps more generally, there exists an integrable distribution of complex subspaces of octonions defining an analog of string world sheet.

What could the interpretation for the events in which the dimension of the extension of rationals increases? Galois extension is extensions of an extension with relative Galois group $Gal(rel) = Gal(new)/Gal(old)$. Here $Gal(old)$ is a normal subgroup of $Gal(new)$. A highly attractive possibility is that evolutionary sequences quite generally (not only in biology) correspond to this kind of sequences of Galois extensions. The relative Galois groups in the sequence would be analogous to conserved genes, and genes could indeed correspond to Galois groups [K11] [L30]. To my best understanding this corresponds to a situation in which the new polynomial P_{m+n} defining the new extension is a polynomial P_m having as argument the old polynomial $P_n(x)$: $P_{m+n}(x) = P_m(P_n(x))$.

What about the interpretation at the level of conscious experience? A possible interpretation is that the quantum jump leading to an extension of an extension corresponds to an emergence of a reflective level of consciousness giving rise to a conscious experience about experience. The abstraction level of the system becomes higher as is natural since number theoretic evolution as an increase of algebraic complexity is in question.

This picture could have a counterpart also in terms of the hierarchy of inclusions of hyperfinite factors of type II_1 (HFFs). The included factor M and including factor N would correspond to extensions of rationals labelled by Galois groups $Gal(M)$ and $Gal(N)$ having $Gal(M) \subset Gal(M)$ as normal subgroup so that the factor group $Gal(N)/Gal(M)$ would be the relative Galois group for the larger extension as extension of the smaller extension. I have indeed proposed [L52] that the inclusions for which included and including factor consist of operators which are invariant under discrete subgroup of $SU(2)$ generalizes so that all Galois groups are possible. One would have Galois confinement analogous to color confinement: the operators generating physical states could have Galois quantum numbers but the physical states would be Galois singlets.

Chapter 13

Unification of Four Approaches to the Genetic Code

13.1 Introduction

A proposal unifying four approaches to genetic code is discussed.

The first approach is introduced by myself and is geometric: genetic code is interpreted as an imbedding of the aminoacid space to DNA space possessing a fiber bundle like structure with DNAs coding for a given aminoacid forming a discrete fiber with a varying number of points. Also Khrennikov has proposed an analogous approach based on the identification of DNAs coding for a given aminoacid as an orbit a discrete flow defined by iteration of a map of DNA space to itself.

Much later (2014) I have introduced a variant of this scenario in which the fiber space structure is by assigning aminoacids to the 20 vertices of icosahedron. This model allows to understand the degeneracies of genetic code group theoretically.

Second approach starts from the 5-adic approach of Dragovich and Dragovich. Codons are labelled by 5-adic integers n which have no non-vanishing 5-digits so that the n is in the range $[31, 124]$. The number of primes in the range $[31, 124]$ is 20. This suggests the labelling of aminoacids by these primes. This inspires an additional condition on the geometric code: if possible, one of the integers n projected to p equals to $p(n)$. This condition fails only for the primes 53,79,101,103 for which some of 5-digits vanishing in 5-ary expansion.

The third approach relies on the generalization of the basic idea of the so called divisor code proposed by Khrennikov and Nilsson. The requirement is that the number of factors for integer n labelling one of DNAs, call it n_d coding for a given aminoacid is the total number of codons coding for the aminoacid, its degeneracy. Therefore a given aminoacid labelled by prime p with no non-vanishing 5-digits is coded by DNAs labelled by p itself and by n_d. A group theoretic and physical interpretation for the origin of the divisor code is proposed.

The fourth approach is a modification of the earlier 4-adic number theoretic thermodynamics approach of Pitkänen.

1. 5-adic thermodynamics involving a maximization of number theoretic negentropy $N_p(n) = -S_p(n) > 0(!)$ as a function of p-adic prime p labelling aminoacids assigns a unique prime to the codon. If no prime in the range divides S_p, the codon is identified as a stopping codon.

2. The number theoretic thermodynamics is assigned with the partitions P of the integer $n_{2)}$ determined by the first two letters of the codon (16 integers belonging to the range $[6, 24]$). The integer valued number theoretic Hamiltonian $h(P) \in Z_{25}$ appearing in the Boltzmann weight $5^{h(P)/T_5}$ is assumed to depend on the number r of summands for the partition only. $h(r)$ is assumed to be tailored by evolution so that it reproduces the code.

3. The effect of the third nucleotide is described in terms of 5-adic temperature $T_5 = 1/n$, $n \in [0, 24]$: the variation of T_5 explains the existence of variants of genetic code and its temporal variation the observed context sensitivity of the codon-aminoacid correspondence for some variants of the code.

A numerical calculation scanning over $N \sim 10^{30}$ candidates for $h(r)$ allows only 11 Hamiltonians and with single additional symmetry inspired condition there are 2 solutions which differ only for 5 largest values of r. Due to the limited computational resources available only 24 percent of the available candidates have been scanned and the naive expectation is that the total number of Hamiltonians is about about 45 unless one poses additional conditions.

The problem of the number theoretic models is that they do not predict but only reproduce. This is in sharp contrst to the model based on dark proton sequences, which leads to a radically new vision about the evolution of prebiotic life and to the vision about how immune system and genetic code evolved and what is the meaning of the genetic code.

The appendix of the book gives a summary about basic concepts of TGD with illustrations. There are concept maps about topics related to the contents of the chapter prepared using CMAP realized as html files. Links to all CMAP files can be found at `http://tgdtheory.fi/cmaphtml.html` [L10]. Pdf representation of same files serving as a kind of glossary can be found at `http://tgdtheory.fi/tgdglossary.pdf` [L11].

13.2 Unifying Various Approaches To The Genetic Code

The understanding of genetic at deeper level has gained increasing attention: mention only the proposals of Khrennikov [A12, A29], Pitkänen [K23, K19, K11], and Dragovich and Dragovich [A18]. Quite recently Khrennikov and Nilsson introduced the idea of divisor code [A30]. The idea is inspired by the observations that the numbers of divisors of integers in the range $[1, 20]$ are rather near to degeneracies of amino-acids for the genetic code. The attempts to realize this idea as such had however only a limited success and this led to a generalization of the basic idea of the divisor code and stimulated the attempt to combining four different approaches to the genetic code to single unified approach.

13.2.1 Geometric Approach To The Genetic Code

The geometric approach of Pitkänen [K23, K19, K11] was inspired by the basic hypothesis of TGD [L5, L4, L3] that space-times can be regarded as 4-surfaces $X^4 \subset H = M^4 \times CP_2$ of 8-dimensional imbedding space H. The idea was to replace H by the discrete space of integers labeling the 64 DNA triplets and X^4 by the discrete space of 20 amino-acids [K19]. Thus genetic code imbeds amino-acid space with points labeled by integers n_A to the DNA space labeled by some subset of integers (not necessarily $0 \leq n \leq 63$) such that the DNAs coding for a given amino-acid A form a discrete fiber like structure. One could also assume that one of the integers $n(DNA)$ labeling one of DNAs coding for A satisfies $n(DNA) = n(A)$ if possible.

As a matter fact, there exists the algebraic-geometric theory for codes based on the identification of code as a subset of subspace of G_p^k where G_p is finite field [A34]. If the points of this subset are labeled by some subset of integers m, the inclusion induces the code as a map $m \to n(m)$ where $n(m)$ consists of k G_p valued numbers. This concept of code does not apply to genetic code but the generalization is obvious: assign to the imbedding a bundle structure assigning to each point $n(m)$ a fiber consisting of points of G_p^k.

[A13] [A12] has proposed identification of codons coding for given amino-acid as an orbit of a discrete flow in the space of codons. It is possible to interpret DNA space as a bundle with fibers identified as orbits of the flow acting as a discrete group Z_n of symmetries in the fiber. The imbedding of amino-acid space to DNA space in the case of 5-adic code is however not quite equivalent with this view since four primes labeling amino-acids do not label codons.

13.2.2 4-Adicity And 5-Adicity As Possible Realizations Of The Symmetries Of The Genetic Code

An important physical constraint on any model is the fact that for the mitochondrial code codons have exact A-C and G-U symmetries with respect to the last codon. For eukaryote code this symmetry is broken only by two codons (Stop-Trp and Ile-Met pairs). A natural origin for this symmetry would be the formation of the 3-codons via fusion of 2-codons and 1-codons as suggested in the model of prebiotic evolution proposed in [K19].

One can consider two mathematical models for this symmetry.

1. 4-adic model of Pitkänen [K11] assumes the labeling of the codons using 4-adic numbers $n = n_0 + n_1 4 + n_3 16$, $n_i \in Z_4$ such that codons with $i = 0, 2$ and $1, 3$, which are 4-adically close to each other, correspond to symmetry related pairs. Also the model of Khrennikov and Kozyrev based on the identification of DNA space as 8×8 diadic plane (chess board!) starts from 4-adicity [A29] and interprets genetic code as a locally constant map from DNA space to amino-acid space. The number of primes $p < 64$ is 18 which leads to the idea that integers $n = 0, 1$ and the primes $p < 64$ code for amino-acids. Note however that 4-adicity as a strict symmetry needs to be assumed only for the third nucleotide.

2. For the 5-adic labeling of the codons suggested Dragovich and Dragovich [A18] codons are labeled by integers $n_0 + n_1 5 + n_2 5^2$ with $n_i \neq 0$ and vary in the range $[31, 124]$. The observation that the number of primes in this range is 20 inspires the hypothesis that that the primes in question label amino-acids. 5-adicity in the weakest sense means 5-adicity with respect to the third nucleotide so that either the codons $(n, n + 50)$ or codon pairs $(n, n + 25)$ and $(n, n + 75)$ code for the same amino-acid in the case of vertebrate mitochondrial code. There are three primes pairs $(p, p_1 = p + 50)$ [(47, 97), (53, 103), (59, 109)] so that $n \to n + 50$ symmetry is not consistent with the labeling of amino-acids by primes. Hence only $(n, n+25)$ and $(n, n + 75)$ option meaning that A-C and G-U pairs correspond to pairs of even and odd integers is acceptable and that the conjugation $n_3 \to 5 - n_3$ cannot correspond to DNA conjugation, which was the original motivation for the 5-adicity, but to the A$\leftrightarrow$C and G$\leftrightarrow$U symmetries.

13.2.3 Number Theoretical Thermodynamics And Genetic Code

The original thermodynamical model for the genetic code developed by Pitkänen [K11] is based on 4-adic labeling of codons. The model assumes that the number theoretical thermodynamics associated with the partitions of integers n labeling codons assigns to a given codon a unique prime labeling the amino-acid coded by DNA as the prime p for which the number theoretic negentropy $S_p = -\sum_k p_k log_p(|p_k|_p) log(p)$ is maximum: here $|x|_p$ denotes p-adic norm. S_p satisfies basic axioms of Shannon entropy but can be also negative so that its negative becomes a genuine measure of information [K32, K11]. Stopping codons would correspond to DNAs for which no prime in the allowed range of primes exists. A possible physical justification could be a breaking of conformal symmetry so that the states of given conformal weight $n = \sum n_i$ associated with the states $\prod L_{n_i}|n = 0\rangle$ are have different number theoretic "energies" depending only on the number r of integers n_i in the partition.

One can consider two variants of the number theoretical thermodynamics.

1. In the 4-adic case $n = 0$ and $n = 1$ amino-acids and codons correspond to DNAs labeled by same integers and are thus in a special role. The number theoretical thermodynamics [K11] is able to reproduce the genetic code and its variants by assuming that the integer valued Boltzmann weights of the thermodynamics are integers in a suitable range tailored by evolution in order to maximize the number theoretical negentropy. Boltzmann weights are assumed to be arbitrary integers in some range rather than powers of some prime so that genuine p-adic thermodynamics for some prime is not in question.

2. The 5-adic thermodynamics is favored by the fact that there are no special amino-acids now ($n = 0$ and $n = 1$). Preliminary calculations suggests that the 5-adic thermodynamics can be reduced to that for the 2-codons defined by the first two nucleotides labeled by integers $n_{2)} = n_0 + n_1 5$, $n_i \neq 0$ belonging to the range $[6, ..., 24]$. The integer valued Hamiltonian $h(P)$ for the thermodynamics of partitions P of $n_{2)}$ and defining Boltzmann weights $5^{h(P)}$ would depend only on the number r of summands in the partition P of n as $n = \sum_{k=1}^{r} n_k$. The dependence of the coded amino-acid on the third letter of the codon would be coded by the integer valued inverse of the 5-adic temperature $T_5 = 1/n$. A-C and G-U symmetries would correspond to the symmetry $T_5(r, k) = T_5(r, 5 - k)$ and the breaking of these symmetries would be due to the variation of temperature. The temporal variation of T_5 would explain the fact that for some variants of code same codon can code for either an amino-acid or stopping sign [K11], [I47].

13.2.4 Group Theoretic Interpretation Of The Divisor Code

The basic question is why the product decompositions of integer n characterizing one of the DNAs coding for a given amino-acid labeled by prime would determine the number of DNAs coding for the amino-acid. The original suggestion was that explanation is group theoretical. The fundamental role of discrete subgroups of rotation group in quantum TGD [K57, K18] suggests that finite subgroups $H \subset G$ of $G \subset SU(2)$ are involved with the code. Finite symmetry groups are indeed naturally associated with codes and the first observation is that product decompositions of integer n correspond naturally to the decompositions of an Abelian group G order n to products of subgroups with orders r and s, $n = r \times s$.

The hypothesis is that integer n characterizing the amino-acid corresponds to the order of G and that the factor pairs (r, s) of $n = rs$ correspond to its subgroups $H_r \times H_s \subset G$. The codons coding for amino-acid characterized by n would correspond to a normal sub-groups of G in general case and to any subgroup in the Abelian case. The simplest identification of G is as the cyclic group Z_n. That the product decompositions (r, s) and (s, r), $r \times s = n$ must be counted as separate can be understood if a wave function invariant under $Z_r = Z_n/Z_s$ characterizes the codon labeled by (r, s). Z_n would naturally act as a symmetry group in the discrete fiber of the fiber bundle defined by the DNA space and defining a discrete flow in the fiber. The p-adic prime p assigned to the amino-acid could in turn characterize the p-adicity of corresponding space-time sheet [K69].

The physical interpretation suggested by TGD and to be discussed later is that the wave functions of (say) free electron pairs (possibly Cooper pairs) defined in the set of points defined by the orbit of $Z_n \subset G_a$ are invariant under the subgroup of $Z_r = Z_n/Z_s \subset Z_n$ for DNA labeled by (r, s), $r \times s = n$. Thus the codons coding for an amino-acid having Z_n as a symmetry group would be characterized by wave functions for free electron pairs transforming under representations of Z_n and remaining invariant under $Z_r \subset Z_n$ and thus reducing to representations of Z_s. Note that $r = 1$ corresponds to all irreps of Z_n and $r = n$ to singlets under Z_n.

13.2.5 Divisor Code

The idea of divisor code discussed in [A30] is inspired by the following observations.

1. Consider the number $N(n)$ of integer divisors for integers n in the range $[1, 21]$ corresponding to amino-acids with stopping sign counted as amino-acid.

2. Denote the number of integers $n \leq 21$ for which the number of divisors is k by $B(k)$. Also stopping sign is counted as an amino-acid and $n = 0$ corresponds to amino-acid also. This number $N(k)$ varies in the range $[1, 6]$. $B(k)$ has the values $(1, 8, 2, 5, 1, 3)$ where k runs from 1 to 6.

3. Denote by $A(k)$ the number of amino-acids coded by k DNA codons. $A(k)$ has the values $2, 9, 2, 5, 0, 3$.

The spectrum of $A(k)$ is very similar to that of $B(k)$ and this raises the question whether one could understand genetic code as a divisor code in the sense that the degeneracy of amino-acid would be dictated by the number of the integers $1 \leq n \leq 21$ coding it. One might also ask whether the amino-acids which are abundant and thus important are coded by integers with a large number of divisors. Also one can ask whether the divisor structure possibly correlates with the structure of the amino-acid.

Divisor code in this form would be only approximate and one can wonder could try to imagine some simple symmetry breaking mechanism. In this respect the crucial observations might be following.

1. The number of DNAs needed to realize divisor code would be 70 instead of 64. One must drop 6 codons and by choosing them suitably one might hope of getting correct degeneracies.

2. The most natural manner to break the symmetry is to drop the 4 codons from the codons coding for 5-plet which would thus become 1-plet. 5-plet corresponds to integer $n = 16$ and its product compositions $(16, 1), (1, 16), (2, 8), (8, 2), (4, 4)$ correspond to the DNAs coding for it. $(4, 4)$ would naturally correspond to singlet.

3. By dropping 2 codons from some 4-plet one obtains 2-plet and correct degeneracies. One candidate for 4-plet corresponds to $n = 8$ and its product decompositions $(1, 8), (8, 1), (2, 4), (4, 2)$. By dropping two of these one obtains correct degeneracies. It might that power of 2 property of $n = 8$ and $n = 16$ somehow relates to 2-adicity and to the special role of these amino-acids.

4. A possible interpretation is in terms of symmetry based on cyclic group $Z(n)$ serving as a symmetry of DNA codons coding for amino-acid labeled n. Z_n allows decompositions $Z_n = Z_{n_1} \times Z_{n_2}$, $n = n_1 \times n_2$ and if the representations are invariant under Z_{n_2} and thus reduce to those of Z_{n_1} codons coding for a given amino-acid correspond to the product decompositions. Symmetry breaking would be due to the lacking 6 codons and would mean that only Z_4 invariant states would be realized for Z_{16} and Z_1 and Z_8 of Z_2 and Z_4 invariant states are realized for $n = 8$. $n = 4$ could correspond to triplet of stopping codons so that powers of 2 would be in special role for vertebrate code suggesting 4-adicity. 4-adicity is also suggests by the almost exact A-G and T-C symmetries of the last nucleotide.

13.2.6 Topological Interpretation Of The Divisor Code In TGD Framework

The most concrete physical interpretation of the divisor code found in TGD framework is topological and based on TGD inspired vision about the role of dark matter in biology.

1. The generalized 8-D imbedding space has a book like structure with pages glued together along back which is 4-D surface of $H = M^4 \times CP_2$ [K18, K39]. Particles at different pages are dark relative to each other since they cannot have local interactions (appear in the same vertex of Feynman diagram). The pages are partially characterized by the value of Planck constant which can be arbitrary large. This explains the macroscopic quantum coherence of living matter. Matter can leak between different pages meaning a phase transition changing Planck constant.

2. The notion of magnetic body with flux tubes carrying dark matter and connecting different bio-molecules central for the TGD inspired model of living matter [K17]. Magnetic bodies of bio-molecules can be also connected by magnetic flux tubes, even those in different pages of the book. For instance, the phase transition reducing $\hbar$ reduces the distance between two bio-molecules connected in this manner and forces them near to each other. This explains the extreme selectivity of bio-catalysis and the miraculous ability of two bio-molecules to find each other in the dense soup of bio-molecules. In particular, DNA and its conjugate codons, mRNA codons, and tRNA would be connected by this kind of flux tubes. Also amino-acids would be connected to tRNA codons in this manner since tRNA molecules catch the amino-acids and bring them to the mRNA-amino-acid translation site. Genetic code could reduce to the selection rules for the flux tube connections connecting in general situation magnetic bodies belonging to different pages of the book.

3. The pages of book are almost copies of $M^4 \times CP_2$. This means that M^4 is replaced with n_a-fold singular covering and CP_2 with n_b-fold singular covering. The coverings have cyclic groups Z_{n_a} and Z_{n_b} act as discrete symmetries for the wave functions of particles in the covering. A given page is thus labeled by two pager numbers (n_a, n_b). Two pages contain common points and thus a direct tunnelling of 3-surfaces between these pages is possible only if the number n_{a_1} of the sheets of covering divides n_{a_2} or vice versa. Same holds true for n_{b_1} and n_{b_2}. This rule is just the basic rule about how symmetries of system can change in phase transition. This number theoretic rule could be behind genetic code and the extreme selectivity of bio-catalysis.

4. Suppose that both bio-molecules correspond to ordinary matter with $n_a = n_b = 1$ but that the magnetic body of a given amino-acid corresponds to $(n_a(A), n_b(A))$ and DNA, RNA, and tRNA codon to $(r_a(DNA), r_b(DNA))$. Since the flux tube from tRNA codon to the amino-acid page is essential for the process in which amino-acid is attached to tRNA, only tRNA for with $r_a(tRNA)$ divides $n_a(A)$ can catch an amino-acid labeled by n_a. Same applies to r_b and n_b.

5. Without the presence of the integer n_b the code would fail since DNA codon labeled by r_a would code for all amino-acids for which n_a has r_a as a factor. n_b can indeed save the situation. Suppose that one has $r_b(tRNA) = n_b(A)$ if DNA codes for an amino-acid. Assume also that $n_b(a)$ is prime: $n_b(A) = p_b(A)$, and different for each amino-acid. This prime does not correspond to p-adic prime, which is expected to be very large in the length scales of atomic physics (electron corresponds to $M_{127} = 2^{127} - 1$). Note that the assumption that amino-acids are labeled by small primes was made in both TGD inspired number theoretical models of the genetic code.

6. The assumptions mean that tRNA and amino-acid can be connected by a magnetic flux tube only if one has

$$p_b(tRNA) = p_b(A)$$

and $r_a(tRNA)$ divides $n_a(A)$. If the pages numbers n_a vary in the range $[1, 21]$ the divisor code follows from the argument of the previous section. Taking the previous argument seriously, one should also understand why there is no amino-acid labeled by $n_a = 4$ and why corresponding DNAs correspond to prime characterizing $n_a = 4$, why the number of DNA codons labeled by the factors of $n_a = 8$ is two, and why the number of codons associated with $n_a = 16$ only one.

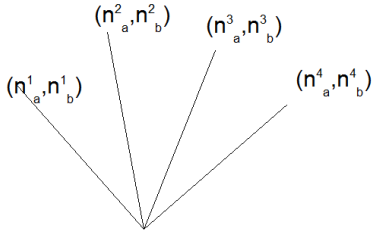

Figure 13.1: Illustration of the book-like structure of the generalized imbedding space.

Some further comments are in order.

1. The realization of the genetic code is not unique since the integers r_a and n_a could be replaced with Nn_a, where N is a product of primes larger than $p = 19$. It is also enough that the integers characterizing amino-acids are relative primes (have not common factors). The simplest assumption would be that the primes $p(A)$ satisfy $p(A) > 19$ so that $p(A)$ does not divide $n(A)$ for any A. If $p(A)$ is as small as possible the value spectrum of $p(A)$ is

$$\{23, 29, 31, 37, 41, 43, 47, 53, 59, 61, 67, 71, 73, 79, 83, 89, 97, 101, 103, 107, 109\} \ .$$

If one assumes that the two additional amino-acids coded in some cases by non-vertebrate genetic code correspond to primes also the primes $113, 127$ are included.

What is interesting is that Mersenne prime $M_7 = 2^7 - 1 = 127$ appears in the model of genetic code based on the notion of Combinatorial Hierarchy [K23]. This model assumes that DNA codons correspond to 64 integers in the range $1, ..., 127$. This realization of the genetic code cannot however be consistent with the divisor code realized in the proposed manner since it would require that the integers $n(A)p(A)$ belong to the range $1, .., 127$. The prime factors of these integers can however belong to this range.

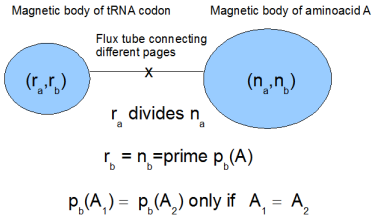

Figure 13.2: Illustration of the selection rules for magnetic flux tubes connecting magnetic bodies of tRNA and amino-acid.

2. The model in principle allows an infinite number of analogous codes and an interesting question is whether the bio-catalysis involves this kind of codes. The quantum antenna model for remote replication discussed in [K24] allows a dynamical interpretation for the flux tube realization of the genetic code as a divisor code in terms of quantum antenna hypothesis [K36], and predicts that sequences of DNA codons serve as names for polar molecules quite generally so that genetic code would define a universal language in living matter. This leads to an identification of the basic mechanism responsible for the functioning and evolution of the immune system.

3. The quantum states of dark baryons realize vertebrate genetic code with very general assumptions group theoretically [L2, K24, **?**], [L2]. Since dark matter is involved in both cases, one might wonder whether these codes could be related somehow. A one-one correspondence between the quantum states of dark nucleons representing codon and the integers r_a, p_b is required in order to have this connection. The simplest possibility is that that energy minimization implies that given dark nucleon resides with high probability at flux tube labeled by unique value of r_a. Same applies to amino-acids.

The number theoretical model discussed in this chapter emerged before the topological explanation of the divisor code. Hence the model becomes somewhat obsolete. In particular, it involves un-necessarily strong assumptions. p-Adic thermodynamics might be used to understand the possible equivalence of the divisor code and the dark baryon code discussed in [**?**] but this problem will not be discussed here.

13.2.7 Is The Fusion Of Geometric, Thermodynamical, And Divisor Code Approaches Possible In The 5-Adic Case?

A very attractive general idea is that genetic code could be understood in two dual manners: as an assignment $n \to p(n)$ and as an assignment $p \to n(p)$.

1. Genetic code could be understood in terms of a 5-adic thermodynamics for the partitions of integers characterizing codons. Here $6 \leq n_{2)} = n_0 + n_1 5 \leq 24$, $n_k \neq 0$, labels the 2-codons formed by the first two letters of the codon. This approach would predict the assignment $n \to p(n)$ once the number theoretic thermodynamics is specified.

2. Genetic code could be understood as a geometric imbedding $p \to n(p)$ of amino-acid space labeled by 20 primes $31 \leq p < 124$ to DNA space such that one has $n(p) = p$ if possible. This cannot the case for 4 primes ($p = 53, 79, 101, 103$). Also the interpretation as an induction of number theoretical bundle structure over amino-acid base space from DNA space is possible. $n(p) = p$ constraint obviously poses strong constraints on the model but it turns out that it is possible to satisfy these constraints for other than exceptional primes.

3. Also the basic idea of the divisor code could be included to the model via the condition that the number of divisors of the integer $n_{2)}$ for one of the DNAs coding for a given amino-acid equals to the number of DNAs coding for the amino-acid. There would be thus *two* labelings of amino-acids so that the model would become highly predictive.

The natural starting point is the vertebrate mitochondrial code with full $A \leftrightarrow C$ and $G \leftrightarrow U$ symmetries and one could interpret the breaking of these symmetries in the case of eukaryote code in terms of the context sensitivity characterized by the number theoretic temperature T_5. The large number of constraints raises the hope that a rather unique code could result. It will be found that for the number theoretic Hamiltonian depending only on the number partitions r of the integer $n_{2)}$ characterizing the first two letters of the 5-adic codon, only 4 solutions to the conditions can be found in the set of $N \sim 10^{30}$ candidates for $h(r)$.

13.3 5-Adicity Or 4-Adicity?

It seems that 5-adic representation of $A - C$ and $T - G$ symmetries allows the unification of the geometric view about genetic code with the number theoretic thermodynamics view and the idea of the divisor code.

13.3.1 The Problems Of The 4-Adic Model Of The Divisor Code

The 4-adic model for the divisor code has some problems.

1. 4-adic model is not consistent with the assumption that the set of DNAs coding for given amino-acid contains both the integer characterizing the degeneracy of the amino-acid as a number of its divisors and the codon labeled by the prime labeling the amino-acid. Hence the geometric realization must be given up unless one assumes that the primes associated with amino-acids associated with columns not containing primes are mapped to the integers in the columns by imbedding map. Even this option fails.

2. It is not easy to understand the emergence of singlets without assuming breaking of the number theoretical symmetries.

3. The proposed TGD inspired topological interpretation of the divisor code is not consistent with the presence of $n = 0$ codons. Also $n = 1$ codons are problematic.

4. There is no obvious connection with the maximization of the number theoretic negentropy assigning primes to amino-acids. 5-adic thermodynamics can do this and one could have dual descriptions. Geometric description in terms of imbedding of amino-acid space to DNA space (assigning DNAs to amino-acids) and thermodynamics description in terms of 5-adic thermodynamics assigning amino-acids to DNAs.

13.3.2 5-Adic Model Works For Thermodynamics Based On Partitions

5-adic variant of the model can overcome the problems of the 4-adic model.

Basic assumptions

1. Stopping codons do not correspond to formal amino-acids. The natural hypothesis is that the stopping codons do not possess negentropy maximizing prime in the range considered.

2. The question is whether conjugation $k \to 5-k$ for the last nucleotide corresponds 1) to DNA conjugation as in [A18] or 2) to a symmetry of the last codon. The naive guess would be 1). The guess turns out to be wrong since it implies that 3 4-plets contain symmetry related primes so that the number of amino-acids would be reduced by 3 due to the $n \to n + 50$ symmetry of the last nucleotide. On the other hand, $k \to 5-k$ as a representation of $A \leftrightarrow C$ and $G \leftrightarrow U$ symmetries takes odd integers to even integers so that there are no problems.

3. DNA codons correspond to 5-adic integers in the range [31, 124] having no vanishing 5-digits. Amino-acids are labeled by the 20 primes in the same range. They are mapped to DNA triplets. For 16 primes this imbedding is just the identification $n(p) = p$. The 4 "outsider" primes $53, 79, 101, 103$, which have a vanishing 5-digit, have necessarily $n(p) \neq p$. The first guess is that the outsider primes $53, 79, 101, 103$ correspond to amino-acids that are somehow special. It turns out that a possible identification for the amino-acids is as Trp, Lys, Met, Gln but that Lys, Gln pair can be replaced by any pair in the set $\{Gln, Lys, Glu\}$. One could also argue that the amino-acids corresponding to 53 and $103 = 53 + 50$ should be related by some kind of symmetry. Trp and Met indeed have the comment feature that a codon coding for them can also act as stopping codon. On the other hand, also Lys, Gln, and Glu share the property of being polar amino-acids.

Further constraints

The observation that there are two 4-columns containing no primes when combined with some facts about the genetic code and its variants give strong constraints on the code.

1. One of the prime-free columns must correspond to shared Ser-Arg column which transforms to Ser-Stop column for mitochondrial code. Otherwise one prime coding for an amino-acid would be lost.

2. In the case of the yeast mitochondria Thr is coded 8 times and Leu only twice. This forces the conclusion that second prime-free 4-column corresponds to Leu.

3. Since Leu must be coded by prime, Leu-Phe 4-column must correspond to the second 4-plet containing two primes. Hence the two 4-columns containing 2 primes give rise to three doublets. 6 additional doublets for eukaryote code and 9 additional doublets for mitochondrial code must be identified.

4. Thr 4-plet should contain n possessing 8 divisors. Only 3 4-columns contain $n = 8$ and correspond to 321, 131, and 231 columns.

Detailed identification of the code

Consider now a more detailed identification of the code.

1. Mitochondrial code is obtained as follows. 4 outsider primes which do not label DNAs directly are imbedded into 4-columns containing single prime. This gives 8 doublets altogether. Stopping codons in the 4-column containing Tyr and corresponding prime give one additional doublet so that a correct number of doublets result.

2. The breaking of the mitochondrial code to eukaryote code is easy to understand in the proposed framework. Trp and Met become singlets and Ile becomes triplet so that 9 doublets result.

3. Outsider primes would in this model correspond to Gln, Lys, Trp, Met. Gln and Lys could be replaced with any pair in the set {Gln, Lys, Glu} for the simple reason that corresponding amino-acid doublets cannot be distinguished from each other number theoretically. The identifications of the integers associated with amino-acids coded by 4 entire 4-column (Val, Ala, Pro, Gly) are unique apart from $4! = 24$ permutations of these amino-acids. It should be noticed that Lys, Gln, Glu belong to the group of 11 polar amino-acids and Met and Trp belong to the group of 8 hydrophobic amino-acids.

4. The multiplet containing Met is unique since there is only single codon ($n = 11^2 = 121$) for which the number of divisors is 3.

5. One can say that Ile and Met compete: either Ile^3-Met results when Ile wins. Ile^2-Met^2 results when Met wins. One can argue that Trp as outsider prime can also correspond to singlet or that Stop can "eat" any any prime and reduce the degeneracy. 5-adicity is broken for the first two nucleotides, which is not surprising.

These number theoretic constraints do not allow a unique identification of the code but pose considerable restrictions. **Table 13.1** represents one example consistent with these conditions. Note that the table does not fix how the primes 53, 79, 101, and 103 are assigned to Trp, Lys, Met, and Gln. Trp and Met are indeed special since they can be replaced by stopping codon some variants of the code.

It will be found that under rather general conditions (roughly 10^{30} candidates for the Hamiltonian $h(r)$ characterizing the thermodynamics of partitions) there are only 4 choices of $h(r)$ reproducing the eukaryote code, vertebrate mitochondrial code as well as other variations of the code. If one requires that the polar amino-acids Lys and Gln (or any pair in the set {Gln, Lys, Glu}) correspond to the conjugation related primes 53 and 103 only single solution for $h(r)$ is found. The 5-adic thermodynamics based on spin-spin interaction fails as do also other simple models.

Table 13.1: An example of a code obeying approximate 5-adic symmetry $k \leftrightarrow 5-k$ with respect to the last codon. Given are the integers associated with the codons of given 4-column in 5-adic and decimal notion, the number of divisors appearing if it belongs to the range of allowed values, and the 2-codon associated with the 4-column. Note that 5-adic symmetry for the first two nucleotides is broken.

(114,106,4,UG)	(214,107,2,GU)	(314,108,GC)	(414,109,2,GA)
(113,81) Trp	(21,82,4) Val	(313,83,2, Ala)	(413,84, Glu)
(112,56,4,Cys)	(212,57,4)	(312,58)	(412,59,2,Asp)
(111,31,2)	(211,32)	(311,33,4)	(411,34,4)
(124,111,4,GG)	(224,112,UA)	(324,113,2,AC)	(424,114,6,CG)
(123,86,4,Gly)	(223,87,4,Stop)	(323,88,8,Thr)	(423,89,2,Arg)
(122,61,2)	(222,62,4,Tyr)	(322,63,4)	(422,64)
(121,36)	(221,37,2)	(321,38,4)	(421,39,4)
(134,116,6,CC)	(234,117,6,UC)	(334,118,4,AA)	(434,119,4,AG)
(133,91,4,Pro)	(233,92,6,Ser)	(333,93,4,Lys)	(433,94,4,Arg)
(132,66,8)	(232,67,2)	(332,68,6,Asn)	(432,69,4,Ser)
(131,41,2)	(231,42,8)	(331,43,2)	(431,44,6)
(144,121,3,AU)	(244,122,4,UU)	(344,123,4,CA)	(444,124,6,CU)
(143,96,Met)	(243,97,2,Leu)	(343,98,6,Gln)	(443,99,6,Leu)
(142,71,2,Ile)	(242,72,Phe)	(342,73,2,His)	(442,74,4)
(141,46,4)	(241,47,2)	(341,48)	(441,49,3)

13.4 5-Adic Thermodynamical Model For The Genetic Code

The challenge is to guess the number theoretic Hamiltonian characterizing the thermodynamical model and the dependence of the 5-adic temperature T_5 on third nucleotide describing the splitting of 4-plets to doublets and further splitting of the doublets in the case of eukaryote code. There are two options concerning the choice of the Hamiltonian.

1. The Hamiltonian depends only on the number r of integers in the partition $n_{2)} = \sum n_k$ of $6 \leq n \leq 24$ of integer $n_{2)} = n_0 + n_1 5$ characterizing the first two nucleotides of the codon. Hamiltonian is tailored by evolution to reproduce the genetic code and its variants.

2. Hamiltonian is a direct analog of spin spin interaction $J \sum n_k n_l$ with n_k interpreted as spin associated with n_k Cooper pairs.

13.4.1 The Simplest Model For The 5-Adic Temperature

The simplest model for 5-adic temperature applies irrespective of the number theoretic Hamiltonian h and relies on the assumption inspired by the comparison of the mitochondrial and eukaryote code tables.

1. $T_5(n_3) = T_5$ hold true for common 4-plets, 4-plet parts of 6-plets, and 6-plets of the mitochondrial and eukaryote codes.

2. $T_5(n_3) = T_5(5-n_3)$ holds true for common 2-plets (A-C and T-G symmetries with respect to the third nucleotide) of eukaryote and mitochondrial code and for all 2-plets of mitochondrial code.

3. For eukaryote code this symmetry of 5-adic temperature would fail for Ile^3-Met, Cys^2-Stop-Trp and only for the second pair of values of n_3 corresponding to Met-Met$\rightarrow$ Ile-Met and Trp-Trp $\rightarrow$ Ttop-Trp $[n_3, 5-n_3) = (2,3)]$. Ser-Stop-Ser-Stop to Ser-Arg-Ser-Arg transition

would in turn be induced by the change of 5-adic temperature. Stop would correspond to a 5-adic temperature for which no prime coding amino-acid divides the partition function.

The condition that the model reproduces correctly the $n \to p(n)$ correspondence to be discussed later in principle allows to fix number theoretic Hamilton and $T_5(n_3)$ to a high degree.

13.4.2 The Simplest Possible Model For Thermodynamics

Before dwelling into complex calculations it is useful to ask what could be the simplest model for the 5-adic thermodynamics.

1. Calculational simplicity would suggest that the partition function must be as small as possible and thus satisfy $Z(n) < 125$. This restriction also maximizes the probability that the prime divisors are in the range $31 \leq p \leq 113$ with stopping codons involving only divisors $p < 31$. This together with the 5-adicity at the level of partition function would suggest that the definition of $Z(n)$ should involve 5-adic cutoff in the form $Z(n) \to Z(n) \ mod \ 5^3$. The natural constraint on the values h of the number theoretical Hamiltonian would thus be $h \in \{0, 1, 2\} \in Z_3$. Modulo three arithmetics fits also nicely with the triplet structure of codons.

2. In this model the effect of changing 5-adic temperature form $T_5 = 1$ to $T_5 = 1/n$, $n = 1, 2$ would be expressed as $h(r) \to n \times h(r)$. Only two possible 5-adic temperatures would be possible and the symmetries of the vertebrate mitochondrial code would be predicted automatically. The symmetry breaking down to eukaryote code could be described in terms of 5-adic temperature if one allows formally infinite temperature for which one would have effectively $h(r) \to h(r) = 0$ so that partition function equivalent with $Z = 1$ would result and the codon in question would code for stopping sign. This is indeed the case for the codon coding originally Trp. For the breaking of Ile-Met doublet the splitting to triplet and singlet can be also understood as the dependence of T_5 on codon in symmetry breaking manner.

3. The simplest possible model would correspond to $Z(n) = p(n) = \sum p_k 5^k$ so that p_k would have interpretation as degeneracies of states modulo 5: this would imply that the doublets would correspond to primes related by exchange of p_1 and p_2, which does not make sense. Hence the integers p_k cannot directly correspond to the degeneracies of states with different energies and the partition function must be obtained via $Z \to Z \ mod \ 125$ prescription from a more complex partition function having values $Z > 125$. The three digits p_k for 5-adic code and Z_3 valuedness of $h(r)$ might relate naturally to 3-letter structure of codons.For $n = p(n)$ one would simply have $Z(n) = n = p(n)$. For the four exceptional amino-acid primes $p = 53, 79, 101, 103$ this would not hold true. The most general model would allow small integer $k \leq 4$ as an additional factor of $Z(n) \leq 124$.

Unfortunately, this simple model does not allow any obvious number theoretical realization. In particular, the models based thermodynamics of partitions and on spin-spin interaction fail with Z_3 valued $h(r)$ and Z_{125} valued $Z(n)$. The simplicity and explanatory power of the model encourage however to keep mind open for the existence of this kind of model.

13.4.3 Number Theoretic Hamilton Depending On The Number OfPartitions Of Integer Characterizing DNA

The number theoretic model for the genetic code discussed in [K11] was based on the assumption that the number theoretic Hamiltonian depends only on the number of summands in the partition $n = \sum_k n_k$.

Generalizing to the recent context, the Hamiltonian $h(r)$ for the 5-adic thermodynamics should depend only on the number r of summands in the partition $n_{2)} = \sum_{k=1}^{r} n_k$. The deviations from the standard code would be explained in terms of the variation 5-adic temperature which has values $T = 1/n$, n positive integer, implying Boltzmann weights $5^{h(r)/T_5}$. The fact that same codon does not always code same amino-acid [K19] , [I47], could be understood in terms of temporal variation of 5-adic temperature. A possible interpretation is in terms of a breaking of conformal invariance characterized completely the number r of subsets in the partition.

A further assumption motivated by 5-adicity is the replacement $X \equiv h(r)/T_5$ in Boltzmann weight with $X \mod N$, where N characterizes the highest power of 5 appearing in partition function. $N = 3$ would be the minimal option but it turns that only $N = 25$ works. It will be assumed that evolution has gradually tailored $h(r)$ so that the observed genetic code maximizes for a given DNA the p-adic information measure defined by the prime $p(DNA)$ coding the corresponding amino-acid in practice this means that partition function is divisible by a power of $p(DNA)$.

The interpretation in terms of the number of sub-condensates of Cooper pairs containing n_k spin 1 Cooper pairs is an alternative interpretation and would look attractive physically but in this case the Hamilton depending on the number r of partitions only does no look natural. The number theoretic Hamiltonian would depend on the number r of bound states only if the interaction energy $E(n_k, n_l)$ between two sub-condensates with n_k and n_l Cooper pairs is a constant integer $E(n_k, n_l) = E$, so that the interaction energy between sub-condensates would behave as $r(r-1)E \mod N$. This could give rise to a rather random looking behavior of $h(r)$ as a function of r. The modulo arithmetic constraint would restrict considerably the number of choices of $h(r)$. This model does not reproduce realistic genetic code.

Formula for the partition function

The formula for the partition function is given as

$$\begin{aligned} Z &= \sum_r d(n,r) 5^{H(r)} \ , \\ H(r) &= \frac{h(r)}{T_5} \mod 25 \ . \end{aligned} \tag{13.4.1}$$

$T_5 = 1/n$ varies in the range $n \in [1, 24]$.

The partition numbers appearing in are conveniently calculated by using the recurrence relation [A6]

$$d(n,r) = P(n,r) = P(n-1, r-1) + P(n-r, r) \ , \ P(n,1) = 1 \ . \tag{13.4.2}$$

The structure of the calculation

The flow of calculation proceeds along the rows of the code table as given in **Table ??** coding for the constraints coming from the assumption that the number of divisors for of the integers labeling DNAs is same as the degeneracy of corresponding amino-acid and from the consistency with the geometric model of the code.

1. It is assumed $0 \leq h(r) \leq h_{max} = 2$ for $r > 1$. $h(1) = 0$ can be assumed without a loss of generality if one assumes that $r = 1$ (trivial partition) corresponds to the most probable minimum energy partition in the sense of 5-adic thermodynamics. This implies that 3^{23} candidates for $h(r)$ must be scanned. All possible $4! = 24$ assignments of Trp, Lys, Met, Gln with the primes $p = 53, 101, 79, 103$ which do not label codons are considered.

2. At the first step those guesses for $h(r)$, $r \leq 6$, for which the DNA-Cys correspondence with $p(Cys) = 31$ is reproduced and stored.

3. At the next step calculation branches to four separate calculations corresponding to the four possible values of $p(Trp) \in \{53, 101, 79, 103\}$. 5-adic temperature T_5 is varied and it is found whether the $p(Trp)$ can be reproduced for some value of $T_5 \in \{1, 2, ..., 24\}$. If this is not possible, the candidate for $h(r)$, $r \leq 6$ is rejected. After this the calculation proceeds for given $p(Trp)$ assignment through next values of $h(r)$ to $r = 18$ where one checks whether $p(Asn) = 43$ can be reproduced. In the transitions to new row corresponding to $r = 10, 11$ and $r = 15, 16$ two values of of $0 \leq h(r) \leq 2$ appear and bring in additional degrees of freedom. In $Glu - Asp$ column at the end of the first row T_5 is varied to see whether also $p(Asp) = 59$ can be reproduced.

Table 13.2: There are 24 different solution types depending on which permutation $xyzu$ of (Trp, Lys, Met, Gln) corresponds to the exceptional primes $(53, 79, 101, 103)$. For instance, lmtg means $(Lys, Met, Trp, Gln) \to (53, 79, 101, 103)$, and tglm means $(Trp, Gln, Lys, Met) \to (53, 79, 101, 103)$. It is convenient to label the 24 possibilities by pairs of integers (m, n). $m = 1, 2, 3, 4$ according to whether Trp, Lys, Met or Gln corresponds to $p = 53$. The second integer $n = 1, ..., 6$ specifies which of the six permutations of remaining three amino-acids corresponds to $(79, 101, 103)$ in a manner expressed by the table. For instance, for $(m, n) = (1, 1) \leftrightarrow (tlmg)$ codes for $(Trp, Lys, Gln, Met) \to (53, 79, 101, 103)$.

(1, 1) tlmg	(1, 2) tglm	(1, 3) tmgl	(1, 4) tlgm	(1, 5) tgml	(1, 6) tmlg
(2, 1) ltmg	(2, 2) gtlm	(2, 3) mtgl	(2, 4) ltgm	(2, 5) gtml	(2, 6) mtlg
(3, 1) lmtg	(3, 2) mgtl	(3, 3) gltm	(3, 4) lgtm	(3, 5) gmtl	(3, 6) mltg
(4, 1) lmgt	(4, 2) glmt	(4, 3) mglt	(4, 4) lgmt	(4, 5) gmlt	(4, 6) mlgt

4. After this the calculation for given value of $p(Trp)$ branches to 6 alternatives corresponding to different assignments of remaining exceptional primes to Lys, Met, Gln. Since Arg-Ser four-column does not give any conditions the values of $h(r)$ for $r = 19, 20, 21$ appear as free parameters. This part of calculation is especially critical since the first 4-columns of the last row of the table contain only doublets. The last 4-column (Leu) corresponding to $r = 24$ does not pose any conditions on $h(24)$ unless one requires that also $n = 49$ gives partition function for $p(Leu) = 97$ is the maximizing prime.

Results

The difficulties involved with the numerical computation were considerable since only University MATLAB was available and for the extensive computations involved its functioning turned out to be somewhat unreliable and reasons for this could not be identified. 22 solutions to the conditions expressed in Table 2 has been found from the set of about 10^{30} candidates, and have been checked separately to satisfy all the conditions.

The 11 number theoretic Hamiltonians $h(r)$ for $r = 1, 2, ..., 23$ are given in**Table 13.3** with conventions expressed in **Table ??**

One can consider additional symmetry assumptions reducing the number of solutions.

1. One might argue that the "unstable" amino-acids Trp and Met naturally correspond to the conjugation related primes 53 and 103. The are only 2 solutions (h_1 and h_2 in Table 3) corresponding to the assignment $(Trp, Met) \to (53, 103)$ or vice versa (the integer pairs (m, n) corresponding to txym and mxyt in Table 2 are (1, 2), (1, 4), (4, 3), (4, 6)). These two solutions differ only for last 5 values of r.

2. One might also argue that the polar amino-acids Lys and Gln (or any pair in the set $\{Lys, Gln, Glu\}$) correspond to the conjugation related primes 53 and 103 (the integer pairs (m, n) corresponding to lxyg and gxyl in Table 2). There are 3 solutions (h_6, h_7 and h_8 in Table 3) corresponding to the assignment $(Lys, Gln) \to (53, 103) orviceversa$ (the integer pairs (m, n) corresponding to txym and mxyt in Table 2 are (2, 1), (2, 4), (3, 1), (3, 4)).

That not too many solutions exist to the conditions together with the fact that the model is consistent with the basic ideas of geometric code and of divisor code and results from 5-adic thermodynamics, raises the hope that something more than a mere complex parameterization of the genetic code might be in question. For $r = 2$ $h(r)$ only the values $h(r) \leq 5$ have been scanned (the reasons were the strange problems that made the continuation of calculations very difficult) so that a portion $6/25 = 24$ per cent of all possible candidates for $h(r)$ are scanned. The number

Table 13.3: Table represents the 11 solutions found for the Hamiltonian of partition thermodynamics consistent with the code table represented in Table 1. The integer pair (m, n) given in the first two rows codes for the correspondence between amino-acids (Trp, Lys, Met, Gln) and exceptional primes $(53, 79, 101, 103)$ according via the correspondence given in **Table 13.2**

m	1	1	1	1	2	3	3	3	3	3	4
n	2	2	5	5	2	1	1	1	2	6	2
r	h_1	h_2	h_3	h_4	h_5	h_6	h_7	h_8	h_9	h_{10}	h_{11}
1	0	0	0	0	0	0	0	0	0	0	0
2	1	1	4	5	3	2	0	0	0	0	0
3	3	3	24	23	11	0	10	10	13	13	13
4	19	19	12	24	2	14	16	16	4	4	4
5	3	3	13	15	9	18	21	21	12	12	12
6	0	0	19	6	5	2	9	9	12	12	12
7	1	1	12	4	14	5	16	16	9	9	9
8	15	15	16	0	10	18	20	20	7	7	7
9	17	17	7	15	9	2	14	14	12	12	12
10	3	3	17	10	15	12	14	14	16	16	16
11	17	17	9	22	3	1	24	24	5	5	5
12	8	8	14	12	18	3	4	4	11	11	11
13	4	4	24	3	17	12	5	5	19	19	19
14	16	16	5	11	19	6	4	4	18	18	18
15	13	13	9	19	3	16	1	1	7	7	7
16	11	11	20	11	20	7	2	2	7	7	7
17	23	23	14	5	17	22	14	14	21	21	21
18	7	7	13	3	4	1	5	5	6	6	6
19	14	16	1	11	8	6	11	14	9	4	4
20	16	14	1	22	22	1	6	12	7	17	23
21	6	19	17	11	19	12	13	15	13	23	22
22	14	0	6	22	2	7	19	5	15	21	16
23	13	12	6	17	7	2	7	12	12	4	15

Table 13.4: Inverse 5-adic temperatures $\beta = 1/t_5$ for doublets of the vertebrate mitochondrial code. The notational conventions and the ordering of solutions are same as in the previous table.

m	n	$\beta(1)$	$\beta(4)$	$\beta(11)$	$\beta(13)$	$\beta(14)$	$\beta(15)$
1	2	19	11	6	5	24	21
1	2	19	11	6	5	23	7
1	5	21	5	15	6	4	7
1	5	15	13	10	23	21	13
2	2	10	16	23	15	16	21
3	1	6	17	16	17	3	19
3	1	10	2	23	17	20	11
3	1	10	2	23	4	4	12
3	2	5	6	5	18	18	7
3	6	5	6	5	8	23	16
4	2	11	6	5	24	23	18

of solutions found is 11. If the solutions are distributed evenly, the estimate for the total number solutions is about 45.

The 5-adic temperature is $T_5 = 1$ for all lower doublets in the code table (the two smallest values of $n(DNA)$ in a given 4-column). The values of 5-adic temperature for the upper vertebrate mitochondrial doublets are given by **Table 13.4** for some cases. For eukaryote code symmetry breaking means only a change of 5-adic temperature for the symmetry breaking codon so that it codes for either Stop as in case of Trp-Cys doublet or for Ile instead of Met. Also the context dependence observed for some variants of the genetic code [I47] can be understood in terms of a temporary change of the 5-adic temperature. Note however that the amino-acid coded temporarily does not belong to the group of standard amino-acids.

For the stopping codon $1/T_5 = 2$ is the minimum temperature implying that no prime $31 \leq p \leq 113$ divides the partition function.

13.4.4 Number Theoretical Hamiltonian Identified As Spin-Spin Interaction

The hypothesis that Hamiltonian depends on the number r of summands in the partition is of course only a very simple working hypothesis allowing a relatively easy numerical search of the Hamiltonian (in the original model one had $n \leq 63$ so that rather large numbers of partitions had to be considered). If one takes seriously the idea about sub-condensates of spin 1 Cooper pairs, one could argue that the interaction energy between blocks of Cooper pairs is spin-spin interaction proportional to the product of net spins of electrons and is therefore of form $E(n_k, n_l) = Jn_kn_l$, $k \neq l$. A number theoretical analog of rather spin glass variant of Ising model would be in question.

In this case one would have $h = J\sum_{k,l} n_kn_l = \sum_k n_k(n - n_k) = n^2 - \sum_k n_k^2$ and thermodynamically equivalent with $h = J\sum_k n_k^2$. This Hamiltonian or rather, its modulo N variant ($N = 3$ in the minimal case), would distinguish between partitions with the same value of r. In the recent model one has $6 \leq n_{2)} \leq 24$ so that the numbers of partitions are quite reasonable.

What makes this Hamiltonian so attractive would be its clear physical interpretation and involve a minimal amount of ad hoc elements.

The simplest working option is that third nucleotide affects only the 5-adic temperature so that one would have

$$h(n_1, ..., n_r) = \frac{J}{T_5} \times \sum_{pairs} n_kn_l \ ,$$

where one has $T_5 = 1, 2$. This interpretation conforms with the idea about living matter as spin glass like structure for which interaction strengths for spin-spin interactions are variable

parameters. This would also conform with the general vision about TGD Universe as a four-dimensional spin glass like structure [L3].

Calculation of the partition function for a model based on spin-spin interaction

The task is to calculate the partition function $Z(T(n_3)) = \sum_P 5^{h(n_2,P)/T_5}$. To achieve this one can generalize the recursion formulas for the numbers $d(n,r)$ of partitions of n to sum of r terms.

1. One can arrange the integers in the partition so that one has always $n_k \leq n_{k+1}$ and start the recursive calculation from $h_r(1,....1,n-r+1) = (n-r+1)(r-1)$.

2. This gives rise to general recursion formula given by

$$\begin{aligned} h_r(n_1,...,n_{r-1},n-r+1-k_1) &= J(n-r+1-k_1)(r-1+k_1) \\ &+ h_{r-1}(n_1,...,n_{r-1}) \ . \end{aligned} \tag{13.4.3}$$

   Using this recursion formula one can express the formula for Hamiltonian as

$$\begin{aligned} &\tfrac{1}{J}h_r(k_r+1,k_{r-1}+1-k_r,...,k_2+1-k_3,k_1+1-k_2,n-r+1-k_1) \\ &= (n-r+1-k_1)(r-1+k_1)+(k_1-r+2-k_2)1)(r-2+k_2) \\ &+...+(k_{s-1}-r+s-k_s)1)(r-s+k_s)+...+(k_{r-1}-k_r)k_r \end{aligned} \tag{13.4.4}$$

   In this formula $h \to h \ \ mod \ \ 25$ operation is not written explicitly.

The expression for the partition function can be written as

$$\begin{aligned} Z(n) &= \sum_r Z(n,r) \\ Z(n,r) &= \sum_{k_1,....,k_r} 5^{h_r(k_r+1,k_{r-1}+1-k_r,...,k_2+1-k_3,k_1+1-k_2,n-r+1-k_1)} \ . \end{aligned} \tag{13.4.5}$$

The lower and up upper bounds for k_s in the summation can be deduced as follows. An upper bound for k_1 obtained from the condition $rk_1 = n$ and gives $k_1 \leq k_{max} = [n/r]$ where $[x]$ denotes the integer $n \leq x$ nearest to x. The corresponding upper bound for k_s reads as $k_s \leq [k_{s-1}/r-s+1]$. A lower bound for k_s comes from the requirement $n_s \geq 1$ and gives $k_s \leq k_{s-1}$.

To avoid problems caused by the fact that the numbers for various loops are dynamical, one can use recursion to calculate $Z(n,r)$ such that the module in question calculates $h(...)$ by calling itself repeatedly. What simplifies the calculation dramatically is that it is not necessary to store the data about the values of Hamiltonian since partition function is all that is needed.

1. At s^{th} level the module first adds to the Hamiltonian of a given branch the contribution from that level and after that adds the contributions from from $(s+1)^{th}$ level.

2. The calculation branches which means a a loop over the values of k_{s+1}. This means that module calls itself at each step of the loop to calculate the contributions of the next level to the Hamiltonian at a given branch.

3. The module adds also to Z the contribution from $(s+1)^{th}$ level is added. The addition is trivial until the r^{th} level is reached and all contributions to the Hamilton are known.

4. At the last level of tree the situation looks like follows. At given branch of the tree at $(r-1)^{th}$ level the module adds in loop-wise manner to Z the contributions from r^{th} level for that branch. After the return to $(r-2)^{th}$ branch next branch at $(r-1)^{th}$ level is selected and same process is repeated. Etc...

5. In order to avoid overflow problems it is safest to express the terms of the partition function in pinary series with respect to the p-adic prime $31 \leq p \leq 113$ considered and perform the addition of contributions to Z in terms of the pinary series.

Structure of the calculation

The general structure of the calculation is following.

1. Perform a loop over n labeling the 2-codons and find for each of them the prime p for which negentropy $S_p(n)$ is minimum and look whether for a suitable choice of T_5 the resulting assignment $n \to p(n)$ is consistent with the geometric model of the code and with the basic idea of the divisor code.

2. For a given n perform a loop over allowed values of p to see whether anyone of them appears as a divisor of the partition function and which of them maximizes the number theoretic negentropy. Unless this occurs the codon in question is identified as a stopping codon. The proposed geometric model of course fixes the integers n associated with the stopping codon.

3. For given n and p perform a loop over the values of r and sum their contributions to the partition function $Z(n, r)$ by applying the recursive procedure described in the previous subsection. In order to avoid overflow problems (possibly appearing in the case of MATLAB), the calculation must be performed for each value of p separately using pinary expansions for $Z(n, r)$. If Hamiltonian belongs to Z_3, overflow problems are of course avoided automatically.

4. An alternative manner to view the calculation is to take the proposal for the $n \to p(n)$ correspondence represented as a table at the end of previous section as an input and by a suitable selection of $0 \leq J(n_{2)}) \leq 2$ try to reproduce it. Note that the correspondence between primes 53, 79, 101, 103 and amino-acids Trp, Met, Gln, Lys if not fixed by the model represented in the table.

5. The most practical manner to perform the calculation is to take $J = 1$ and allow T_5 to run from 1 to 2 for every value of n and look whether the resulting spectrum of primes is consistent with the proposed $n \to n(p)$ correspondence or possible modification of it. At the roughest level the calculation serves as a test for 5-adicity that is whether the integer $n = n_0 + n_1 5$ corresponds to prime of form $n + 25$ or $n + 75$.

Results

The proposed spin-spin interaction model allowing varying value of T_5 cannot reproduce the model summarized by **Table 13.3**. The roughest test for the model is whether 5-adic description of A-C and T-G symmetries works. For mod 25 thermodynamics with $n = n_0 + n_1 5$ determining the thermodynamics the fails to be consistent with the predictions of the simplest model.

13.5 A Possible Physical Interpretation Of Various Codes In TGD Framework

The inspiration for attempts to interpret physically the origin of various codes in TGD framework (summaries of quantum TGD, TGD inspired theory of consciousness, and TGD inspired view about quantum biology are given in articles [L5, L4, L3]) springs from the following ideas.

1. At fundamental level quantum TGD reduces to almost topological quantum field theory at light-like 3-surfaces of $H = M^4 \times CP_2$ having also interpretation as random light-like orbits of 2-dimensional partons, which can have arbitrarily large sizes. Quantum TGD involves fusion of real physics and its p-adic variants relying crucially to the assumption that S-matrix involves only data at intersections of real 2-surfaces and their p-adic counterparts obeying same algebraic equations consisting of rational pointsandalgebraic points in the algebraic extension of p-adic numbers characterization physical states in question. These intersections consist of discrete points giving rise to cognitive representations which should naturally relate to the genetic code.

2. TGD based view about dark matter as a hierarchy of quantum coherent phases labeled by symmetry groups $G_a \times G_b \subset SU(2) \times SU(2) \subset SL(2,C) \times SU(3)$, where $SL(2,C)$ is Lorentz group and $SU(3)$ corresponds to the gauge group of color interactions. These phases are characterized by arbitrarily large values of Planck constants and are assumed to be responsible for the quantum control in living matter.

3. The generalization of the notion of imbedding space $H = M^4 \times CP_2$ based on the geometric realization of the dark matter hierarchy and involving a hierarchy of discrete sub-groups $G_a \times G_b$.

The basic idea is that the maximal cyclic subgroup Z_n of G_a could correspond to the group Z_n assigned with amino-acid and corresponding codons in the proposed group theoretic interpretation of the divisor code. n would give the order of the maximal cyclic subgroup $Z_n \subset G_a$ acting as symmetry group of wave functions of free electron pairs and (r,s), $rs = n$ could define a decomposition of $Z_n = Z_r \times Z_s$ with Z_r leaving invariant the electronic wave function.

13.5.1 Generalization Of Imbedding Space And Interpretation Of Discrete Bundle Like Structures

One should understand how the discrete number theoretical structures associated with various realizations of the genetic code emerge from TGD based physics. TGD suggests a very general geometric realization of the geometric codes in terms of points in the intersection of p-adic and real space-time sheets (actually a 2-D "partonic" surfaces having arbitrarily large size) consisting of algebraic points and of the TGD based generalization of imbedding space obtained by gluing together infinite number of copies of the imbedding space having singular bundle structure $H = M^4 \times CP_2 \to H/G_a \times G_b$, where one has $G_a \times G_b \subset SU(2) \times SU(2) \subset SL(2,C) \times SU(3)$.

G_a would manifest itself directly as discrete rotational symmetries of biomolecules basically due the presence of dark matter having G_a as exact group of rotational symmetries. Hence only G_a would be interesting in the recent case. In fact, the maximal cyclic subgroup Z_n for arbitrary G_a is in a special physical role and it might be possible to identify the group characterizing amino-acid and DNA as this group.

The bundle structure $H \to H/G_a \times G_b$ has singular points corresponding to the points of H for which $G_a \times G_b$ or its subgroup acts as an isotropy group leaving the point invariant. Quite generally, the singular points, in particular those for which G_a acts as isotropies, are involved with the phase transitions changing Planck constant and interpreted as a leakage of 3-surfaces between sectors of H labeled by different groups $G_a \times G_b$.

The interpretation of G_r characterizing DNA as an isotropy of singular point of bundle structure does not seem however natural. Rather, the wave functions of (say) free electron pairs (possibly Cooper pairs) defined in the set of points defined by the orbit of $Z_n \subset G_a$ could be invariant under some subgroup of $Z_r \subset Z_n$ for DNA labeled by (r,s), $r \times s = n$. Thus codons coding for an amino-acid having Z_n as a symmetry group would be characterized by wave functions for free electron pairs transforming under representations of Z_n and remaining invariant under $Z_r \subset Z_n$ and thus reducing to representations of $Z_s = Z_n/Z_r$. Note that $r = 1$ corresponds to all irreps of Z_n and $r = n$ to singlets under Z_n.

13.5.2 A Possible Interpretation For The Divisor Code

Consider now a model for what might happen in the coding of amino-acid by DNA.

1. Suppose that the maximal cyclic subgroup $Z_n \subset G_a$ acts as symmetries of "dark" space-time sheets and wave functions of "dark" free electron pairs for the amino-acid and corresponding DNAs so that the 2-surfaces in question are n-fold coverings of CP_2 points by M^4 points (corresponding to positions of say 5 molecules in a cyclic molecule) and corresponding codons. Free electron pairs could correspond to the dark matter in question.

2. Suppose that DNA characterized by n and its particular divisor r has electronic wave functions invariant under Z_r and thus forming irreducible representations of $Z_s = Z_n/Z_r$, $n = r \times s$. The electronic wave functions assignable to the amino-acid would in general

transform according to some irreducible representations of $Z_n = \prod_i Z_{p_i}$, $n = \prod_i p_i$, where same prime p_i can appear several times. This assumption would explain why the product decompositions (r, s) and (s, r) are not equivalent.

13.5.3 About The Geometric Interpretation For The Thermodynamics Of Partitions Of $N_{2)}$

Suppose that the maximization of the information content for the thermodynamics for the partitions of the integer $n_2 = n \ mod \ 5^2$ belonging to the range $[6, 24]$ and labeling 2-codons provides a dual manner to understand the genetic code. $n \to n \ mod \ 25$ would have an interpretation in terms of reduction to a subset of the finite finite field $G(5, 2)$ and would be natural in 5-adic context.

One could try to interpret the modulo arithmetics in terms of the generalized notion of imbedding space.

1. One could label the points of M^4 covering of CP_2 by integers $0 \leq m \leq n$. The sheets points m and $m + k25$ should be equivalent from the point of view of mitochondrial genetic code so that Z_{25} equivalence classes would give rise to $n_{2)}$ points.

2. A more concrete interpretation would be that first nucleotide along gives rise to n_0-fold covering, second nucleotide adds $5n_1$ sheets so that $n_{2)} = n_0 + 5n_1$-fold covering results, and third nucleotide adds $n_3 5^2$ sheets so that to $n = n_{2)} + n_3 \times 5^2$-fold covering results. The sheets contributed by the third nucleotide would not participate in the partition thermodynamics and the third nucleotide would only determine the 5-adic temperature $T_5 = 1/n$.

13.5.4 About The Physical Interpretation For The Thermodynamics Of Partitions Of $N_{2)}$

The 5-adic thermodynamics relies on the partitions of $n_2 = n \ mod \ 5^2$. n_2 could have interpretation both as a net conformal weight or spin associated with spin one electronic Cooper pairs.

1. Modulo 5^2 property could be due to the invariance of electronic wave functions under Z_{25} acting as rotations. There would be 25-periodicity of physics in the covering, the analog of a lattice structure in angle degree of freedom with sub-lattices forming dynamical units. Also quantum group with quantum phase $q = exp(i\pi/25)$ implies the analog of lattice structure in angle degrees of freedom.

2. Each equivalence class analogous to a sub-lattice with points having distance of 25 units would effectively carry one unit conformal weight or one unit of spin (L_0 and iL_0 act as infinitesimal scaling and rotation respectively). At the concrete physical level the following alternative interpretations suggest themselves.

The interpretation in terms of conformal symmetry

The partitions of the integer $n_{2)} = n_0 + n_1 5$, $n_i \neq 0$ could have interpretation as partitions of the set of equivalence classes to a union of subsets with the number n_k of elements in the subset giving the total conformal weight created by L_{n_k} rather than L_1^k. These partitions could be interpreted as partitions of a molecular Z_{25} equivalence classes of building blocks of the molecular structure with Z_n rotational symmetry to subsets of basic building blocks and Virasoro generators L_{n_k} would act on various building blocks. A formation of bound states each binding single particle states associated with n_k sheets and created by L_1 suggests itself. The reduction of Virasoro algebra defined in Z to a Virasoro algebra defined in the finite field $G(5, 2)$ or in the ring Z_{25} is natural in this framework.

Interpretation in terms of irreducible representations of symmetric group and braids

Partitions label the conjugacy classes of symmetric group S_n consisting of the permutations of n objects. The summand n_k corresponds to a cyclic permutation of n_k objects. Partitions label also

the irreducible representations of S_n. S_n can be defined by generators e_m representing permutation of m^{th} and $(m+1)^{th}$ object satisfying the conditions

$$\begin{aligned} e_m e_m &= e_n e_m \text{ for } |m-n|>1, \\ e_n e_{n+1} e_n &= e_n e_{n+1} e_n e_{n+1} \text{ for } n=1,...,n-2 \ , \\ e_n^2 &= 1 \ . \end{aligned} \tag{13.5.1}$$

By dropping the condition $e_n^2 = 1$ one obtains the defining relations of the braid group B_n of braid consisting of n strands. The irreducible representations of B_n are projective representations of S_n and give as a special case the representations of S_n.

1. Could the dynamics for partitions of n correspond to the dynamics for irreducible representations of S_n?

S_n brings in mind braids and topological quantum computation and the suggestion of [**?**] that DNA and/or RNA might act as a topological quantum computer. The so called number theoretical braids, which provide representations for Galois groups permuting roots of an n^{th} order irreducible polynomial are subgroups of S_n (and equal to S_n in the generic case), are in a central role in the formulation of quantum TGD [K9], [A4].

This interpretation would assign to a given codon a braid with n strands, whose states would correspond to irreducible representations of S_n [A7]. The thermodynamics would be for the irreducible representations of S_n with the number n of braids varying in the range $[6, 24]$. Braid would be a 5-adic thermodynamical system such that all $d(n,r)$ irreducible representations with a given value of r would have the same value of the 5-adic Hamiltonian $h(r)$ (definitely not the most general dynamics now). The reason for the absence of n-braids for which n has zeros in its 5-adic expansion could relate to the fact that the quantum phase $q = exp(i\pi/m)$ defines a universal topological quantum computer for $m \geq 5$. $m = 5$ is suggested strongly in case of DNA since it manifests itself in the geometry of DNA (twisting angle for single nucleotide and the presence of 5-cycles).

2. More general dynamics?

The alternative interpretation forces to reconsider the definition of 5-adic thermodynamics. Let us denote by (n,r,i) the irrep of S_n corresponding to a particular partition of n with r summands. It would seem natural to interpret the dimension $D_{n,r,i}$ of the irrep as the additional degeneracy factor replacing $d(n,r)$ so that the number $d(n,r)$ of partitions with r summands (subsets) would be replaced by the degeneracy factor

$$D(n,r) = \sum_i D_{n,r,i} \ ,$$

and $D_{n,r,i}$ is the dimension of the irrep in question. The irreps $d(n,r,i)$ are in one-one-correspondence with Yang tableaus consisting of n boxes in r rows and $D(n,r,i)$ can be calculated using standard formulas [A10].

One might hope that this modification could allow to simplify the dynamics. The best one might dream of would be that $h(r)$ could be taken to be Z_3 valued: $0 \leq h(r) \leq 2$. One could also check whether the definition of the partition sum using modulo 125 arithmetics as $Z = \sum_r D(n,r) 5^{h(r)} \ mod \ 125$ gives sensible results. Only two possible temperatures $1/T_5 = 1, 2$ besides $1/T_5 = 0$ corresponding to stopping codon are possible so that doublets pose very strong conditions on the model. The transformation $Z = Z_0 + Z_1 5 + Z_2 5^2 \to Z_0 + Z_2 5 + Z_1 5^2$ corresponds to the temperature scaling by 2. Hence it is not surprising that the simplest model does not work. In any case, the modification of earlier computational model to this case involves only the replacement of $d(n,r)$ with $D(n,r)$.

The dynamics could be however much more flexible. The 5-adic thermodynamics for irreducible representations of S_n instead of partitions allows the replacement of $h(r)$ with $h(n,r,i)$, say $h(n,r,d(n,r,i))$, where $d(n,r,i)$ is the dimension of the representation in question. The dynamics for a given n would be independent of the dynamics for other values of n unless one assumes that $h(n,r,d(n,r,i))$ is some simple function, say $h = d(n,r,i) \ mod \ 3$. In the most general case the number of parameters $h(n,r,i)$ would be the number of irreps given by the number

$d(n) = \sum_r d(n,r)$ of partitions. For $n = 6$ one has $d(6) = 11$ partitions and $n = 24$ would give $d(24) = 3^2 \times 5^2 \times 7 = 1575$ partitions. Even for $h(n,r,i) \in Z_3$ this would increase the number of parameters dramatically and might allow to reproduce the genetic code in consistency with the constraints from the divisor code.

3. What could be the physical interpretation?

One can ask how this picture could relate to the picture provided by the divisor code in which representations of cyclic group Z_n reduced to some of its subgroup with integer $31 \leq n \leq 124$ being one of the integers associated with a given amino-acid. Is there place in TGD Universe for these two discrete symmetries? This might be the case if one takes seriously both the hierarchy of Planck constants involving the generalization of the imbedding space concept and the notion of number theoretic braid.

1. The permutation group $S_{n_{2)}}$, $n_{2)} \in [6,24]$ for braid strands associated with the first two letters of the codon $n > n_{2)}$ would act on the number theoretical braids with $n_{2)}$ strands. The increase of n_2 could have interpretation as an increase of complexity in the sense that the number of braid strands increases.

2. The cyclic group Z_n, $n \in [31, ..., 124]$, possibly associated with electron pairs, could correspond to the G_a covering of $M^4_\pm$ defined by the hierarchy of Planck constants associated with the hierarchy of fiber bundle structures $H_\pm = M^4_\pm \times CP_2 \to H_\pm/G_a \times G_b$, $G_a \times G_b \subset SU(2) \times SU(2) \subset SL(2,C) \times SU(3)$. Cyclic group Z_n would be identified as the maximal cyclic group of G_a. Note however that topological quantum computer considerations would suggest that G_a has Z_5 as maximal cyclic subgroup so that Z_n cannot correspond to the number of sheets in the cyclic covering essential for topological quantum computation. A more natural interpretation would be as a cyclic group of symmetries for the magnetic flux quanta action as rotations permuting the flux tubes of the topologically quantized dipole type magnetic field. What remains a mystery is why $n_1 = n \ mod \ 5$, $n_2 = n - n_1 \ mod \ 5^2$, ... cannot vanish. Could the irreducible representation of $S_{n_{2)}}$ corresponding to the partition $n_{2)} = \sum_k n_k 5^k$ defined by 5-adic expansion and having $r = 2$ summands have a special role? IR could the sub-group $\prod_k S_{n_k 5^k}$ of S_n have a special role?

The interpretation in terms of decomposition to many-particle states consisting of free electron pairs or Cooper pairs

The fact that iL_0 corresponds to rotations allows to consider also the interpretation of the partitions in terms of decompositions of the state to a product of angular momentum eigen states with values of $J_z = n_k$. Basic building blocks could have spin $S_z = 1$ so that codon would be characterized by its total spin $S_z = n_2 = n \ mod \ 5^2$ possible associated with dark Cooper pairs with spin quantum number $S_z = 1$. The blocks of the partition would be coherent sub-Bose-Einstein condensates of dark Cooper pairs and the number theoretic Hamiltonian would characterize the change of energy like quantity as this kind of state is formed.

This interpretation conforms with the general TGD based view about living matter. High T_c superconductivity indeed plays a key role in TGD based model of living matter [K6, K7] and there is experimental evidence that DNA can have anomalously high conductivity [I70]. TGD based model [K7] relies on the hypothesis that free electron pairs associated with the 5- and/or 6-rings of sugars in the backbone of DNA correspond to dark matter with Planck constant $\hbar = n\hbar_0$, $n = 5$ and/or $n = 6$. Also the observation that the twist angle of single nucleotide in double helix is $\pi/5$ is suggestive of 5-adicity. Note that $n = 5$ defines the minimum value of n making possible universal topological quantum computation and in [**?**] it is proposed that DNA and/or RNA could act as topological quantum computer.

13.5.5 A Possible Interpretation For The P-Adic Prime Labeling Amino-Acid And DNAs Coding It

The notion of field body or magnetic body is central for the TGD inspired model of living matter [K15] , [L3]. This notion is justified by so called topological quantization of classical fields making it possible to assign to a given physical system a field body which is typically much larger than

the physical body. For instance, in case of brain the magnetic body is of astrophysical size (EEG wavelengths are of order Earth size). Dark magnetic body containing Bose Einstein condensates of ions with large value of Planck constant would be the fundamental bio-controller utilizing biological body as a sensory receptor and motor instrument [K15].

A possible interpretation for the p-adic prime labeling amino-acid and DNAs coding for it could be as a characterizer of the effective p-adic topology associated with their magnetic bodies and the genuine p-adic topology for their p-adic counterparts obeying same algebraic equations. This is possible since for large values of Planck constant possibly associated with the magnetic body the small p-adic primes could correspond to size scales of order EEG wave lengths. Notice however that the p-adic primes characterizing elementary particles are much larger. For instance, electron is characterized by Mersenne prime $M_{127} = 2^{127} - 1$.

The preferred values of n_a and n_b are given by $n_i = 2^k \prod F_i$, where F_i are distinct Fermat primes (only four of them corresponding to $F = 3, 5, 17, 257, 2^{16} + 1$ are known). The 2-adic hierarchy $n_a = 2^k$ could provide a deeper justification for the p-adic length scales hypothesis.

The 2-adic sub-hierarchy $n_a = 2^{k11}$, $k = 0, 1, 2...$ is especially interesting. For $n_b = 1$ $k = 11$ would correspond to the time scale $T_{121} = T(127)/64$, $T_{127}(2) = .1$ s, which defines the fundamental 10 Hz biorhythm. $T_{121} \simeq 1.6$ ms corresponds to a typical time scale for nerve pulse activity. For this option primary *resp.* secondary p-adic length scales associated with an amino-acid labeled by prime p would be $T_p = \sqrt{p}T_{121}$ *resp.* $T_p = pT_{121}$ and could define a small-p p-adic hierarchy of time scales of neuronal activity.

Obviously, the maximal cyclic subgroup of G_a containing 2^{121} elements and acting naturally as symmetries of magnetic and electric flux tube structures accompanying DNA and amino-acids cannot correspond to the group Z_n, $n \leq 124$ associated with DNA and amino-acid molecules.

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I want to thank Andrei Kozyrev and Marcus Nilsson for interesting discussions about models of genetic code, in particular the idea of divisor code.

13.6 Appendix: 4-Adic Realization Of $N \to N + 32$ Symmetry,Divisor Code, And Labeling Of Amino-Acids By Primes Are Not Mutually Consistent

For the four-adic realization of the divisor code geometrically 18 amino-acids would correspond to primes $p < 63$ whereas the integers $n = 0$ and $n = 1$ would correspond to special amino-acids. $n \to n + 32$ symmetry means that 4-columns of the code table contain either even or odd integers depending on whether the row is odd or even. Hence the 4-columns containing even integers cannot contain the prime coding for the amino-acid so that the geometric realization in which DNAs coding amino-acid contain both prime labeling for the amino-acid and the integer characterizing the degeneracy of the amino-acid as the number of its divisors is not possible.

One could weaken the condition by requiring that $n(p) = p$ holds true only when one of the coding codons is labeled by a prime. This however leads to a further difficulty since the primes $(5, 5 + 32 = 27)$ and $(11, 11 + 32 = 43)$ belong to same 4-column and should code for same amino-acid. Hence the assumption that amino-acids correspond to $n = 0, 1$ and 18 primes $p < 63$ does not look natural. One could however consider a less ambitious realization of the divisor code by giving up this requirement altogether and requiring only that one of the DNAs is labeled by an integer for which the number of divisors equals to the degeneracy of the corresponding codon.

For eukaryote code Met would naturally correspond to $n = 1$. For mitochondrial code the multiplets containg $n = 0$ and $n = 1$ DNA would contain also second DNA. The problem is that the number of its divisors should be $n = 2$ for the mitochondrial code for both Met and Ile and one end ups with a contradiction unless one somehow loosens the rules. One could say that the prime $n = 17$ determines the degeneracy of Ile for mitochondrial code so that Met takes the rest.

The multiplet coding for a particular amino-acid would contain DNA labeled by the prime coding for amino-acid and an integer with a number of divisors equal to the degeneracy of the codon. For odd rows of the code table 4-columns contain only even primes so that primes are contained in 4-columns in even rows of the table.

Table 13.5: Best variant of the code table

UCC Ser	AGC Ser	CCC Pro	CUC Leu
UCA Ser	AGA Stop	CCA Pro	CUA Leu (16)
UCU Ser 20	AGU Ser	CCU Pro	CUU Leu 0
UCG Ser (4)	AGG Stop 8	CCG Pro 12	CUG Leu
(49) AUC Ile 53	CAC His 57	GUC Val 61	UUC Leu (33)
AUA Ile (37)	CAA Gln (41)	GUA Val (45)	UUA Phe 17
AUU Ile	CAU His	GUU Val 29	UUU Leu 1
AUG Met 5	CAG Gln (9)	GUG Val 13	UUG Phe
CGC Arg	GCC Ala	ACC Thr	GGC Gly 34
GGA Arg	GCA Ala	ACA Thr	GGA Gly 18
GGU Arg	GCU Ala	ACU Thr	GGU Gly 2
GGG Arg 6	GCG Ala 10	ACG Thr 14	GGG Gly
GAC Asp	UGC Cys 59	AACAsn 63	UAC Tyr
GAA Glu 39	UGA Trp (43)	AAA Lys (47)	UAA Stop 19
GAU Asp 23	UGU Cys	AAU Asn (31)	UAU Tyr 3
GAG Glu 7	UGG Trp 11	AAG Lys (15)	UAG Stop

Table 13.5 represents the best variant found hitherto. One of the integers in 4-column is consistent with the degeneracy of amino-acid according to divisor code and for each amino-acid one of DNAs corresponds to the integers consistent with the degeneracy. For Trp in case of eukaryote code stop breaks the symmetry. 7 codes only for a singlet (Trp).

Chapter i

Appendix

Originally this appendix was meant to be a purely technical summary of basic facts but in its recent form it tries to briefly summarize those basic visions about TGD which I dare to regarded stabilized. I have added illustrations making it easier to build mental images about what is involved and represented briefly the key arguments. This chapter is hoped to help the reader to get fast grasp about the concepts of TGD.

The basic properties of imbedding space and related spaces are discussed and the relationship of CP_2 to standard model is summarized. The notions of induction of metric and spinor connection, and of spinor structure are discussed. Many-sheeted space-time and related notions such as topological field quantization and the relationship many-sheeted space-time to that of GRT space-time are discussed as well as the recent view about induced spinor fields and the emergence of fermionic strings. Various topics related to p-adic numbers are summarized with a brief definition of p-adic manifold and the idea about generalization of the number concept by gluing real and p-adic number fields to a larger book like structure. Hierarchy of Planck constants can be now understood in terms of the non-determinism of Kähler action and the recent vision about connections to other key ideas is summarized.

A-1 Imbedding Space $M^4 \times CP_2$ And Related Notions

Space-times are regarded as 4-surfaces in $H = M^4 \times CP_2$ the Cartesian product of empty Minkowski space - the space-time of special relativity - and compact 4-D space CP_2 with size scale of order 10^4 Planck lengths. One can say that imbedding space is obtained by replacing each point m of empty Minkowski space with 4-D tiny CP_2. The space-time of general relativity is replaced by a 4-D surface in H which has very complex topology. The notion of many-sheeted space-time gives an idea about what is involved.

Fig. 1. Imbedding space $H = M^4 \times CP_2$ as Cartesian product of Minkowski space M^4 and complex projective space CP_2. `http://tgdtheory.fi/appfigures/Hoo.jpg`

Denote by M^4_+ and M^4_- the future and past directed lightcones of M^4. Denote their intersection, which is not unique, by CD. In zero energy ontology (ZEO) causal diamond (CD) is defined as cartesian product $CD \times CP_2$. Often I use CD to refer just to $CD \times CP_2$ since CP_2 factor is relevant from the point of view of ZEO.

Fig. 2. Future and past light-cones M^4_+ and M^4_-. Causal diamonds (CD) are defined as their intersections. `http://tgdtheory.fi/appfigures/futurepast.jpg`

Fig. 3. Causal diamond (CD) is highly analogous to Penrose diagram but simpler. `http://tgdtheory.fi/appfigures/penrose.jpg`

A rather recent discovery was that CP_2 is the only compact 4-manifold with Euclidian signature of metric allowing twistor space with Kähler structure. M^4 is in turn is the only 4-D space with Minkowskian signature of metric allowing twistor space with Kähler structure so that $H = M^4 \times CP_2$ is twistorially unique.

One can loosely say that quantum states in a given sector of "world of classical worlds" (WCW) are superpositions of space-time surfaces inside CDs and that positive and negative energy parts of zero energy states are localized and past and future boundaries of CDs. CDs form a hierarchy. One can have CDs within CDs and CDs can also overlap. The size of CD is characterized by the proper time distance between its two tips. One can perform both translations and also Lorentz boosts of CD leaving either boundary invariant. Therefore one can assign to CDs a moduli space and speak about wave function in this moduli space.

In number theoretic approach it is natural to restrict the allowed Lorentz boosts to some discrete subgroup of Lorentz group and also the distances between the tips of CDs to multiples of CP_2 radius defined by the length of its geodesic. Therefore the moduli space of CDs discretizes. The quantization of cosmic recession velocities for which there are indications, could relate to this quantization.

A-2 Basic Facts About CP_2

CP_2 as a four-manifold is very special. The following arguments demonstrates that it codes for the symmetries of standard models via its isometries and holonomies.

A-2.1 CP_2 As A Manifold

CP_2, the complex projective space of two complex dimensions, is obtained by identifying the points of complex 3-space C^3 under the projective equivalence

$$(z^1, z^2, z^3) \equiv \lambda(z^1, z^2, z^3) \ . \tag{A-2.1}$$

Here λ is any non-zero complex number. Note that CP_2 can be also regarded as the coset space $SU(3)/U(2)$. The pair z^i/z^j for fixed j and $z^i \neq 0$ defines a complex coordinate chart for CP_2. As j runs from 1 to 3 one obtains an atlas of three coordinate charts covering CP_2, the charts being holomorphically related to each other (e.g. CP_2 is a complex manifold). The points $z^3 \neq 0$ form a subset of CP_2 homoeomorphic to R^4 and the points with $z^3 = 0$ a set homeomorphic to S^2. Therefore CP_2 is obtained by "adding the 2-sphere at infinity to R^4".

Besides the standard complex coordinates $\xi^i = z^i/z^3$, $i = 1, 2$ the coordinates of Eguchi and Freund [A21] will be used and their relation to the complex coordinates is given by

$$\begin{aligned} \xi^1 &= z + it \ , \\ \xi^2 &= x + iy \ . \end{aligned} \tag{A-2.2}$$

These are related to the "spherical coordinates" via the equations

$$\begin{aligned} \xi^1 &= rexp(i\frac{(\Psi+\Phi)}{2})cos(\frac{\Theta}{2}) \ , \\ \xi^2 &= rexp(i\frac{(\Psi-\Phi)}{2})sin(\frac{\Theta}{2}) \ . \end{aligned} \tag{A-2.3}$$

The ranges of the variables r, Θ, Φ, Ψ are $[0, \infty], [0, \pi], [0, 4\pi], [0, 2\pi]$ respectively.

Considered as a real four-manifold CP_2 is compact and simply connected, with Euler number Euler number 3, Pontryagin number 3 and second $b = 1$.

Fig. 4. CP_2 as manifold. `http://tgdtheory.fi/appfigures/cp2.jpg`

A-2.2 Metric And Kähler Structure Of CP_2

In order to obtain a natural metric for CP_2, observe that CP_2 can be thought of as a set of the orbits of the isometries $z^i \to exp(i\alpha)z^i$ on the sphere S^5: $\sum z^i \bar{z}^i = R^2$. The metric of CP_2 is obtained by projecting the metric of S^5 orthogonally to the orbits of the isometries. Therefore the distance between the points of CP_2 is that between the representative orbits on S^5.

The line element has the following form in the complex coordinates

$$ds^2 = g_{a\bar{b}} d\xi^a d\bar{\xi}^b \ , \tag{A-2.4}$$

where the Hermitian, in fact Kähler metric $g_{a\bar{b}}$ is defined by

$$g_{a\bar{b}} = R^2 \partial_a \partial_{\bar{b}} K \ , \tag{A-2.5}$$

where the function K, Kähler function, is defined as

$$\begin{aligned} K &= log(F) \ , \\ F &= 1 + r^2 \ . \end{aligned} \tag{A-2.6}$$

The Kähler function for S^2 has the same form. It gives the S^2 metric $dzd\bar{z}/(1+r^2)^2$ related to its standard form in spherical coordinates by the coordinate transformation $(r, \phi) = (tan(\theta/2), \phi)$.

The representation of the CP_2 metric is deducible from S^5 metric is obtained by putting the angle coordinate of a geodesic sphere constant in it and is given

$$\frac{ds^2}{R^2} = \frac{(dr^2 + r^2\sigma_3^2)}{F^2} + \frac{r^2(\sigma_1^2 + \sigma_2^2)}{F} \ , \tag{A-2.7}$$

where the quantities σ_i are defined as

$$\begin{aligned} r^2\sigma_1 &= Im(\xi^1 d\xi^2 - \xi^2 d\xi^1) \ , \\ r^2\sigma_2 &= -Re(\xi^1 d\xi^2 - \xi^2 d\xi^1) \ , \\ r^2\sigma_3 &= -Im(\xi^1 d\bar{\xi}^1 + \xi^2 d\bar{\xi}^2) \ . \end{aligned} \tag{A-2.8}$$

R denotes the radius of the geodesic circle of CP_2. The vierbein forms, which satisfy the defining relation

$$s_{kl} = R^2 \sum_A e_k^A e_l^A \ , \tag{A-2.9}$$

are given by

$$\begin{aligned} e^0 &= \tfrac{dr}{F} \ , \quad e^1 = \tfrac{r\sigma_1}{\sqrt{F}} \ , \\ e^2 &= \tfrac{r\sigma_2}{\sqrt{F}} \ , \quad e^3 = \tfrac{r\sigma_3}{F} \ . \end{aligned} \tag{A-2.10}$$

The explicit representations of vierbein vectors are given by

$$\begin{aligned} e^0 &= \tfrac{dr}{F} \ , & e^1 &= \tfrac{r(sin\Theta cos\Psi d\Phi + sin\Psi d\Theta)}{2\sqrt{F}} \ , \\ e^2 &= \tfrac{r(sin\Theta sin\Psi d\Phi - cos\Psi d\Theta)}{2\sqrt{F}} \ , & e^3 &= \tfrac{r(d\Psi + cos\Theta d\Phi)}{2F} \ . \end{aligned} \tag{A-2.11}$$

The explicit representation of the line element is given by the expression

$$ds^2/R^2 = \frac{dr^2}{F^2} + \frac{r^2}{4F^2}(d\Psi + cos\Theta d\Phi)^2 + \frac{r^2}{4F}(d\Theta^2 + sin^2\Theta d\Phi^2) \ . \tag{A-2.12}$$

The vierbein connection satisfying the defining relation

$$de^A = -V_B^A \wedge e^B \ , \tag{A-2.13}$$

is given by

$$\begin{array}{lllllll} V_{01} & = & -\frac{e^1}{r_2} \ , & & V_{23} & = & \frac{e^1}{r_2} \ , \\ V_{02} & = & -\frac{e^2}{r} \ , & & V_{31} & = & \frac{e^2}{r} \ , \\ V_{03} & = & (r - \frac{1}{r})e^3 \ , & & V_{12} & = & (2r + \frac{1}{r})e^3 \ . \end{array} \tag{A-2.14}$$

The representation of the covariantly constant curvature tensor is given by

$$\begin{array}{lllllll} R_{01} & = & e^0 \wedge e^1 - e^2 \wedge e^3 \ , & & R_{23} & = & e^0 \wedge e^1 - e^2 \wedge e^3 \ , \\ R_{02} & = & e^0 \wedge e^2 - e^3 \wedge e^1 \ , & & R_{31} & = & -e^0 \wedge e^2 + e^3 \wedge e^1 \ , \\ R_{03} & = & 4e^0 \wedge e^3 + 2e^1 \wedge e^2 \ , & & R_{12} & = & 2e^0 \wedge e^3 + 4e^1 \wedge e^2 \ . \end{array} \tag{A-2.15}$$

Metric defines a real, covariantly constant, and therefore closed 2-form J

$$J = -ig_{a\bar{b}} d\xi^a d\bar{\xi}^b \ , \tag{A-2.16}$$

the so called Kähler form. Kähler form J defines in CP_2 a symplectic structure because it satisfies the condition

$$J^k_{\ r} J^{rl} = -s^{kl} \ . \tag{A-2.17}$$

The form J is integer valued and by its covariant constancy satisfies free Maxwell equations. Hence it can be regarded as a curvature form of a $U(1)$ gauge potential B carrying a magnetic charge of unit $1/2g$ (g denotes the gauge coupling). Locally one has therefore

$$J = dB \ , \tag{A-2.18}$$

where B is the so called Kähler potential, which is not defined globally since J describes homological magnetic monopole.

It should be noticed that the magnetic flux of J through a 2-surface in CP_2 is proportional to its homology equivalence class, which is integer valued. The explicit representations of J and B are given by

$$\begin{aligned} B &= 2re^3 \ , \\ J &= 2(e^0 \wedge e^3 + e^1 \wedge e^2) = \frac{r}{F^2} dr \wedge (d\Psi + cos\Theta d\Phi) + \frac{r^2}{2F} sin\Theta d\Theta d\Phi \ . \end{aligned} \tag{A-2.19}$$

The vierbein curvature form and Kähler form are covariantly constant and have in the complex coordinates only components of type (1, 1).

Useful coordinates for CP_2 are the so called canonical coordinates in which Kähler potential and Kähler form have very simple expressions

$$
\begin{aligned}
B &= \sum_{k=1,2} P_k dQ_k \ , \\
J &= \sum_{k=1,2} dP_k \wedge dQ_k \ .
\end{aligned}
\tag{A-2.20}
$$

The relationship of the canonical coordinates to the "spherical" coordinates is given by the equations

$$
\begin{aligned}
P_1 &= -\frac{1}{1+r^2} \ , \\
P_2 &= \frac{r^2 cos\Theta}{2(1+r^2)} \ , \\
Q_1 &= \Psi \ , \\
Q_2 &= \Phi \ .
\end{aligned}
\tag{A-2.21}
$$

A-2.3 Spinors In CP_2

CP_2 doesn't allow spinor structure in the conventional sense [A17]. However, the coupling of the spinors to a half odd multiple of the Kähler potential leads to a respectable spinor structure. Because the delicacies associated with the spinor structure of CP_2 play a fundamental role in TGD, the arguments of Hawking are repeated here.

To see how the space can fail to have an ordinary spinor structure consider the parallel transport of the vierbein in a simply connected space M. The parallel propagation around a closed curve with a base point x leads to a rotated vierbein at x: $e^A = R^A_B e^B$ and one can associate to each closed path an element of $SO(4)$.

Consider now a one-parameter family of closed curves $\gamma(v) : v \in (0,1)$ with the same base point x and $\gamma(0)$ and $\gamma(1)$ trivial paths. Clearly these paths define a sphere S^2 in M and the element $R^A_B(v)$ defines a closed path in $SO(4)$. When the sphere S^2 is contractible to a point e.g., homologically trivial, the path in $SO(4)$ is also contractible to a point and therefore represents a trivial element of the homotopy group $\Pi_1(SO(4)) = Z_2$.

For a homologically nontrivial 2-surface S^2 the associated path in $SO(4)$ can be homotopically nontrivial and therefore corresponds to a nonclosed path in the covering group Spin(4) (leading from the matrix 1 to -1 in the matrix representation). Assume this is the case.

Assume now that the space allows spinor structure. Then one can parallel propagate also spinors and by the above construction associate a closed path of Spin(4) to the surface S^2. Now, however this path corresponds to a lift of the corresponding $SO(4)$ path and cannot be closed. Thus one ends up with a contradiction.

From the preceding argument it is clear that one could compensate the non-allowed -1-factor associated with the parallel transport of the spinor around the sphere S^2 by coupling it to a gauge potential in such a way that in the parallel transport the gauge potential introduces a compensating -1-factor. For a $U(1)$ gauge potential this factor is given by the exponential $exp(i2\Phi)$, where Φ is the magnetic flux through the surface. This factor has the value -1 provided the $U(1)$ potential carries half odd multiple of Dirac charge $1/2g$. In case of CP_2 the required gauge potential is half odd multiple of the Kähler potential B defined previously. In the case of $M^4 \times CP_2$ one can in addition couple the spinor components with different chiralities independently to an odd multiple of $B/2$.

A-2.4 Geodesic Sub-Manifolds Of CP_2

Geodesic sub-manifolds are defined as sub-manifolds having common geodesic lines with the imbedding space. As a consequence the second fundamental form of the geodesic manifold vanishes, which means that the tangent vectors h^k_α (understood as vectors of H) are covariantly constant quantities with respect to the covariant derivative taking into account that the tangent vectors are vectors both with respect to H and X^4.

In [A33] a general characterization of the geodesic sub-manifolds for an arbitrary symmetric space G/H is given. Geodesic sub-manifolds are in 1-1-correspondence with the so called Lie triple systems of the Lie-algebra g of the group G. The Lie triple system t is defined as a subspace of g characterized by the closedness property with respect to double commutation

$$[X,[Y,Z]] \in t \ \text{ for } \ X,Y,Z \in t \ . \tag{A-2.22}$$

$SU(3)$ allows, besides geodesic lines, two nonequivalent (not isometry related) geodesic spheres. This is understood by observing that $SU(3)$ allows two nonequivalent $SU(2)$ algebras corresponding to subgroups $SO(3)$ (orthogonal 3×3 matrices) and the usual isospin group $SU(2)$. By taking any subset of two generators from these algebras, one obtains a Lie triple system and by exponentiating this system, one obtains a 2-dimensional geodesic sub-manifold of CP_2.

Standard representatives for the geodesic spheres of CP_2 are given by the equations

$$S^2_I \ : \ \xi^1 = \bar{\xi}^2 \ \text{ or equivalently } \ (\Theta = \pi/2, \Psi = 0) \ ,$$

$$S^2_{II} \ : \ \xi^1 = \xi^2 \ \text{ or equivalently } \ (\Theta = \pi/2, \Phi = 0) \ .$$

The non-equivalence of these sub-manifolds is clear from the fact that isometries act as holomorphic transformations in CP_2. The vanishing of the second fundamental form is also easy to verify. The first geodesic manifold is homologically trivial: in fact, the induced Kähler form vanishes identically for S^2_I. S^2_{II} is homologically nontrivial and the flux of the Kähler form gives its homology equivalence class.

A-3 CP_2 Geometry And Standard Model Symmetries

A-3.1 Identification Of The Electro-Weak Couplings

The delicacies of the spinor structure of CP_2 make it a unique candidate for space S. First, the coupling of the spinors to the $U(1)$ gauge potential defined by the Kähler structure provides the missing $U(1)$ factor in the gauge group. Secondly, it is possible to couple different H-chiralities independently to a half odd multiple of the Kähler potential. Thus the hopes of obtaining a correct spectrum for the electromagnetic charge are considerable. In the following it will be demonstrated that the couplings of the induced spinor connection are indeed those of the GWS model [B15] and in particular that the right handed neutrinos decouple completely from the electro-weak interactions.

To begin with, recall that the space H allows to define three different chiralities for spinors. Spinors with fixed H-chirality $e = \pm 1$, CP_2-chirality l, r and M^4-chirality L, R are defined by the condition

$$\begin{aligned} \Gamma\Psi &= e\Psi \ , \\ e &= \pm 1 \ , \end{aligned} \tag{A-3.1}$$

where Γ denotes the matrix $\Gamma_9 = \gamma_5 \times \gamma_5$, $1 \times \gamma_5$ and $\gamma_5 \times 1$ respectively. Clearly, for a fixed H-chirality CP_2- and M^4-chiralities are correlated.

The spinors with H-chirality $e = \pm 1$ can be identified as quark and lepton like spinors respectively. The separate conservation of baryon and lepton numbers can be understood as a consequence of generalized chiral invariance if this identification is accepted. For the spinors with a definite H-chirality one can identify the vielbein group of CP_2 as the electro-weak group: $SO(4) = SU(2)_L \times SU(2)_R$.

The covariant derivatives are defined by the spinorial connection

$$A = V + \frac{B}{2}(n_+ 1_+ + n_- 1_-) \ . \tag{A-3.2}$$

Here V and B denote the projections of the vielbein and Kähler gauge potentials respectively and $1_{+(-)}$ projects to the spinor H-chirality $+(-)$. The integers $n_\pm$ are odd from the requirement of a respectable spinor structure.

The explicit representation of the vielbein connection V and of B are given by the equations

$$\begin{aligned} V_{01} &= -\frac{e^1}{r} \ , & V_{23} &= \frac{e^1}{r} \ , \\ V_{02} &= -\frac{e^2}{r} \ , & V_{31} &= \frac{e^2}{r} \ , \\ V_{03} &= (r-\frac{1}{r})e^3 \ , & V_{12} &= (2r+\frac{1}{r})e^3 \ , \end{aligned} \tag{A-3.3}$$

and

$$B = 2re^3 \ , \tag{A-3.4}$$

respectively. The explicit representation of the vielbein is not needed here.

Let us first show that the charged part of the spinor connection couples purely left handedly. Identifying Σ_3^0 and Σ_2^1 as the diagonal (neutral) Lie-algebra generators of $SO(4)$, one finds that the charged part of the spinor connection is given by

$$A_{ch} = 2V_{23}I_L^1 + 2V_{13}I_L^2 \ , \tag{A-3.5}$$

where one have defined

$$\begin{aligned} I_L^1 &= \frac{(\Sigma_{01}-\Sigma_{23})}{2} \ , \\ I_L^2 &= \frac{(\Sigma_{02}-\Sigma_{13})}{2} \ . \end{aligned} \tag{A-3.6}$$

A_{ch} is clearly left handed so that one can perform the identification

$$W^\pm = \frac{2(e^1 \pm ie^2)}{r} \ , \tag{A-3.7}$$

where $W^\pm$ denotes the charged intermediate vector boson.

Consider next the identification of the neutral gauge bosons γ and Z^0 as appropriate linear combinations of the two functionally independent quantities

$$\begin{aligned} X &= re^3 \ , \\ Y &= \frac{e^3}{r} \ , \end{aligned} \tag{A-3.8}$$

appearing in the neutral part of the spinor connection. We show first that the mere requirement that photon couples vectorially implies the basic coupling structure of the GWS model leaving only the value of Weinberg angle undetermined.

To begin with let us define

$$\begin{aligned} \bar{\gamma} &= aX + bY \ , \\ \bar{Z}^0 &= cX + dY \ , \end{aligned} \tag{A-3.9}$$

where the normalization condition

$$ad - bc = 1 \ ,$$

is satisfied. The physical fields γ and Z^0 are related to $\bar{\gamma}$ and $\bar{Z}^0$ by simple normalization factors.

Expressing the neutral part of the spinor connection in term of these fields one obtains

$$\begin{aligned} A_{nc} &= [(c+d)2\Sigma_{03} + (2d-c)2\Sigma_{12} + d(n_+1_+ + n_-1_-)]\bar{\gamma} \\ &+ [(a-b)2\Sigma_{03} + (a-2b)2\Sigma_{12} - b(n_+1_+ + n_-1_-)]\bar{Z}^0 \ . \end{aligned} \tag{A-3.10}$$

Identifying Σ_{12} and $\Sigma_{03} = 1 \times \gamma_5\Sigma_{12}$ as vectorial and axial Lie-algebra generators, respectively, the requirement that γ couples vectorially leads to the condition

$$c = -d \ . \tag{A-3.11}$$

Using this result plus previous equations, one obtains for the neutral part of the connection the expression

$$A_{nc} = \gamma Q_{em} + Z^0(I_L^3 - sin^2\theta_W Q_{em}) \ . \tag{A-3.12}$$

Here the electromagnetic charge Q_{em} and the weak isospin are defined by

$$\begin{aligned} Q_{em} &= \Sigma^{12} + \frac{(n_+1_+ + n_-1_-)}{6} \ , \\ I_L^3 &= \frac{(\Sigma^{12} - \Sigma^{03})}{2} \ . \end{aligned} \tag{A-3.13}$$

The fields γ and Z^0 are defined via the relations

$$\begin{aligned} \gamma &= 6d\bar{\gamma} = \frac{6}{(a+b)}(aX + bY) \ , \\ Z^0 &= 4(a+b)\bar{Z}^0 = 4(X - Y) \ . \end{aligned} \tag{A-3.14}$$

The value of the Weinberg angle is given by

$$sin^2\theta_W = \frac{3b}{2(a+b)} \ , \tag{A-3.15}$$

and is not fixed completely. Observe that right handed neutrinos decouple completely from the electro-weak interactions.

The determination of the value of Weinberg angle is a dynamical problem. The angle is completely fixed once the YM action is fixed by requiring that action contains no cross term of type γZ^0. Pure symmetry non-broken electro-weak YM action leads to a definite value for the Weinberg angle. One can however add a symmetry breaking term proportional to Kähler action and this changes the value of the Weinberg angle.

To evaluate the value of the Weinberg angle one can express the neutral part F_{nc} of the induced gauge field as

$$F_{nc} = 2R_{03}\Sigma^{03} + 2R_{12}\Sigma^{12} + J(n_+1_+ + n_-1_-) \ , \tag{A-3.16}$$

where one has

$$\begin{aligned} R_{03} &= 2(2e^0 \wedge e^3 + e^1 \wedge e^2) \ , \\ R_{12} &= 2(e^0 \wedge e^3 + 2e^1 \wedge e^2) \ , \\ J &= 2(e^0 \wedge e^3 + e^1 \wedge e^2) \ , \end{aligned} \tag{A-3.17}$$

in terms of the fields γ and Z^0 (photon and Z- boson)

$$F_{nc} = \gamma Q_{em} + Z^0(I_L^3 - sin^2\theta_W Q_{em}) \ . \tag{A-3.18}$$

Evaluating the expressions above one obtains for γ and Z^0 the expressions

$$\begin{aligned} \gamma &= 3J - sin^2\theta_W R_{03} \ , \\ Z^0 &= 2R_{03} \ . \end{aligned} \tag{A-3.19}$$

For the Kähler field one obtains

$$J = \frac{1}{3}(\gamma + sin^2\theta_W Z^0) \ . \tag{A-3.20}$$

Expressing the neutral part of the symmetry broken YM action

$$\begin{aligned} L_{ew} &= L_{sym} + fJ^{\alpha\beta}J_{\alpha\beta} \ , \\ L_{sym} &= \frac{1}{4g^2}Tr(F^{\alpha\beta}F_{\alpha\beta}) \ , \end{aligned} \tag{A-3.21}$$

where the trace is taken in spinor representation, in terms of γ and Z^0 one obtains for the coefficient X of the γZ^0 cross term (this coefficient must vanish) the expression

$$\begin{aligned} X &= -\frac{K}{2g^2} + \frac{fp}{18} \ , \\ K &= Tr\left[Q_{em}(I_L^3 - sin^2\theta_W Q_{em})\right] \ , \end{aligned} \tag{A-3.22}$$

In the general case the value of the coefficient K is given by

$$K = \sum_i \left[-\frac{(18 + 2n_i^2)sin^2\theta_W}{9}\right] \ , \tag{A-3.23}$$

where the sum is over the spinor chiralities, which appear as elementary fermions and n_i is the integer describing the coupling of the spinor field to the Kähler potential. The cross term vanishes provided the value of the Weinberg angle is given by

$$sin^2\theta_W = \frac{9\sum_i 1}{(fg^2 + 2\sum_i(18 + n_i^2))} \ . \tag{A-3.24}$$

In the scenario where both leptons and quarks are elementary fermions the value of the Weinberg angle is given by

$$sin^2\theta_W = \frac{9}{(\frac{fg^2}{2} + 28)} \ . \tag{A-3.25}$$

The bare value of the Weinberg angle is 9/28 in this scenario, which is quite close to the typical value 9/24 of GUTs [B3] .

A-3.2 Discrete Symmetries

The treatment of discrete symmetries C, P, and T is based on the following requirements:

1. Symmetries must be realized as purely geometric transformations.
2. Transformation properties of the field variables should be essentially the same as in the conventional quantum field theories [B4] .

The action of the reflection P on spinors of is given by

$$\Psi \rightarrow P\Psi = \gamma^0 \otimes \gamma^0 \Psi \ . \tag{A-3.26}$$

in the representation of the gamma matrices for which γ^0 is diagonal. It should be noticed that W and Z^0 bosons break parity symmetry as they should since their charge matrices do not commute with the matrix of P.

The guess that a complex conjugation in CP_2 is associated with T transformation of the physicist turns out to be correct. One can verify by a direct calculation that pure Dirac action is invariant under T realized according to

$$\begin{aligned} m^k &\rightarrow T(M^k) \ , \\ \xi^k &\rightarrow \bar{\xi}^k \ , \\ \Psi &\rightarrow \gamma^1\gamma^3 \otimes 1\Psi \ . \end{aligned} \tag{A-3.27}$$

The operation bearing closest resemblance to the ordinary charge conjugation corresponds geometrically to complex conjugation in CP_2:

$$\begin{aligned} \xi^k &\rightarrow \bar{\xi}^k \ , \\ \Psi &\rightarrow \Psi^\dagger \gamma^2\gamma^0 \otimes 1 \ . \end{aligned} \tag{A-3.28}$$

As one might have expected symmetries CP and T are exact symmetries of the pure Dirac action.

A-4 The Relationship Of TGD To QFT And String Models

TGD could be seen as a generalization of quantum field theory (string models) obtained by replacing pointlike particles (strings) as fundamental objects with 3-surfaces.

Fig. 5. TGD replaces point-like particles with 3-surfaces. `http://tgdtheory.fi/appfigures/particletgd.jpg`

The fact that light-like 3-surfaces are effectively metrically 2-dimensional and thus possess generalization of 2-dimensional conformal symmetries with light-like radial coordinate defining the analog of second complex coordinate suggests that this generalization could work and extend the super-conformal symmetries to their 4-D analogs.

The boundary $\delta M^4_+ = S^2 \times R_+$- of 4-D light-cone M^4_+ is also metrically 2-dimensional and allows extended conformal invariance. Also the group of isometries of light-cone boundary and of light-like 3-surfaces is infinite-dimensional since the conformal scalings of S^2 can be compensated by S^2-local scaling of the light-like radial coordinate of R_+. These simple facts mean that 4-dimensional Minkowski space and 4-dimensional space-time surfaces are in completely unique position as far as symmetries are considered.

String like objects obtained as deformations of cosmic strings $X^2 \times Y^2$, where X^2 is minimal surface in M^4 and Y^2 a holomorphic surface of CP_2 are fundamental extremals of Kähler action having string world sheet as M^4 projections. Cosmic strings dominate the primordial cosmology of TGD Universe and inflationary period corresponds to the transition to radiation dominated cosmology for which space-time sheets with 4-D M^4 projection dominate.

Also genuine string like objects emerge from TGD. The conditions that the em charge of modes of induces spinor fields is well-defined requires in the generic case the localization of

the modes at 2-D surfaces -string world sheets and possibly also partonic 2-surfaces. This in Minkowskian space-time regions.

Fig. 6. Well-definedness of em charge forces the localization of induced spinor modes to 2-D surfaces in generic situtation in Minkowskian regions of space-time surface. `http://tgdtheory.fi/appfigures/fermistring.jpg`

TGD based view about elementary particles has two aspects.

1. The space-time correlates of elementary particles are identified as pairs of wormhole contacts with Euclidian signature of metric and having 4-D CP_2 projection. Their throats behave effectively as Kähler magnetic monopoles so that wormhole throats must be connected by Kähler magnetic flux tubes with monopole flux so that closed flux tubes are obtained.

2. Fermion number is carried by the modes of the induced spinor field. In Minkowskian space-time regions the modes are localized at string world sheets connecting the wormhole contacts.

Fig. 7. TGD view about elementary particles. a) Particle corresponds 4-D generalization of world line or b) with its light-like 3-D boundary (holography). c) Particle world lines have Euclidian signature of the induced metric. d) They can be identified as wormhole contacts. e) The throats of wormhole contacts carry effective Kähler magnetic charges so that wormhole contacts must appear as pairs in order to obtain closed flux tubes. f) Wormhole contacts are accompnied by fermionic strings connecting the throats at same sheet: the strings do not extend inside the wormhole contacts. `http://tgdtheory.fi/appfigures/elparticletgd.jpg`

Particle interactions involve both stringy and QFT aspects.

1. The boundaries of string world sheets correspond to fundamental fermions. This gives rise to massless propagator lines in generalized Feynman diagrammatics. One can speak of "long" string connecting wormhole contacts and having hadronic string as physical counterpart. Long strings should be distinguished from wormhole contacts which due to their superconformal invariance behave like "short" strings with length scale given by CP_2 size, which is 10^4 times longer than Planck scale characterizing strings in string models.

2. Wormhole contact defines basic stringy interaction vertex for fermion-fermion scattering. The propagator is essentially the inverse of the superconformal scaling generator L_0. Wormhole contacts containing fermion and antifermion at its opposite throats beheave like virtual bosons so that one has BFF type vertices typically.

3. In topological sense one has 3-vertices serving as generalizations of 3-vertices of Feynman diagrams. In these vertices 4-D "lines" of generalized Feynman diagrams meet along their 3-D ends. One obtains also the analogs of stringy diagrams but stringy vertices do not have the usual interpretation in terms of particle decays but in terms of propagation of particle along two different routes.

Fig. 8. a) TGD analogs of Feynman and string diagrammatics at the level of space-time topology. b) The 4-D analogs of both string diagrams and QFT diagrams appear but the interpretation of the analogs stringy diagrams is different. `http://tgdtheory.fi/appfigures/tgdgraphs.jpg`

A-5 Induction Procedure And Many-Sheeted Space-Time

Since the classical gauge fields are closely related in TGD framework, it is not possible to have space-time sheets carrying only single kind of gauge field. For instance, em fields are accompanied by Z^0 fields for extremals of Kähler action.

Classical em fields are always accompanied by Z^0 field and some components of color gauge field. For extremals having homologically non-trivial sphere as a CP_2 projection em and Z^0 fields are the only non-vanishing electroweak gauge fields. For homologically trivial sphere only W fields are non-vanishing. Color rotations does not affect the situation.

For vacuum extremals all electro-weak gauge fields are in general non-vanishing although the net gauge field has U(1) holonomy by 2-dimensionality of the CP_2 projection. Color gauge

field has $U(1)$ holonomy for all space-time surfaces and quantum classical correspondence suggest a weak form of color confinement meaning that physical states correspond to color neutral members of color multiplets.

Induction procedure for gauge fields and spinor connection

Induction procedure for gauge potentials and spinor structure is a standard procedure of bundle theory. If one has imbedding of some manifold to the base space of a bundle, the bundle structure can be induced so that it has as a base space the imbedded manifold, whose points have as fiber the fiber if imbedding space at their image points. In the recent case the imbedding of space-time surface to imbedding space defines the induction procedure. The induced gauge potentials and gauge fields are projections of the spinor connection of the imbedding space to the space-time surface (see **Fig. ??**).

Induction procedure makes sense also for the spinor fields of imbedding space and one obtains geometrization of both electroweak gauge potentials and of spinors. The new element is induction of gamma matrices which gives their projections at space-time surface.

As a matter fact, the induced gamma matrices cannot appear in the counterpart of massless Dirac equation. To achieve super-symmetry, Dirac action must be replaced with Kähler-Dirac action for which gamma matrices are contractions of the canonical momentum currents of Kähler action with imbedding space gamma matrices. Induced gamma matrices in Dirac action would correspond to 4-volume as action.

Fig. 9. Induction of spinor connection and metric as projection to the space-time surface. `http://tgdtheory.fi/appfigures/induct.jpg`

Induced gauge fields for space-times for which CP_2 projection is a geodesic sphere

If one requires that space-time surface is an extremal of Kähler action and has a 2-dimensional CP_2 projection, only vacuum extremals and space-time surfaces for which CP_2 projection is a geodesic sphere, are allowed. Homologically non-trivial geodesic sphere correspond to vanishing W fields and homologically non-trivial sphere to non-vanishing W fields but vanishing γ and Z^0. This can be verified by explicit examples.

$r = \infty$ surface gives rise to a homologically non-trivial geodesic sphere for which e_0 and e_3 vanish imply the vanishing of W field. For space-time sheets for which CP_2 projection is $r = \infty$ homologically non-trivial geodesic sphere of CP_2 one has

$$\gamma = (\frac{3}{4} - \frac{sin^2(\theta_W)}{2})Z^0 \simeq \frac{5Z^0}{8} \quad .$$

The induced W fields vanish in this case and they vanish also for all geodesic sphere obtained by $SU(3)$ rotation.

$Im(\xi^1) = Im(\xi^2) = 0$ corresponds to homologically trivial geodesic sphere. A more general representative is obtained by using for the phase angles of standard complex CP_2 coordinates constant values. In this case e^1 and e^3 vanish so that the induced em, Z^0, and Kähler fields vanish but induced W fields are non-vanishing. This holds also for surfaces obtained by color rotation. Hence one can say that for non-vacuum extremals with 2-D CP_2 projection color rotations and weak symmetries commute.

A-5.1 Many-Sheeted Space-Time

TGD space-time is many-sheeted: in other words, there are in general several space-sheets which have projection to the same M^4 region. Second manner to say this is that CP_2 coordinates are many-valued functions of M^4 coordinates. The original physical interpretation of many-sheeted space-time time was not correct: it was assumed that single sheet corresponds to GRT space-time and this obviously leads to difficulties since the induced gauge fields are expressible in terms of only four imbedding space coordinates.

Fig. 10. Illustration of many-sheeted space-time of TGD. `http://tgdtheory.fi/appfigures/manysheeted.jpg`

Superposition of effects instead of superposition of fields

The first objection against TGD is that superposition is not possible for induced gauge fields and induced metric. The resolution of the problem is that it is effects which need to superpose, not the fields.

Test particle topologically condenses simultaneously to all space-time sheets having a projection to same region of M^4 (that is touches them). The superposition of effects of fields at various space-time sheets replaces the superposition of fields.This is crucial for the understanding also how GRT space-time relates to TGD space-time, which is also in the appendix of this book).

Wormhole contacts

Wormhole contacts are key element of many-sheeted space-time. One does not expect them to be stable unless there is non-trivial Kähler magnetic flux flowing through then so that the throats look like Kähler magnetic monopoles.

Fig. 11. Wormhole contact. `http://tgdtheory.fi/appfigures/wormholecontact.jpg`

Since the flow lines of Kähler magnetic field must be closed this requires the presence of another wormhole contact so that one obtains closed monopole flux tube decomposing to two Minkowskian pieces at the two space-time sheets involved and two wormhole contacts with Euclidian signature of the induced metric. These objects are identified as space-time correlates of elementary particles and are clearly analogous to string like objects.

The relationship between the many-sheeted space-time of TGD and of GRT space-time

The space-time of general relativity is single-sheeted and there is no need to regard it as surface in H although the assumption about representability as vacuum extremal gives very powerful constraints in cosmology and astrophysics and might make sense in simple situations.

The space-time of GRT can be regarded as a long length scale approximation obtained by lumping together the sheets of the many-sheeted space-time to a region of M^4 and providing it with an effective metric obtained as sum of M^4 metric and deviations of the induced metrics of various space-time sheets from M^4 metric. Also induced gauge potentials sum up in the similar manner so that also the gauge fields of gauge theories would not be fundamental fields.

Fig. 12. The superposition of fields is replaced with the superposition of their effects in many-sheeted space-time. `http://tgdtheory.fi/appfigures/fieldsuperpose.jpg`

Space-time surfaces of TGD are considerably simpler objects that the space-times of general relativity and relate to GRT space-time like elementary particles to systems of condensed matter physics. Same can be said about fields since all fields are expressible in terms of imbedding space coordinates and their gradients, and general coordinate invariance means that the number of bosonic field degrees is reduced locally to 4. TGD space-time can be said to be a microscopic description whereas GRT space-time a macroscopic description. In TGD complexity of space-time topology replaces the complexity due to large number of fields in quantum field theory.

Topological field quantization and the notion of magnetic body

Topological field quantization also TGD from Maxwell's theory. TGD predicts topological light rays ("massless extremals (MEs)") as space-time sheets carrying waves or arbitrary shape propagating with maximal signal velocity in single direction only and analogous to laser beams and carrying light-like gauge currents in the generi case. There are also magnetic flux quanta and electric flux quanta. The deformations of cosmic strings with 2-D string orbit as M^4 projection gives rise to magnetic flux tubes carrying monopole flux made possible by CP_2 topology allowing homological Kähler magnetic monopoles.

Fig. 13. Topological quantization for magnetic fields replaces magnetic fields with bundles of them defining flux tubes as topological field quanta. `http://tgdtheory.fi/appfigures/field.jpg`

The imbeddability condition for say magnetic field means that the region containing constant magnetic field splits into flux quanta, say tubes and sheets carrying constant magnetic field. Unless one assumes a separate boundary term in Kähler action, boundaries in the usual sense are forbidden except as ends of space-time surfaces at the boundaries of causal diamonds. One obtains typically

pairs of sheets glued together along their boundaries giving rise to flux tubes with closed cross section possibly carrying monopole flux.

These kind of flux tubes might make possible magnetic fields in cosmic scales already during primordial period of cosmology since no currents are needed to generate these magnetic fields: cosmic string would be indeed this kind of objects and would dominated during the primordial period. Even superconductors and maybe even ferromagnets could involve this kind of monopole flux tubes.

A-5.2 Imbedding Space Spinors And Induced Spinors

One can geometrize also fermionic degrees of freedom by inducing the spinor structure of $M^4 \times CP_2$.

CP_2 does not allow spinor structure in the ordinary sense but one can couple the opposite H-chiralities of H-spinors to an $n = 1$ ($n = 3$) integer multiple of Kähler gauge potential to obtain a respectable modified spinor structure. The em charges of resulting spinors are fractional (integer valued) and the interpretation as quarks (leptons) makes sense since the couplings to the induced spinor connection having interpretation in terms electro-weak gauge potential are identical to those assumed in standard model.

The notion of quark color differs from that of standard model.

1. Spinors do not couple to color gauge potential although the identification of color gauge potential as projection of $SU(3)$ Killing vector fields is possible. This coupling must emerge only at the effective gauge theory limit of TGD.

2. Spinor harmonics of imbedding space correspond to triality $t = 1$ ($t = 0$) partial waves. The detailed correspondence between color and electroweak quantum numbers is however not correct as such and the interpretation of spinor harmonics of imbedding space is as representations for ground states of super-conformal representations. The wormhole pairs associated with physical quarks and leptons must carry also neutrino pair to neutralize weak quantum numbers above the length scale of flux tube (weak scale or Compton length). The total color quantum numbers or these states must be those of standard model. For instance, the color quantum numbers of fundamental left-hand neutrino and lepton can compensate each other for the physical lepton. For fundamental quark-lepton pair they could sum up to those of physical quark.

The well-definedness of em charge is crucial condition.

1. Although the imbedding space spinor connection carries W gauge potentials one can say that the imbedding space spinor modes have well-defined em charge. One expects that this is true for induced spinor fields inside wormhole contacts with 4-D CP_2 projection and Euclidian signature of the induced metric.

2. The situation is not the same for the modes of induced spinor fields inside Minkowskian region and one must require that the CP_2 projection of the regions carrying induced spinor field is such that the induced W fields and above weak scale also the induced Z^0 fields vanish in order to avoid large parity breaking effects. This condition forces the CP_2 projection to be 2-dimensional. For a generic Minkowskian space-time region this is achieved only if the spinor modes are localized at 2-D surfaces of space-time surface - string world sheets and possibly also partonic 2-surfaces.

3. Also the Kähler-Dirac gamma matrices appearing in the modified Dirac equation must vanish in the directions normal to the 2-D surface in order that Kähler-Dirac equation can be satisfied. This does not seem plausible for space-time regions with 4-D CP_2 projection.

4. One can thus say that strings emerge from TGD in Minkowskian space-time regions. In particular, elementary particles are accompanied by a pair of fermionic strings at the opposite space-time sheets and connecting wormhole contacts. Quite generally, fundamental fermions would propagate at the boundaries of string world sheets as massless particles and wormhole contacts would define the stringy vertices of generalized Feynman diagrams. One obtains geometrized diagrammatics, which brings looks like a combination of stringy and Feynman diagrammatics.

5. This is what happens in the the generic situation. Cosmic strings could serve as examples about surfaces with 2-D CP_2 projection and carrying only em fields and allowing delocalization of spinor modes to the entire space-time surfaces.

A-5.3 Space-Time Surfaces With Vanishing Em, Z^0, Or Kähler Fields

In the following the induced gauge fields are studied for general space-time surface without assuming the extremal property. In fact, extremal property reduces the study to the study of vacuum extremals and surfaces having geodesic sphere as a CP_2 projection and in this sense the following arguments are somewhat obsolete in their generality.

Space-times with vanishing em, Z^0, or Kähler fields

The following considerations apply to a more general situation in which the homologically trivial geodesic sphere and extremal property are not assumed. It must be emphasized that this case is possible in TGD framework only for a vanishing Kähler field.

Using spherical coordinates (r, Θ, Ψ, Φ) for CP_2, the expression of Kähler form reads as

$$\begin{aligned} J &= \frac{r}{F^2} dr \wedge (d\Psi + cos(\Theta) d\Phi) + \frac{r^2}{2F} sin(\Theta) d\Theta \wedge d\Phi \ , \\ F &= 1 + r^2 \ . \end{aligned} \tag{A-5.1}$$

The general expression of electromagnetic field reads as

$$\begin{aligned} F_{em} &= (3+2p)\frac{r}{F^2} dr \wedge (d\Psi + cos(\Theta) d\Phi) + (3+p)\frac{r^2}{2F} sin(\Theta) d\Theta \wedge d\Phi \ , \\ p &= sin^2(\Theta_W) \ , \end{aligned} \tag{A-5.2}$$

where Θ_W denotes Weinberg angle.

1. The vanishing of the electromagnetic fields is guaranteed, when the conditions

$$\begin{aligned} \Psi &= k\Phi \ , \\ (3+2p)\frac{1}{r^2 F}(d(r^2)/d\Theta)(k + cos(\Theta)) &+ (3+p) sin(\Theta) = 0 \ , \end{aligned} \tag{A-5.3}$$

hold true. The conditions imply that CP_2 projection of the electromagnetically neutral space-time is 2-dimensional. Solving the differential equation one obtains

$$\begin{aligned} r &= \sqrt{\frac{X}{1-X}} \ , \\ X &= D \left[|\frac{(k+u}{C}| \right]^{\epsilon} \ , \\ u &\equiv cos(\Theta) \ , \ C = k + cos(\Theta_0) \ , \ D = \frac{r_0^2}{1+r_0^2} \ , \ \epsilon = \frac{3+p}{3+2p} \ , \end{aligned} \tag{A-5.4}$$

where C and D are integration constants. $0 \leq X \leq 1$ is required by the reality of r. $r = 0$ would correspond to $X = 0$ giving $u = -k$ achieved only for $|k| \leq 1$ and $r = \infty$ to $X = 1$ giving $|u + k| = [(1 + r_0^2)/r_0^2)]^{(3+2p)/(3+p)}$ achieved only for

$$sign(u+k) \times [\frac{1+r_0^2}{r_0^2}]^{\frac{3+2p}{3+p}} \leq k + 1 \ ,$$

where $sign(x)$ denotes the sign of x.

The expressions for Kähler form and Z^0 field are given by

$$\begin{aligned} J &= -\frac{p}{3+2p} X du \wedge d\Phi \ , \\ Z^0 &= -\frac{6}{p} J \ . \end{aligned} \tag{A-5.5}$$

The components of the electromagnetic field generated by varying vacuum parameters are proportional to the components of the Kähler field: in particular, the magnetic field is parallel to the Kähler magnetic field. The generation of a long range Z^0 vacuum field is a purely TGD based feature not encountered in the standard gauge theories.

2. The vanishing of Z^0 fields is achieved by the replacement of the parameter ϵ with $\epsilon = 1/2$ as becomes clear by considering the condition stating that Z^0 field vanishes identically. Also the relationship $F_{em} = 3J = -\frac{3}{4}\frac{r^2}{F} du \wedge d\Phi$ is useful.

3. The vanishing Kähler field corresponds to $\epsilon = 1, p = 0$ in the formula for em neutral space-times. In this case classical em and Z^0 fields are proportional to each other:

$$\begin{aligned} Z^0 &= 2e^0 \wedge e^3 = \frac{r}{F^2}(k+u)\frac{\partial r}{\partial u} du \wedge d\Phi = (k+u) du \wedge d\Phi \ , \\ r &= \sqrt{\frac{X}{1-X}} \ , \ X = D|k+u| \ , \\ \gamma &= -\frac{p}{2} Z^0 \ . \end{aligned} \tag{A-5.6}$$

For a vanishing value of Weinberg angle ($p = 0$) em field vanishes and only Z^0 field remains as a long range gauge field. Vacuum extremals for which long range Z^0 field vanishes but em field is non-vanishing are not possible.

The effective form of CP_2 metric for surfaces with 2-dimensional CP_2 projection

The effective form of the CP_2 metric for a space-time having vanishing em,Z^0, or Kähler field is of practical value in the case of vacuum extremals and is given by

$$\begin{aligned} ds^2_{eff} &= (s_{rr}(\frac{dr}{d\Theta})^2 + s_{\Theta\Theta}) d\Theta^2 + (s_{\Phi\Phi} + 2k s_{\Phi\Psi}) d\Phi^2 = \frac{R^2}{4}[s^{eff}_{\Theta\Theta} d\Theta^2 + s^{eff}_{\Phi\Phi} d\Phi^2] \ , \\ s^{eff}_{\Theta\Theta} &= X \times \left[\frac{\epsilon^2(1-u^2)}{(k+u)^2} \times \frac{1}{1-X} + 1 - X \right] \ , \\ s^{eff}_{\Phi\Phi} &= X \times \left[(1-X)(k+u)^2 + 1 - u^2 \right] \ , \end{aligned} \tag{A-5.7}$$

and is useful in the construction of vacuum imbedding of, say Schwartchild metric.

Topological quantum numbers

Space-times for which either em, Z^0, or Kähler field vanishes decompose into regions characterized by six vacuum parameters: two of these quantum numbers (ω_1 and ω_2) are frequency type parameters, two (k_1 and k_2) are wave vector like quantum numbers, two of the quantum numbers (n_1 and n_2) are integers. The parameters ω_i and n_i will be referred as electric and magnetic quantum numbers. The existence of these quantum numbers is not a feature of these solutions alone but represents a much more general phenomenon differentiating in a clear cut manner between TGD and Maxwell's electrodynamics.

The simplest manner to avoid surface Kähler charges and discontinuities or infinities in the derivatives of CP_2 coordinates on the common boundary of two neighboring regions with different vacuum quantum numbers is topological field quantization, 3-space decomposes into disjoint topological field quanta, 3-surfaces having outer boundaries with possibly macroscopic size.

Under rather general conditions the coordinates Ψ and Φ can be written in the form

$$\begin{aligned} \Psi &= \omega_2 m^0 + k_2 m^3 + n_2\phi + \text{Fourier expansion} \ , \\ \Phi &= \omega_1 m^0 + k_1 m^3 + n_1\phi + \text{Fourier expansion} \ . \end{aligned} \tag{A-5.8}$$

m^0,m^3 and ϕ denote the coordinate variables of the cylindrical M^4 coordinates) so that one has $k = \omega_2/\omega_1 = n_2/n_1 = k_2/k_1$. The regions of the space-time surface with given values of the vacuum parameters ω_i,k_i and n_i and m and C are bounded by the surfaces at which space-time surface becomes ill-defined, say by $r > 0$ or $r < \infty$ surfaces.

The space-time surface decomposes into regions characterized by different values of the vacuum parameters r_0 and Θ_0. At $r = \infty$ surfaces n_2,ω_2 and m can change since all values of Ψ correspond to the same point of CP_2: at $r = 0$ surfaces also n_1 and ω_1 can change since all values of Φ correspond to same point of CP_2, too. If $r = 0$ or $r = \infty$ is not in the allowed range space-time surface develops a boundary.

This implies what might be called topological quantization since in general it is not possible to find a smooth global imbedding for, say a constant magnetic field. Although global imbedding exists it decomposes into regions with different values of the vacuum parameters and the coordinate u in general possesses discontinuous derivative at $r = 0$ and $r = \infty$ surfaces. A possible manner to avoid edges of space-time is to allow field quantization so that 3-space (and field) decomposes into disjoint quanta, which can be regarded as structurally stable units a 3-space (and of the gauge field). This doesn't exclude partial join along boundaries for neighboring field quanta provided some additional conditions guaranteeing the absence of edges are satisfied.

For instance, the vanishing of the electromagnetic fields implies that the condition

$$\Omega \equiv \frac{\omega_2}{n_2} - \frac{\omega_1}{n_1} = 0 \ , \tag{A-5.9}$$

is satisfied. In particular, the ratio ω_2/ω_1 is rational number for the electromagnetically neutral regions of space-time surface. The change of the parameter n_1 and n_2 (ω_1 and ω_2) in general generates magnetic field and therefore these integers will be referred to as magnetic (electric) quantum numbers.

A-6 P-Adic Numbers And TGD

A-6.1 P-Adic Number Fields

p-Adic numbers (p is prime: 2, 3, 5, ...) can be regarded as a completion of the rational numbers using a norm, which is different from the ordinary norm of real numbers [A16]. p-Adic numbers are representable as power expansion of the prime number p of form

$$x = \sum_{k \geq k_0} x(k) p^k, \ x(k) = 0, ..., p-1 \ . \tag{A-6.1}$$

The norm of a p-adic number is given by

$$|x| = p^{-k_0(x)} \ . \tag{A-6.2}$$

Here $k_0(x)$ is the lowest power in the expansion of the p-adic number. The norm differs drastically from the norm of the ordinary real numbers since it depends on the lowest pinary digit of the p-adic number only. Arbitrarily high powers in the expansion are possible since the norm of the

p-adic number is finite also for numbers, which are infinite with respect to the ordinary norm. A convenient representation for p-adic numbers is in the form

$$x = p^{k_0}\varepsilon(x) \ , \tag{A-6.3}$$

where $\varepsilon(x) = k + ...$ with $0 < k < p$, is p-adic number with unit norm and analogous to the phase factor $exp(i\phi)$ of a complex number.

The distance function $d(x,y) = |x-y|_p$ defined by the p-adic norm possesses a very general property called ultra-metricity:

$$d(x,z) \leq max\{d(x,y), d(y,z)\} \ . \tag{A-6.4}$$

The properties of the distance function make it possible to decompose R_p into a union of disjoint sets using the criterion that x and y belong to same class if the distance between x and y satisfies the condition

$$d(x,y) \leq D \ . \tag{A-6.5}$$

This division of the metric space into classes has following properties:

1. Distances between the members of two different classes X and Y do not depend on the choice of points x and y inside classes. One can therefore speak about distance function between classes.

2. Distances of points x and y inside single class are smaller than distances between different classes.

3. Classes form a hierarchical tree.

Notice that the concept of the ultra-metricity emerged in physics from the models for spin glasses and is believed to have also applications in biology [B14]. The emergence of p-adic topology as the topology of the effective space-time would make ultra-metricity property basic feature of physics.

A-6.2 Canonical Correspondence Between P-Adic And Real Numbers

The basic challenge encountered by p-adic physicist is how to map the predictions of the p-adic physics to real numbers. p-Adic probabilities provide a basic example in this respect. Identification via common rationals and canonical identification and its variants have turned out to play a key role in this respect.

Basic form of canonical identification

There exists a natural continuous map $I : R_p \to R_+$ from p-adic numbers to non-negative real numbers given by the "pinary" expansion of the real number for $x \in R$ and $y \in R_p$ this correspondence reads

$$\begin{aligned} y &= \sum_{k>N} y_k p^k \to x = \sum_{k<N} y_k p^{-k} \ , \\ y_k &\in \{0,1,..,p-1\} \ . \end{aligned} \tag{A-6.6}$$

This map is continuous as one easily finds out. There is however a little difficulty associated with the definition of the inverse map since the pinary expansion like also decimal expansion is not unique ($1 = 0.999...$) for the real numbers x, which allow pinary expansion with finite number of pinary digits

$$
\begin{aligned}
x &= \sum_{k=N_0}^{N} x_k p^{-k} \ , \\
x &= \sum_{k=N_0}^{N-1} x_k p^{-k} + (x_N - 1)p^{-N} + (p-1)p^{-N-1} \sum_{k=0,..} p^{-k} \ .
\end{aligned}
\tag{A-6.7}
$$

The p-adic images associated with these expansions are different

$$
\begin{aligned}
y_1 &= \sum_{k=N_0}^{N} x_k p^{k} \ , \\
y_2 &= \sum_{k=N_0}^{N-1} x_k p^{k} + (x_N - 1)p^{N} + (p-1)p^{N+1} \sum_{k=0,..} p^{k} \\
&= y_1 + (x_N - 1)p^N - p^{N+1} \ ,
\end{aligned}
\tag{A-6.8}
$$

so that the inverse map is either two-valued for p-adic numbers having expansion with finite pinary digits or single valued and discontinuous and non-surjective if one makes pinary expansion unique by choosing the one with finite pinary digits. The finite pinary digit expansion is a natural choice since in the numerical work one always must use a pinary cutoff on the real axis.

The topology induced by canonical identification

The topology induced by the canonical identification in the set of positive real numbers differs from the ordinary topology. The difference is easily understood by interpreting the p-adic norm as a norm in the set of the real numbers. The norm is constant in each interval $[p^k, p^{k+1})$ (see **Fig. A-6.2**) and is equal to the usual real norm at the points $x = p^k$: the usual linear norm is replaced with a piecewise constant norm. This means that p-adic topology is coarser than the usual real topology and the higher the value of p is, the coarser the resulting topology is above a given length scale. This hierarchical ordering of the p-adic topologies will be a central feature as far as the proposed applications of the p-adic numbers are considered.

Ordinary continuity implies p-adic continuity since the norm induced from the p-adic topology is rougher than the ordinary norm. p-Adic continuity implies ordinary continuity from right as is clear already from the properties of the p-adic norm (the graph of the norm is indeed continuous from right). This feature is one clear signature of the p-adic topology.

Fig. 14. The real norm induced by canonical identification from 2-adic norm. `http://tgdtheory.fi/appfigures/norm.png`

The linear structure of the p-adic numbers induces a corresponding structure in the set of the non-negative real numbers and p-adic linearity in general differs from the ordinary concept of linearity. For example, p-adic sum is equal to real sum only provided the summands have no common pinary digits. Furthermore, the condition $x +_p y < max\{x, y\}$ holds in general for the p-adic sum of the real numbers. p-Adic multiplication is equivalent with the ordinary multiplication only provided that either of the members of the product is power of p. Moreover one has $x \times_p y < x \times y$ in general. The p-Adic negative -1_p associated with p-adic unit 1 is given by $(-1)_p = \sum_k (p-1)p^k$ and defines p-adic negative for each real number x. An interesting possibility is that p-adic linearity might replace the ordinary linearity in some strongly nonlinear systems so these systems would look simple in the p-adic topology.

These results suggest that canonical identification is involved with some deeper mathematical structure. The following inequalities hold true:

$$
\begin{aligned}
(x+y)_R &\leq x_R + y_R \ , \\
|x|_p |y|_R \leq (xy)_R &\leq x_R y_R \ ,
\end{aligned}
\tag{A-6.9}
$$

where $|x|_p$ denotes p-adic norm. These inequalities can be generalized to the case of $(R_p)^n$ (a linear vector space over the p-adic numbers).

$$\begin{aligned} (x+y)_R &\leq x_R + y_R \ , \\ |\lambda|_p |y|_R \leq (\lambda y)_R &\leq \lambda_R y_R \ , \end{aligned} \tag{A-6.10}$$

where the norm of the vector $x \in T_p^n$ is defined in some manner. The case of Euclidian space suggests the definition

$$(x_R)^2 = (\sum_n x_n^2)_R \ . \tag{A-6.11}$$

These inequalities resemble those satisfied by the vector norm. The only difference is the failure of linearity in the sense that the norm of a scaled vector is not obtained by scaling the norm of the original vector. Ordinary situation prevails only if the scaling corresponds to a power of p.

These observations suggests that the concept of a normed space or Banach space might have a generalization and physically the generalization might apply to the description of some non-linear systems. The nonlinearity would be concentrated in the nonlinear behavior of the norm under scaling.

Modified form of the canonical identification

The original form of the canonical identification is continuous but does not respect symmetries even approximately. This led to a search of variants which would do better in this respect. The modification of the canonical identification applying to rationals only and given by

$$I_Q(q = p^k \times \frac{r}{s}) = p^k \times \frac{I(r)}{I(s)} \tag{A-6.12}$$

is uniquely defined for rationals, maps rationals to rationals, has also a symmetry under exchange of target and domain. This map reduces to a direct identification of rationals for $0 \leq r < p$ and $0 \leq s < p$. It has turned out that it is this map which most naturally appears in the applications. The map is obviously continuous locally since p-adically small modifications of r and s mean small modifications of the real counterparts.

Canonical identification is in a key role in the successful predictions of the elementary particle masses. The predictions for the light elementary particle masses are within extreme accuracy same for I and I_Q but I_Q is theoretically preferred since the real probabilities obtained from p-adic ones by I_Q sum up to one in p-adic thermodynamics.

Generalization of number concept and notion of imbedding space

TGD forces an extension of number concept: roughly a fusion of reals and various p-adic number fields along common rationals is in question. This induces a similar fusion of real and p-adic imbedding spaces. Since finite p-adic numbers correspond always to non-negative reals n-dimensional space R^n must be covered by 2^n copies of the p-adic variant R_p^n of R^n each of which projects to a copy of R_+^n (four quadrants in the case of plane). The common points of p-adic and real imbedding spaces are rational points and most p-adic points are at real infinity.

Real numbers and various algebraic extensions of p-adic number fields are thus glued together along common rationals and also numbers in algebraic extension of rationals whose number belong to the algebraic extension of p-adic numbers. This gives rise to a book like structure with rationals and various algebraic extensions of rationals taking the role of the back of the book. Note that Neper number is exceptional in the sense that it is algebraic number in p-adic number field Q_p satisfying $e^p \ mod \ p = 1$.

Fig. 15. Various number fields combine to form a book like structure. `http://tgdtheory.fi/appfigures/book.jpg`

For a given p-adic space-time sheet most points are literally infinite as real points and the projection to the real imbedding space consists of a discrete set of rational points: the interpretation in terms of the unavoidable discreteness of the physical representations of cognition is natural. Purely local p-adic physics implies real p-adic fractality and thus long range correlations for the real space-time surfaces having enough common points with this projection.

p-Adic fractality means that M^4 projections for the rational points of space-time surface X^4 are related by a direct identification whereas CP_2 coordinates of X^4 at these points are related by I, I_Q or some of its variants implying long range correlates for CP_2 coordinates. Since only a discrete set of points are related in this manner, both real and p-adic field equations can be satisfied and there are no problems with symmetries. p-Adic effective topology is expected to be a good approximation only within some length scale range which means infrared and UV cutoffs. Also multi-p-fractality is possible.

A-6.3 The Notion Of P-Adic Manifold

The notion of p-adic manifold is needed in order to fuse real physics and various p-adic physics to a larger structure which suggests that real and p-adic number fields should be glued together along common rationals bringing in mind adeles. The notion is problematic because p-adic topology is totally disconnected implying that p-adic balls are either disjoint or nested so that ordinary definition of manifold using p-adic chart maps fails. A cure is suggested to be based on chart maps from p-adics to reals rather than to p-adics (see the appendix of the book)

The chart maps are interpreted as cognitive maps, "thought bubbles".

Fig. 16. The basic idea between p-adic manifold. `http://tgdtheory.fi/appfigures/padmanifold.jpg`

There are some problems.

1. Canonical identification does not respect symmetries since it does not commute with second pinary cutoff so that only a discrete set of rational points is mapped to their real counterparts by chart map arithmetic operations which requires pinary cutoff below which chart map takes rationals to rationals so that commutativity with arithmetics and symmetries is achieved in finite resolution: above the cutoff canonical identification is used

2. Canonical identification is continuous but does not map smooth p-adic surfaces to smooth real surfaces requiring second pinary cutoff so that only a discrete set of rational points is mapped to their real counterparts by chart map requiring completion of the image to smooth preferred extremal of Kähler action so that chart map is not unique in accordance with finite measurement resolution

3. Canonical identification vreaks general coordinate invariance of chart map: (cognition-induced symmetry breaking) minimized if p-adic manifold structure is induced from that for p-adic imbedding space with chart maps to real imbedding space and assuming preferred coordinates made possible by isometries of imbedding space: one however obtains several inequivalent p-adic manifold structures depending on the choice of coordinates: these cognitive representations are not equivalent.

A-7 Hierarchy Of Planck Constants And Dark Matter Hierarchy

Hierarchy of Planck constants was motivated by the "impossible" quantal effects of ELF em fields on vertebrate cyclotron energies $E = hf = \hbar \times eB/m$ are above thermal energy is possible only if $\hbar$ has value much larger than its standard value. Also Nottale's finding that planetary orbits migh be understood as Bohr orbits for a gigantic gravitational Planck constant.

Hierachy of Planck constant would mean that the values of Planck constant come as integer multiples of ordinary Planck constant: $h_{eff} = n \times h$. The particles at magnetic flux tubes characterized by h_{eff} would correspond to dark matter which would be invisible in the sense that only particle with same value of h_{eff} appear in the same vertex of Feynman diagram.

Hierarchy of Planck constants would be due to the non-determism of the Kähler action predicting huge vacuum degeneracy allowing all space-time surfaces which are sub-manfolds of any $M^4 \times Y^2$, where Y^2 is Lagrangian sub-manifold of CP_2. For agiven Y^2 one obtains new manifolds Y^2 by applying symplectic transformations of CP_2.

Non-determinism would mean that the 3-surface at the ends of causal diamond (CD) can be connected by several space-time surfaces carrying same conserved Kähler charges and having same values of Kähler action. Conformal symmetries defined by Kac-Moody algebra associated with the imbedding space isometries could act as gauge transformations and respect the light-likeness property of partonic orbits at which the signature of the induced metric changes from Minkowskian to Euclidian (Minkowskianb space-time region transforms to wormhole contact say). The number of conformal equivalence classes of these surfaces could be finite number n and define discrete physical degree of freedom and one would have $h_{eff} = n \times h$. This degeneracy would mean "second quantization" for the sheets of n-furcation: not only one but several sheets can be realized.

This relates also to quantum criticality postulated to be the basic characteristics of the dynamics of quantum TGD. Quantum criticalities would correspond to an infinite fractal hierarchy of broken conformal symmetries defined by sub-algebras of conformal algebra with conformal weights coming as integer multiples of n. This leads also to connections with quantum criticality and hierarchy of broken conformal symmetries, p-adicity, and negentropic entanglement which by consistency with standard quantum measurement theory would be described in terms of density matrix proportional $n \times n$ identity matrix and being due to unitary entanglement coefficients (typical for quantum computing systems).

Formally the situation could be described by regarding space-time surfaces as surfaces in singular n-fold singular coverings of imbedding space. A stronger assumption would be that they are expressible as as products of n_1 -fold covering of M^4 and n_2-fold covering of CP_2 meaning analogy with multi-sheeted Riemann surfaces and that M^4 coordinates are n_1-valued functions and CP_2 coordinates n_2 -valued functions of space-time coordinates for $n = n_1 \times n_2$. These singular coverings of imbedding space form a book like structure with singularities of the coverings localizable at the boundaries of causal diamonds defining the back of the book like structure.

Fig. 17. Hierarchy of Planck constants. `http://tgdtheory.fi/appfigures/planckhierarchy.jpg`

A-8 Some Notions Relevant To TGD Inspired Consciousness And Quantum Biology

Below some notions relevant to TGD inspired theory of consciousness and quantum biology.

A-8.1 The Notion Of Magnetic Body

Topological field quantization inspires the notion of field body about which magnetic body is especially important example and plays key role in TGD inspired quantum biology and consciousness theory. This is a crucial departure fromt the Maxwellian view. Magnetic body brings in third level to the description of living system as a system interacting strongly with environment. Magnetic body would serve as an intentional agent using biological body as a motor instrument and sensory receptor. EEG would communicated the information from biological body to magnetic body and Libet's findings from time delays of consciousness support this view.

The following pictures illustrate the notion of magnetic body and its dynamics relevant for quantum biology in TGD Universe.

Fig. 18. Magnetic body associated with dipole field. `http://tgdtheory.fi/appfigures/fluxquant.jpg`

Fig. 19. Illustration of the reconnection by magnetic flux loops. `http://tgdtheory.fi/appfigures/reconnect1.jpg`

Fig. 20. Illustration of the reconnection by flux tubes connecting pairs of molecules. http://tgdtheory.fi/appfigures/reconect2.jpg

Fig. 21. Flux tube dynamics. a) Reconnection making possible magnetic body to "recognize" the presence of another magnetic body, b) braiding, knotting and linking of flux tubes making possible topological quantum computation, c) contraction of flux tube in phase transition reducing the value of h_{eff} allowing two molecules to find each other in dense molecular soup. http://tgdtheory.fi/appfigures/fluxtubedynamics.jpg

A-8.2 Number Theoretic Entropy And Negentropic Entanglement

TGD inspired theory of consciousness relies heavily p-Adic norm allows an to define the notion of Shannon entropy for rational probabilities (and even those in algebraic extension of rationals) by replacing the argument of logarithm of probability with its p-adic norm. The resulting entropy can be negative and the interpretation is that number theoretic entanglement entropy defined by this formula for the p-adic prime minimizing its value serves as a measure for conscious information. This negentropy characterizes two-particle system and has nothing to do with the formal negative negentropy assignable to thermodynamic entropy characterizing single particle. Negentropy Maximization Principle (NMP) implies that number theoretic negentropy increases during evolution by quantum jumps. The condition that NMP is consistent with the standard quantum measurement theory requires that negentropic entanglement has a density matrix proportional to unit matrix so that in 2-particle case the entanglement matrix is unitary.

Fig. 22. Schrödinger cat is neither dead or alive. For negentropic entanglement this state would be stable. http://tgdtheory.fi/appfigures/cat.jpg

A-8.3 Life As Something Residing In The Intersection Of Reality And P-Adicities

In TGD inspired theory of consciousness p-adic space-time sheets correspond to space-time correlates for thoughts and intentions. The intersections of real and p-adic preferred extremals consist of points whose coordinates are rational or belong to some extension of rational numbers in preferred imbedding space coordinates. They would correspond to the intersection of reality and various p-adicities representing the "mind stuff" of Descartes. There is temptation to assign life to the intersection of realities and p-adicities. The discretization of the chart map assigning to real space-time surface its p-adic counterpart would reflect finite cognitive resolution.

At the level of "world of classical worlds" (WCW) the intersection of reality and various p-adicities would correspond to space-time surfaces (or possibly partonic 2-surfaces) representable in terms of rational functions with polynomial coefficients with are rational or belong to algebraic extension of rationals.

The quantum jump replacing real space-time sheet with p-adic one (vice versa) would correspond to a buildup of cognitive representation (realization of intentional action).

Fig. 23. The quantum jump replacing real space-time surface with corresponding p-adic manifold can be interpreted as formation of though, cognitive representation. Its reversal would correspond to a transformation of intention to action. http://tgdtheory.fi/appfigures/padictoreal.jpg

A-8.4 Sharing Of Mental Images

The 3-surfaces serving as correlates for sub-selves can topologically condense to disjoint large space-time sheets representing selves. These 3-surfaces can also have flux tube connections and this makes possible entanglement of sub-selves, which unentangled in the resolution defined by the size of sub-selves. The interpretation for this negentropic entanglement would be in terms of sharing of mental images. This would mean that contents of consciousness are not completely private as assumed in neuroscience.

Fig. 24. Sharing of mental images by entanglement of subselves made possible by flux tube connections between topologically condensed space-time sheets associated with mental images. http://tgdtheory.fi/appfigures/sharing.jpg

A-8.5 Time Mirror Mechanism

Zero energy ontology (ZEO) is crucial part of both TGD and TGD inspired consciousness and leads to the understanding of the relationship between geometric time and experience time and how the arrow of psychological time emerges. One of the basic predictions is the possibiity of negative energy signals propagating backwards in geometric time and having the property that entropy basically associated with subjective time grows in reversed direction of geometric time. Negative energy signals inspire time mirror mechanism (see **Fig.** http://tgdtheory.fi/appfigures/timemirror.jpg or **Fig.** 24 in the appendix of this book) providing mechanisms of both memory recall, realization of intentational action initiating action already in geometric past, and remote metabolism. What happens that negative energy signal travels to past and is reflected as positive energy signal and returns to the sender. This process works also in the reverse time direction.

Fig. 25. Zero energy ontology allows time mirror mechanism as a mechanism of memory recall. Essentially "seeing" in time direction is in question. http://tgdtheory.fi/appfigures/timemirror.jpg

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