Article

Evolution in Many-Sheeted Space-Time: General Ideas

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Abstract

In this article 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) , the idea that primitive life forms evolved in "Mother Gaia's womb", 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). A weaker assumption is that ATP ADP makes only possible to generate negentropic entanglement.

1 Introduction

This article is part of a chapter [53] of "Genes and Memes", which 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 [36, 39] . There are many constraints on the models for prebiotic evolution. The models have also many difficulties [20, 35] .

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 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 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.

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.

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) [58]. 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

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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 [67]. 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. Tqc programs correspond to asymptotic self organization patterns for liquid flows inducing braidings and are non-trivial in presence of external energy feed.

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 [50] 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.

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 aminoacid 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-aminoacid 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 aminoacid sequences were formed. After a period of symbiosis involving all these three tRNAs a transition to DNA-RNA-aminoacid world took place as an aminoacid sequence acting like reverse transcriptase emerged.

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 [31] 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 [12] .

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 [27] and same might be true in the case of exotic RNA.

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

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 these articles are in order.

1. The idea about hierarchy of Josephson junctions discussed in [49] (cell membrane would provide the basic realization leading to a model of nerve pulse [62]) is central and emerged already around 2000 as I learned by looking at old CASYS conference proceedings [68].

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 [52, 61] 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 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 [51].

3. In [66] the identification of biophotons 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 biophotons nor the notions of zero energy ontology [58] having profound biological implications [45, 67] are not discussed. The reason is that all the articles in this series are prepared from the chapters of online book "Genes and Memes" - 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.

In this article - the first part of a 4-part article - 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) [67], the idea that primitive life forms evolved in "Mother Gaia's womb" [54] (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) [58]. A weaker assumption is that ATP→ ADP makes only possible to generate negentropic entanglement.

Some important topics have been left out since they have been discussed in [51]: 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. 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 [67] 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 What is known about pre-biotic evolution?

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

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 environement provide by the surface of young Earth.

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.

2.3 The notion of primordial ocean

The following discussion uses basic facts which I have learned from articles of Chris King [36] representing updated view about facts and theories about pre-biotic evolution as well as articles criticing the existing theories [20, 35] .

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 precessors of the cell. Haldade 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 outgassing associated with volcanic eruptions but aund 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 [17] . 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 [20] 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 [43] and others to be discussed below would not been satisfied.

2.4 Urey-Miller experiment

Urey-Miller experiment [43] 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 [21] . 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 [26] 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 mimick the situation prevaling 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.

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 [33, 31] 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 [36] 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 [34] . These chains attached to the surface of the clay, and when more nucleotides were feeded 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 [19] . Second crucial finding was that these RNAs could act as catalysts in transesterifications crucial for the protein synthesis [33] . Even high fidelity complementary replication of arbitrary short RNA sequences has been demonstrated [29] . 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 [32] and modified ribozymes are able to act as amino-acyl esterases [23] . 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 retro-viruses (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.

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 [57] . Chris King has formulated the same idea in a more concrete manner in his article [36] 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.

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 [28] . 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 [18] . 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.

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 [41, 36] . 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 [28] 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 [20, 35] .

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.

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. Superconducting 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.

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 [35] .

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 unstable 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.

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 [20] .

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.

3.2.1 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 [58] 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 [64, 60] . 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 [59] explains cold fusion [2] ,[4] as well as biological nuclear transmutations for which there is considerable empirical support [1] . 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 [6] . 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 [51] 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 [46] 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.

3.2.2 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 [49] . 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 [38] . 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.

3.2.3 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 [52, 49] . 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 [49] . 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 $r \equiv \hbar/\hbar_0$ [52] 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 [65] . 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 p-adic length scales sith $k \in \{151, 157, 163, 167\}$ 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 [49] . 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 $B \rightarrow B/r$ 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 quantition 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.

3.2.4 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 [46, 51] . 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-acidthis 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.

3.2.5 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 [56]). 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 bio-polymers 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.

3.2.6 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.

3.2.7 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 [47, 48] . 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 [49] . 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 [41] discussed from TGD viewpoint in [62] , 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 bio-polymers 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 [51] . 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.

3.2.8 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 depolymerization. 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.

3.2.9 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 [30, 22] 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.

3.2.10 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 [57, 49] . 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.

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.

3.3.1 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.

3.3.2 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 [51] and also for amino-acids [44] .

3.3.3 Evolution of pre-biotic chemistry as a sequence of bifurcations

In his article "Biocosmology" [36] 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 magneticbody using plasmoids and plasma oscillation patterns.

3.3.4 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.

3.3.5 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. $ATP \rightarrow ADP$ process

AMP, ADP , ATP are phosphorylated RNA nucleosides [8] and the hydrolysis of ATP to ADP [9] 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 Coulombic 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 $ATP + F_1$ $\rightarrow$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 [40] .

Step 2 Hydrolysis: F_1·ATP$\rightarrow$ F_1·ADP·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·ADP·$P_i \rightarrow F_1 \cdot ADP + P_i$. Free energy $\Delta G \sim .31$ eV is liberated at this step.

Step 4: ADP is released from the catalyst site: F_1·ADP+$P_i \rightarrow F_1 + ADP + P_i$. $\Delta G \sim 0$ 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 [5, 3] ,[37] . 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 $ATP \rightarrow ADP$ 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 $ATP \rightarrow$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 [44] . The model is relies on ideas inspired by the model of DNA as topological quantum computer [51] . 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 $ATP \rightarrow ADP + P_i$ 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 assocaited 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 fluix 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 shorterining of the magnetic flux tube connecting them and associated with the innermost phophate. This would liberate .42 eV of metabolic energy.

3. At Step 2 hydrolysis would induce F_1·ADP·$P_i \rightarrow F_1 \cdot ADP + P_i$. Since no energy is released at this step, there is temptation to concludde 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 disappaerence of this flux tubeso 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 ineed 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 Coulombic interaction energy of proton with PO^{4-}. The Coulombic 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 instabilization 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^+ [13] 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 $NADH \rightarrow NAD^+$ 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. Alfwen 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 $\mathrm{PO_4H_2^{2-}}$ 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-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-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 destabilizes 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.

3.3.6 Why DNA is stable inside cell nucleus?

Inside membrane bound surface both DNA and RNA nucleotides and polymers are stable. The unstability 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→ 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 $C\text{-}OH^-$ 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.

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.

3.4.1 Basic ideas

Before continuing general motivating comments about implications of negentropic entanglement 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) [58] 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 [44] 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.

3.4.2 General formulation of the model

Consider now the model. High energy phosphate bond [11] assigned with the two outer-most phosphates of ATP [8] is fundamental for the basic processes in living matter. The $ATP \rightarrow ADP + P_i$ liberates metabolic energy loaded to ATP in the cellular respiration process [10] 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 [7] and phosphate ion $P_i = PO_4^{3-}$ [14] . The notion of high energy phosphate bond has been however challenged as being meaningless [5, 3] ,[37] .

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 $ATP \rightarrow ADP + P_i$ 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).

3. With an inspiration coming from DNA as topological quantum computer model [51] 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 [51, 44] . 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 [63] 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 patways. Why this happens would be easy to understand in Indra's net model.

5. In $ATP \rightarrow ADP+P_i$ 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.

3.4.3 Quantitative estimates

Consider now a more detailed model for $ATP \rightarrow ADP + P_i$. 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 $ATP + F_1 \rightarrow ATP \cdot F_1$ 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 [40] .

   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

$$\Delta g_1 = E_0 + 3T/2 - T\Delta s = .42 \ \ eV \ \ . \tag{3.1}$$

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. 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.

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.

3.5.1 Water memory: general considerations

With few exceptions so called "serious" scientists remain silent about the experiments of Benveniste and others relating to water memory [15, 16, 24, 25] 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 [42] . 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.

3.5.2 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 [24] . 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 [25] ,[42] .

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 superconductivity 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 [47] . 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) [25] .

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