# Evolution in Many-Sheeted Space-Time

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## Contents

**Abstract**

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

1. Basic facts about and TGD based model for pre-biotic evolution are discussed.
2. A model for the ATP-ADP process based on DNA as topological quantum computer vision, the identification of universal metabolic energy quanta in terms of zero point kinetic energies, and the notion of remote metabolism is discussed.
3. A model for the evolution of the recent genetic code (3-codons) as a fusion of codes for which codons are nucleotides (1-codons) and di-nucleotides (2-codons) is discussed. The symmetries of the genetic code, the observation that tRNA can be seen as a fusion of two hairpin like DNA molecules, and the finding that the first nucleotides of 3-codon code for the reaction path leading from a precursors of the amino-acid to amino-acids for hydrophobic/hydrophilic dichotomy, serve as motivations of the model. 1- and 2-codes corresponding to the two forms of RNA (the exotic $2' - 5'$ RNA and the usual $3' - 5'$ RNA) would have prevailed in RNA world. Amino-acids would have served as catalysts for the copying of RNA on one hand, and RNA molecules would have catalyzed the formation of amino-acids from their precursors on one hand, meaning the presence of a positive feedback loop. In the transition to DNA-amino-acid era RNA began to be translated to amino-acid sequences.
4. Cambrian explosion represents a rather mysterious period in biology: new highly developed phylae emerged out of nowhere. A second strange finding is that continents would fit together to form single super-continent covering entire Earth's surface at time of Cambrian explosion if the radius of Earth would have been one half of its recent value. This finding has inspired Expanding Earth theories but it has not been possible to identify the mechanism causing the expansion. The success of the standard tectonic plate theory requires that possible expansion must have occurred in relatively short geological time scale. The hierarchy of Planck constants implies that cosmic expansion has occurred in quantum leaps increasing the value of $h_{eff}$ and thus of quantum scales by factors which tend to be powers of 2. Cosmic expansion would have occurred as jerks even in the case of planets. In the proposed model Cambrian explosion would have accompanied the expansion of the Earth's radius by a factor of 2: during this period an outburst of highly developed life forms from underground seas to the surface of Earth would have taken place.
5. The last section of the chapter compares TGD based view about the evolution of genetic code to the views of McFadden. This section is a little bit out of date. For instance, the hypothesis that magnetic body of DNA could induce mutations purposefully is not discussed. This hypothesis is natural if one believes that magnetic flux tubes connecting bio-molecules play a key role in bio-catalysis. This idea is discussed in the chapter devoted to protein folding.
6. A vision about biological evolution and evolution of brain is discussed on basis of the wisdom gained from the construction of the models of sensory receptor and generalized EEG.
7. TGD inspired theory of consciousness in its recent form predicts that life is a universal phenomenon. The possibility that oil droplets could be seen as a primitive life form is discussed in the last section of the chapter.

# 1 Introduction

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

If was already early that the notion of many-sheeted space-time could allow to understand many puzzles related to the pre-biotic evolution [I43, I71]. There are many constraints on the models for pre-biotic evolution. The models have also many difficulties [I44, I65].

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

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## 1.1 Questions And Answers About Evolution

A good manner to introduce the essentials of the TGD inspired model for the prebiotic evolution is by a sequence of questions and answers relating to evolution. The progress occurred during last years in the understanding of water as primitive lifeform has modified considerably the original answers and I have comments about this.

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

A: Quantum TGD predicts a genuine cosmic evolution occurring by quantum jumps for which dynamics is characterized by Negentropy Maximization Principle (NMP) [K22]. The generalization of the notion of space-time implies dark matter hierarchy with levels characterized by arbitrarily large values of effective Planck constant so that macroscopic quantum coherence is possible even in astrophysical length scales. Even astrophysical systems are analogous to atomic systems which implies a strong standardization of planetary system so that Earth like planets are abundant. There are also other good reasons for why the evolution of life would not have been accident in TGD Universe and life should appear everywhere in TGD Universe.

Even stronger conclusions follow from NMP in zero energy ontology (ZEO). The view about quantum jump in ZEO implies that the formation of what might be regarded as generalizations of sensory and other representations defining reflective level of consciousness appearing universally. These representations would be kind of Akashic records. The braiding of the magnetic flux tubes would serve as a geometric correlate of the negentropic entanglement, which together with Negentropy Maximization Principle (NMP) guarantees approximate invariance of representations under quantum jumps. Also the sensory-motor dichotomy characterizing living matter is a universal property of quantum jump sequence in ZEO [K35]. This would strongly suggest that consciousness and even life has not emerged but has been present already at elementary particle level. These ideas are however newcomers and do not yet appear in the formulations represented in the article series.

Q: What were the most primitive living systems?

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

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

Q: How metabolic machinery emerged?

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

Q: What is behind biocatalytic machinery?

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

Q: How symbolic dynamics emerged?

A: There is a temptation to assign the origin of the symbolic dynamics with the magnetic body. The notion of fractional atom [K11] suggested by the fractionization of electron and nucleon quantum numbers for dark matter hierarchy brings in a candidate for a symbolic dynamics assigning to molecules "names" which need not correlate very strongly with the chemical properties of the molecule but would dictate to a high degree its biochemical behavior. Molecular "sex" emerges in the sense that molecules labeled with "names" and "co-names" tend to pair. The model of DNA as TQC assumes a 4-coloring of braid strands realized by an assignment of DNA nucleotides to quarks and anti-quarks. Also this means symbolic dynamics since only molecules connected by colored braids have high probability to participate in same biochemical reaction and do it in a very specific manner. Since the quarks involved with braid strands can have fractional charges, molecular sex can be realized also in this manner.

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

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

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

Q: How biochemical pathways emerged?

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

The lock and key mechanism can be generalized with key being replaced with a password. In computer languages like LISP lock-key pair corresponds to a memory position represented as a pair formed by its own address and the address to which the memory position points and the

program consisting of sequence of this kind of associations. These addresses can be represented also as collections of resonance frequencies.

Q: How genetic code evolved?

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

More strongly TGD based approach is provided by the vision about water as a primitive life-form inspired by Pollack's findings about fourth phase of water and exclusion zones [L7]. In this framework the dark proton strings defining "dark amino-acid" sequences [L2, K18] could have coded the 2-braiding (braiding in space-time) patterns of invader molecules as their own 2-braidings, and dark DNA would have provided symbolic coding of "dark proteins". Therefore dark DNA would originally have coded dynamical patterns for magnetic bodies of invader molecules. This would make possible pre-biotic immune system, which would be a part of the recent immune system.

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

A: The model for the evolution of the genetic code forces to conclude tha RNA world [I83] 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 [I16].

Another and more plausuible option in TGD framework is water as a primitive lifeform with dark counterparts of basic biomolecules realizes as dark protonic strings (dark nuclei). RNA world could have followed this period but the fact that both DNA, RNA, tRNA and aminoacids can have dark counterparts does not suggest special role for RNA.

Q: Does the notion of protocell make sense?

A: The model of DNA as TQC involves essentially the magnetic flux tubes connecting DNA nucleotides and cell membrane. Since topological quantum computation should have taken place also during the RNA era, some kind of cell membrane consisting of exotic RNA should have been present. It has been found that DNA indeed forms membrane like structures which are liquid crystals consisting of sequences of DNA nucleotides with length up to 20 nucleotides [I58] and same might be true in the case of exotic RNA.

Another very attractive option is that the counterparts of exclusion zone carrying negative charge due to the transfer of protons to the flux tubes of the magnetic body of exclusion zone [L7] defines protocell.

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

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

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

1. The idea about hierarchy of Josephson junctions discussed in [K10] (cell membrane would

provide the basic realization leading to a model of nerve pulse [K27]) is central and emerged already around 2000 as I learned by looking at old CASYS conference proceedings [L1].

2. The considerations rely also heavily on the notion of magnetic body and the identification of dark matter as a hierarchy of phases of ordinary matter (at least) labelled by an effective value of Planck constant $\hbar_{eff} = n\hbar$ coming as an integer multiple of the ordinary Planck constant (this idea [K13, K25] was introduced around 2005). These phases are assumed to reside at flux tubes and sheets appearing as parts of the magnetic body assignable to any physical system.

   The basic implication is that basic quantum scales proportional to $\hbar$ are scaled up so that nanoscopic and even macroscopic quantum phases become possible for sufficiently large values of Planck constant. Magnetic body is assumed to act as an intentional agent receiving sensory data from cell membranes and controlling biological body with the mediation of genome. Signals are realized as dark photons and cyclotron Bose-Einstein condensates at magnetic bodies are central in this picture. Photon with given energy can correspond to arbitrarily long wavelengths and one can understand the effects of ELF radiation on vertebrate brain in terms of dark photons. DNA as topological quantum computer is one of the implications [K12].

3. In [K34] the identification of bio-photons as ordinary photons resulting in decays of (say) dark photons with same energy and frequency in EEG range is discussed. In this and subsequent articles neither bio-photons nor the notions of zero energy ontology [K22] having profound biological implications [K2, K35] are not discussed. The reason is that all the articles in this series are prepared from the chapters of online book "Genes and Memes" [K17] - 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.

## 1.2 Topics Of The Chapter

The topics of the chapter has been restricted to those, which seem to represent the most well-established ideas. The topics of the article have been restricted to those, which seem to represent the most well-established ideas about evolution in TGD Universe. There are many other, more speculative, ideas such as the notion of fractional atom [K11] based on fractalization of electron charge and strong form of the hypothesis that some life forms has evolved in "Mother Gaia's womb", maybe even in the hot environment defined by the boundary of mantle and core.

1. The basic facts believed to be known about pre-biotic evolution are discussed first. After that the TGD inspired vision about prebiotic evolution is introduced. The key ideas discussed are the notion of magnetic body and plasmoids as primitive life-forms, emergence of symbolic dynamics as dynamics of dark matter, universal metabolic currencies identified as increments of zero point kinetic energies in many-sheeted space-time, time mirror mechanism giving rise to models of intentional action, memory and remote metabolism and finding justification in zero energy ontology (ZEO) [K35], the idea that primitive life forms evolved in "Mother Gaia's womb" [K15] (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) [K22]. A weaker assumption is that ATP$\rightarrow$ ADP makes only possible to generate negentropic entanglement.

   Some important topics have been left out since they have been discussed in [K20] and in an earlier article [L3, L4]. 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 [L3, L4]. 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 [K35] gives also rise to a universal representations (sensory -. memory -. etc...) suggests that topological quantum computation like processes must have been present from already during pre-biotic period.

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

   TGD based view about the evolution of genetic code is compared to the views of McFadden [I67]. This section is a little bit out of date. For instance, the hypothesis that magnetic body of DNA could induce mutations purposefully is not discussed. This hypothesis is natural if one believes that magnetic flux tubes connecting bio-molecules play a key role in bio-catalysis. This idea is discussed in the chapter devoted to protein folding [K1].

3. A vision about biological evolution and evolution of brain is discussed on basis of the wisdom gained from the construction of the models of sensory receptor and generalized EEG [K16, K10]. As I started to develop this vision. several obvious questions popped up. The preferred values of (effective) Planck constant are assumed to be integer multiples of ordinary Planck constant: does this integer have preferred values? For eight years later I take the original speculative answer to this question with a grain of salt. Can one distinguish between evolution of biological and magnetic body and identify cultural evolution as evolution of magnetic body? EEG and its variants (and the predicted scaled variants of these) are expected to characterize living organisms, even super organisms like ant nest, bee hive, and bacterial colony: is this really the case? Does bee hive possess a long term memory and what is the role of the queen? One can also ask questions about the evolution of nervous system in the same conceptual framework. Are the magnetic bodies of neurons and larger structures characterized by $\hbar_{eff}$? What about collective and transpersonal levels of consciousness?

   Sheldrake's vision [I74, I75], [J4] about species memory is also highly interesting from TGD point of view but is not considered in the article series about prebiotic evolution. The interested reader can however consult the article at [L5]. The latest view about TGD inspired theory of consciousness justifying Sheldrake's vision in terms of negentropically entangled states defining representations invariant under quantum jump sequence and in this manner giving rise to "Akashic records" defining sensory -. memory -. etc. representations can be found at [K35].

   Dark photons characterized by the value of $\hbar_{eff}$ and transforming to ordinary photons with the same energy identified as bio-photons are becoming a central element of TGD inspired quantum biology [K34]: in particular the non-destructive conscious reading of the memories represented in terms of negentropically entangled states by interaction free measurement is very attractive idea [K35]. The communications by dark photons might have been present already during the prebiotic era before the emergence of biochemical signalling and neural communications. The role of dark photons is not discussed in the vision as it was formulated for more than five years ago.

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

period an outburst of highly developed life forms from underground seas to the surface of Earth would have taken place. This topic is discussed in separate chapter [K15].

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

The appendix of the book gives a summary about basic concepts of TGD with illustrations. Pdf representation of same files serving as a kind of glossary can be found at `http://tgdtheory.fi/tgdglossary.pdf` [L6].

# 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 environment 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 [I43] representing updated view about facts and theories about pre-biotic evolution as well as articles criticizing the existing theories [I44, I65].

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

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

The assumption that the atmosphere is reducing is essential: the presence of oxygen would be fatal for the biomonomers. This assumption can be however questioned. The primordial atmosphere was due to the outgassign associated with volcanic eruptions but due to volcanic fumes the atmosphere is oxidizing which means that biomonomers would have been rapidly destroyed by oxidation. Interestingly, the photographs of Earth taken during the Apollo 16 mission allow to conclude that a gigantic cloud of hydrogen, extending 40, 000 miles into space surrounds the Earth. The only source of hydrogen can be water vapour, bombarded by high energy UV light rays above ozone layer [I80]. 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 [I44] 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 [J10] and others to be discussed below would not been satisfied.

## 2.4 Urey-Miller Experiment

Urey-Miller experiment [J10] 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 [I45]. 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 [I50] thin ice at temperature of 10 K containing $H_2O$, ammonia, CO, $CO_2$ methanol was located in vacuum and bombarded by UV radiation to mimic the situation prevailing in the interstellar space. Contrary to expectations, hundreds of different complex organic molecules appearing also in meteorites were generated. Thus it seems that the molecules generated by pre-biotic evolution appear everywhere in cosmos but ironically, the environment provided by the surface of young Earth's does not seem to favor the pre-biotic evolution.

## 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 [I66, I83] 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 [I43] 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 [I61]. These chains attached to the surface of the clay, and when more nucleotides were fed by washing them with the solution, they grew up to 55 nucleotides long. It seems that reversible dehydration in a medium containing phosphates, bases and sugars provides the routes to polynucleotide formations. Besides water, $Mg_{++}$ plays a key role in stabilizing mono- and oligonucleotides by compensating the negative charges of the phosphates.

2. RNA can form double helices and has 3-dimensional tertiary structures analogous to that of proteins so that one might expect the ability to act as catalyst. The discovery of spontaneous splicing of RNAs in living systems is possible meant a breakthrough in this respect [I81]. Second crucial finding was that these RNAs could act as catalysts in trans-esterifications crucial for the protein synthesis [I66]. Even high fidelity complementary replication of arbitrary short RNA sequences has been demonstrated [I55]. 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 [I42] and modified ribozymes are able to act as amino-acyl esterases [I59]. Thus RNA seems able to serve synthetizing, transfer, messenger and ribosomal functions so that it can guide both its own replication and ordered polymerization of proteins.

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

## 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 [K20]. Chris King has formulated the same idea in a more concrete manner in his article [I43] 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 [I52]. 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 [I39]. 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 [I62, I43] . 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 [I52] 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 [I44, I65].

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.

Super-conducting magnetosphere can be seen as a higher level life-form which controls and guides the biological evolution from the very beginning. Second key element is dark matter hierarchy.

## 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 [I65].

4. The formation of the biological polymers such as proteins, nucleic acids, lipids, and carbohydrates occurs universally by dehydration. The problem is that in water environment polymers are un-stable against decay by hydration: it would seem that a metabolic energy feed is required already at this stage to guarantee non-equilibrium situation. The assembly of these macro-molecules into organized aggregates like chromosomes, micro-tubules and cell organelles suggests the emergence of symbolic representations and only a weak independence of hard facts of chemistry which makes the problem even more difficult from the point of view of standard physics.

5. The emergence of catalysts and metabolism, should be understood. Here one encounters an egg-hen problem. Standardized metabolic currency seems to be necessary for effective catalysis but metabolism according to the standard view involves extremely complex web of reaction pathways needing refined catalytic actions.

6. Membrane bound structures are essential for life and one should understand how they emerge and even predict correctly basic facts about them.

7. The emergence of the genetic code has remained a mystery in various scenarios of pre-biotic evolution.

8. How the incredible ability of the components of bio-systems to co-operate pops up from primordial soup is not always included to the list of mysteries since everything smelling "holism" is regarded as pseudo science in reductionistic circles.

## 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 [I44] .

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 [K22] 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 [K29, K24]. Only very few orbital radii are possible and for a star with mass around solar mass planets at distance of Earth are possible and probable irrespective of the mass of the planet. Hence solar systems are standardized to high degree. Also the quantization of masses of stars is highly suggestive and the number of stars with mass not far from solar mass is large. Obviously this raises the probability for having Earth like environments dramatically.

3. TGD based nuclear physics [L2] , [L2] explains cold fusion [C2] , [D7] as well as biological nuclear transmutations for which there is considerable empirical support [C1] . 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 [E6]. 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 [K12] 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 [K3] 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 [K10]. 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 [I70]. 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 [K13, K10]. 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 [K10] . 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 $r \equiv \hbar/\hbar_0$ [K13] 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 [K32] . The values of $n_i$ for which quantum phase is expressible in terms of squared roots are number theoretically preferred and correspond to integers $n$ expressible as $n_i = 2^k \prod_n F_{s_n}$, where $F_s = 2^{2^s} + 1$ is Fermat prime and each of them can appear only once The lowest Fermat primes are $F_0 = 3, F_1 = 5, F_2 = 17$. The prediction is that also $r$-multiples of p-adic length scales are possible as preferred length scales.

TGD inspired quantum biology and number theoretical considerations suggest preferred values for $r = \hbar/\hbar_0$. For the most general option the values of $\hbar$ are products and ratios of two integers $n_a$ and $n_b$. Ruler and compass integers defined by the products of distinct Fermat primes and power of two are number theoretically favored values for these integers because the phases $exp(i2\pi/n_i)$, $i \in \{a, b\}$, in this case are number theoretically very simple and should have emerged first in the number theoretical evolution via algebraic extensions of p-adics and of rationals. p-Adic length scale hypothesis favors powers of two as values of $r$.

The hypothesis that Mersenne primes $M_k = 2^k - 1$, $k \in \{89, 107, 127\}$, and Gaussian Mersennes $M_{G,k} = (1+i)k - 1$, $k \in \{113, 151, 157, 163, 167, 239, 241..\}$ (the number theoretical miracle is that

all the four scaled up electron Compton lengths $L_e(k) = \sqrt{5}L(k)$ with $k \in \{151, 157, 163, 167\}$ are in the biologically highly interesting range 10 nm-2.5 $\mu$m) define scaled up copies of electroweak 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 [K10]. This hypothesis - to be referred to as Mersenne hypothesis - replaces the earlier rather ad hoc proposal $r = \hbar/\hbar_0 = 2^{11k}$ for the preferred values of Planck constant.

In the case of magnetic flux simplest quantization suggests the scaling $B \to B/r$ for the magnetic fields. This is assumed to hold true also in more general case when the quantization condition reads as $\oint(p - ZeA)dl = n\hbar$ and involves currents flowing at the boundaries of flux quanta so that magnetic flux need not be anymore quantized to a multiple of Planck constant. For axonal membranes the flux quantization with $n = 0$ is natural since the size of flux quantum does not depend on the value of Planck constant. Assuming flux quantization and standard value of Planck constant $B_{end} = .2$ Gauss would give flux tube radius $L = \sqrt{5/2} \times L(169) \simeq 1.58L(169)$, which does not correspond to any p-adic length scale as such.

Concerning the interpretation of $B_{end}$ there are two options. It could correspond to a personal magnetic body or to a dark variant of the Earth's magnetic field. At this moment it is impossible to say which if any hypothesis is right. However the fact that the ELF fields have no direct effect on conscious experience mildly supports the identification as the dark variant of $B_E$.

### 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 [K3, K12]. In this case DNA nucleotides are analogous to colors of braid strands and base pairing corresponds to molecular sex for DNA molecules. The color of braid strand implies long ranged highly selective interactions between DNA and distant molecules, such as lipids of the lipid layer of cell membrane or amino-acids. Free amino-acids inherit the colors of the first two nucleotides in the codon $XYZ$ whereas the color of the third nucleotide corresponds to a quantum superposition of colors for codons coding for the amino-acid this defines the quantum counterpart of wobble base pairing. Amino-acids can be divided into amino-acids and their conjugates analogous to opposite sexes and generalized base pairing determines the interactions of the amino-acids to a high degree. Hydrogen bond can be identified as a special case of flux tube. There are also flux tubes connecting acceptors of hydrogen bonds acting as plugs in the connection lines formed by the magnetic flux tubes and $Y$ corresponds to this kind of plug at the level of amino-acids.

*2. Second vision*

The mathematical realization for the hierarchy of Planck constants leads to a generalization of the notion of imbedding space and this leads to four kinds of phases resulting as combinations of phases with increased or reduced unit of spin and quantum numbers associated with $CP_2$ degrees of freedom. Each phase corresponds to its own Planck constant and is characterized by a discrete symmetry group.

Especially interesting are phases with large value of Planck constant involving charge fractionization and increase of spin unit. The electrons of free electron pairs of aromatic cycle are reasonable candidates for dark electrons of this kind. One can consider variants of hydrogen atom containing $n \leq N$ fractionally charged electrons with with lepton number and electronic charge equal to $n/N$. The values $n/N$ and $(N-n)/N$ for the fractional charge would correspond "name" and "conjugate name" since their combination would give a maximal charge and a state analogous to a full electron shell. Thermal stability poses strong constraints since atomic and molecular energy scales are reduced as Planck constant increases.

The notion of fractional electron inspires the notion of "half" hydrogen bond for which electron

has a fractionized fermion number. The full hydrogen bond would be formed in the fusion of half hydrogen bonds and give rise to a structure analogous to a full electron shell expected to be especially stable. Catalyst sites might correspond to half hydrogen bonds and the basic recognition mechanism could be the fusion of half bond and its conjugate to form a full hydrogen bond. One could speak about "molecular sex". The sequences of half bonds would represent words so that molecules would have names. Also interpretation as quantum computer codes might make sense. The problem of this vision is the lack of direct contact with experimental facts and for this reason it will not be discussed in the sequel.

### 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 [K19] ). It will be found that this mechanism is involved also with the dehydration leading to polymerization and phosphorylation. The reversal of this process also implies the in-stability of DNA in an ordinary aqueous environment.

The interpretation of the role of phosphate ions as metabolic energy batteries seems to be wrong in TGD framework: the main function of negatively charge phosphates would be to make biopolymers critical against local modifications making them thus ideal for catalytic manipulations. Even deeper function would be the role as standard plugs to which magnetic flux tube can attach and which second flux tube can begin. $ATP \rightarrow$ADP would in this framework mean reconnection process for a magnetic flux tubes modifying the hardware of TQC.

### 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.

In many-sheeted space-time particles topologically condense at all space-time sheets having projection to given region of space-time so that this option makes sense only near the boundaries of space-time sheet of a given system. Also p-adic phase transition increasing the size of the space-time sheet could take place and the liberated energy would correspond to the reduction of zero point kinetic energy. Particles could be transferred from a portion of magnetic flux tube portion to another one with different value of magnetic field and possibly also of Planck constant $h_{eff}$ so that cyclotron energy would be liberated. In the following only the "dropping" option is discussed.

### 3.2.7 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 [K4, K5]. 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 [K10]. 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 [I62] discussed from TGD viewpoint in [K27], 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 [K12]. 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 de-polymerization. The coherent structure of gel would be due to the braiding of distant molecules. The phase transitions of gel phase are good candidates for a basic mechanism of bio-control and would stabilize these polymers via the formation of structured water around them preventing hydrolysis. The developing life forms should be shielded from UV radiation and meteor bombardment.

The combination of these constraints leads to the idea that life as we define it could have evolved in the womb of Mother Gaia in underground seas with the Earth's crust shielding from UV and meteors. The necessary ingredients of biomolecules, in particular phosphates making possible phosphorylation making DNA and RNA charged and appearing also in hydrophilic ends of phospholipids, would have dissolved to the water from the ground. Cambrian revolution would have meant the burst of these highly developed life-forms to the Earth surface and resulting as a phase transition increasing the value of Planck constant for Earth's space-time sheet by a factor of two would have occurred. This would also provide a justification of Expanding Earth theory explaining the strange finding that the continents fits nicely together to form a single super continent covering entire Earth's surface if the radius of Earth is one half of its recent value and actually the same as the recent radius of Mars, which is now known to contain reservoirs of underground water.

*2. Mother Gaia's womb as mantle-core boundary?*

What about the period before the life in underground seas?

1. The plasma like aspects of cytoplasm suggests that some kind of plasma phase must have been present. Also the postulated Bose-Einstein condensates of bosonic ions at dark magnetic flux quanta represent kind of quantum plasma.

2. Plasmoids involving magnetic flux tubes and charged particles could have been predecessors of more complex molecular life forms and could have developed in the interstellar space. Their metabolism could have been based on universal metabolic energy quanta. Simple

metabolic cycles and short term chemical storage of energy based on fusion and decay of simple molecules induced by say UV radiation from the nearby stars might have developed during this era. Quite high temperatures can be considered so that after the interstellar period this kind of life forms could have survived and developed in the hot interior of planets receiving their metabolic energy from radiation by high temperature plasma. A possible candidate for the womb of Mother Gaia is the mantle-core boundary, where intensive self-organization processes are expected to take place.

3. Ultimately the charged molecules must have come in contact with ordinary water in underground seas. One can imagine that the polymerization of the charged molecules and the formation of structured water around them stabilizing them and giving rise to a gel phase took place simultaneously in presence of metabolic energy feed.

The primordial womb containing plasmoid like life forms could have been located somewhere below the boundary at which $k = 137$ atomic space-time sheets transform to very hot $k = 131$ space-time sheets: this should occur when the thermal de Broglie wave length becomes equal to the p-adic length scale $L(131)$. The transition occurs above the crust-mantle boundary (1300 K). Mantle-core boundary (4000 K) is a good candidate for a seat of high-$T$ life forms.

The dropping of O, C, N ions from the hot $k = 131$ space-time sheets to larger space-time sheets generates light at visible frequencies replacing solar light so that even intra-terrestrial counterpart of photosynthesis could develop. The dropping of oxygen atoms could make also possible development of oxygen based metabolism.

Magnetic flux quantum structure of the magnetosphere acting as a nervous system and a metabolic circuitry of the magnetic Mother Gaia could make possible controlled metabolism already during the pre-biotic period and allow to circumvent these difficulties.

### 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 [I76, I56] 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 [K20, K10]. 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 [K12] and also for amino-acids [K1].

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

In his article "Biocosmology" [I43] Chris King discusses biochemistry from the point of view of mathematician using the notions of symmetry breaking and bifurcation. This discussion allows for a physicists to get a wider perspective to the complexities of biochemistry. In the following I modify the arguments of King to TGD framework. The first basic new element is that generation of new space-time sheets corresponds to a sequence of symmetry breakings.

Besides hydrogen C, N, and O atoms with charges 6, 7, and 8 are the most important elements appearing in basic bio-monomers. The bonds with hydrogen are formed between 1s and $2p^3$ orbitals. The covalent bonds between C, N, and O atoms are the bonds appearing in various bio-monomers like ribose. Also peptide bonds between C and N in amino-acid sequence are covalent bonds. In standard chemistry one can characterize the atom in given molecule by its electronegativity telling how effectively it attracts electrons.

Electronegativity increases in the sequence C, N, O so that the bonds are more and more polar. Also Si, P, and S in the next row of the periodic table form covalent bonds but the bond energy tends to be lower which reflects itself as lower boiling points. For instance, the boiling point of $H_2S$ is below the freezing point of water). Consider now the bifurcations.

1. Polar-non-polar bifurcation is fundamental in biology. Non-polar molecules are hydrophobic and are not water-soluble whereas polar molecules are hydrophilic and water-soluble. For

instance, the formation of biological membranes is based on hydrophobic character of the second ends of lipids. A rough characterization of amino-acids is by polar-non-polar dichotomy. Also DNA base stacking is based on polarity.

2. Second bifurcation corresponds to acid-base dichotomy. Acids are able to act as donors of positive and bases donors of negative charge. For instance, this allows to classify polar amino-acids to acidic and basic ones. A working hypothesis worth of studying is that many-sheeted physics is involved in the sense that the protons in acid and electrons in base have dropped to some larger space-time sheet from the atomic space-time sheet.

3. The third bifurcation corresponds to that between second and third row of the periodic table that is $Na^+$-$K^+$ and $Mg^{++}$-$Ca^{++}$ bifurcations. The covalent bonds involving K and Ca are in general weaker. $Na^+$ concentration is higher outside cell whereas $K^+$ concentration is higher inside cell. Same applies to gel phase, a possible predecessor of cell membrane bound regions. $Mg^{++}$ acts as stabilizer of polymers and $Ca^{++}$ ions are key players in cellular and intracellular control. In particular, $Ca^{++}$ waves appear in extremely wide range of frequencies and conduction velocities.

4. The fourth bifurcation corresponds to the d-orbital elements forming a catalytic group. Almost all transition elements Mn, Fe, Co, Cu, Zn are essential biological trace elements, promote pre-biotic synthesis and are optimal in their catalytic ligand-forming capacity and valency transitions. For instance, $Zn^{2^+}$ catalyzes RNA polymerization in pre-biotic synthesis and occurs in both polymerases and DNA binding proteins.

5. The fifth bifurcation corresponds to chiral symmetry breaking not easy to understand in standard model predicting extremely small parity breaking. There is empirical evidence such as circular polarization of light from the region of star formation in the constellation of Orion suggests that parity breaking occurs also in interstellar space. Also the amino-acids in Murchison meteorite were found to be dominantly left handed.

In TGD Universe the interpretation of bifurcations is not quite the same as in the world obeying standard chemistry.

1. The polar-non-polar bifurcation corresponds to hydrophilic-hydrophobic dichotomy. The model for protein folding and bio-catalysis relies on the hypothesis that wormhole flux tubes connect conjugate amino-acids. This process is analogous to base pairing. Stating it roughly, amino-acid and its conjugate correspond hydrophilic and hydrophobic amino-acid. This bifurcation is thus important from the point of view of molecular symbolism and bio-catalysis if is based on the coding of DNA are nucleotides and amino-acids by quarks and antiquarks at the ends of wormhole magnetic flux tubes connecting them to other molecules. The emergence of wormhole magnetic flux tubes could be seen almost as a definition of emergence of life. This might have happened already during prebiotic molecular evolution if water molecules have been present from the beginning.

2. Acid-non-acid bifurcation brings in protons and there is obviously a connection with the role of protons in the basic mechanisms of metabolism and catalysis. What is also essential is the role of negative charge of bio-polymers making bio-polymers critical against local deformations so that a wide repertoire of catalytic actions using $\hbar$ changing phase transitions of wormhole magnetic flux tubes and their reconnections becomes possible. Phosphate ions would not serve as batteries of metabolic energy but make bio-polymers sensitive to catalytic actions.

3. Fifth bifurcation is difficult to understand in standard physics framework but is consistent with the presence long ranged weak fields predicted by TGD and possibly associated with dark matter. This bifurcation is not the last one in TGD Universe since already plasmoids identified as rotating magnetic systems break parity because the sign of the charge density generated by the induced radial ohmic current depends on the orientation of rotation and only the second orientation is favored energetically. $W$ MEs induce charge entanglement giving rise to plasma oscillation patterns in turn inducing various physiological waves. This

mechanism can be used as a control tool by magnetic bodies at various levels of hierarchy. Long range weak forces due to the exotic ionization of atomic nuclei could provide a tool for controlling conformations of nucleic acid polymers. Same applies to kaolinite clays consisting of Al, Si, O suggested to be of biological importance (Al can have three different states at a given lattice site): in this case the state of Al atoms in the lattice might be manipulated using weak forces.

4. The hierarchy of bifurcations defines also a hierarchy of decreasing cyclotron frequencies. The cyclotron frequencies would be associated with both with Bose-Einstein condensates of ordinary and exotic bosonic ions at magnetic flux sheets. For the bosonic ions cyclotron frequencies in the $B_{end} = 2B_E/5$ are in alpha band and in TGD Universe they play a fundamental role in communications to and control by magnetic body using hierarchy of generalized EEGs. $Ca^{++}$ and other waves associated with bosonic ions are of special importance in the bio-control by magnetic body using plasmoids and plasma oscillation patterns.

### 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. $ATP \to ADP$ process*

AMP, $ADP$, $ATP$ are phosphorylated RNA nucleosides [I2] and the hydrolysis of $ATP$ to $ADP$ [I4] plays a key role in the metabolism. Obviously also the molecules XMP, X=U, C, G are important biologically. Each $PO_3$ in $ATP$ corresponds to one unit of negative charge except for the last one which carries two units of negative charge. According to the standard chemistry $ATP \leftrightarrow ADP$ corresponds to the hydrolysis

$$ATP^{4-} + H_2O \leftrightarrow ADP^{2-} + P_i$$

where $P_i$ denotes orthophosphate $HPO_4^{-2}$. In $ADP$ the last phosphate group is $HO - PO_2^{-2}$ rather than $O = PO_2^{-2}$ as in the case of $ATP$.

The actual process is however much more complex than this.

1. The process involves several steps such that energy is liberated in two steps in which the change of Gibbs free energy is $\Delta G = .42$ eV and $\Delta G = .31$ eV making altogether.73 eV, which should closely relate to the liberated metabolic energy.

2. Three protons are accelerated in electric field during the generation of $ATP$. The interpretation would be in terms of driving of electrons from larger space-time sheet to $k = 137$ atomic space-time sheet. If the larger space-time sheet corresponds to $k = 139$, the increment of the zero point kinetic energy of proton is $(1 - 1/4) \times \times E_0(137) = .375$ eV for $E_0(137) = .5$ eV of metabolic energy quantum. Three protons would give net zero point kinetic energy increment of 1.125 eV which is higher than $\Delta G_{tot} = .73$ eV. The explanation of the discrepancy should relate to Coulomb binding energy of protons with $ATP$ and $F_1$. This interpretation conforms with the observation that the liberated energy is higher for the third proton.

Consider now a more detailed model for the process. The binding of $ATP$ to the catalytic site involves several steps.

Step 1: The binding $ATP + F_1 \rightarrow$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 [I72].

Step 2 Hydrolysis: $F_1\cdot$ATP$\rightarrow F_1\cdot$ADP$\cdot P_i$. The change of free energy is small during this step: $\Delta G \sim 0$.

Step 3: Ortophosphate is released from the catalyst site: $F_1\cdot$ADP$\cdot P_i \rightarrow F_1 \cdot ADP + P_i$. Free energy $\Delta G \sim .31$ eV is liberated at this step.

Step 4: $ADP$ is released from the catalyst site: $F_1\cdot$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 [D8, D4], [I63]. 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 $XMP$s, $X = A, T, C, G$ 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 [K1]. The model is relies on ideas inspired by the model of DNA as topological quantum computer [K12]. In this model hydrogen bonds are assumed to correspond or to be accompanied by (wormhole) magnetic flux tubes. Also flux tubes connecting acceptor atoms or molecules of hydrogen bonds are assumed to be connected long flux tubes and represent genuinely new physics. Examples of acceptors are $O =$ atoms in phosphates and amino-acids and aromatic rings in DNA and also in some amino-acids. The model for protein folding has tight connections with existing chemistry and leads to a very simple criterion for the formation of hydrogen bond between $N-H$ and $O =$ in the constant part of amino-acid and to a proposal for the folding code.

4. DNA as TQC model gives further constraints. The structure of the phospholipids suggest that in the case DNA nucleotides long flux tubes connect the aromatic ring of the nucleotide to the $O =$ atom at the hydrophilic end of the lipid acting as a standard plug which in turn can be connected to another acceptor and eventually terminates to a donor of hydrogen bond. The detailed charge structure of the aromatic ring(s) should determine the quark-nucleotide correspondence. The connection line to the lipid could involve several intermediate $O =$ plugs and the first plug in the series would be the $O =$ atom of the monophosphate of the nucleotide. Not surprisingly, phosphorylation would be absolutely essential for the operation of DNA as topological quantum computer. $O = -O =$ flux tubes could also act as switches inducing a shortcut of the flux tube connection by reconnecting with a hydrogen bond connecting two water molecules. This is an essential step in the model for how DNA acts as topological quantum computer.

A possible model (perhaps the simplest one found hitherto) for the reaction $ATP \to ADP + P_i$ is based on the assumption that it splits a flux tube connection defining strand of a braid defining topological quantum computation. A change of the hardware of topological quantum computer would be therefore in question.

1. Suppose that $ATP$ defines a standard plug in flux tube connections. This would mean that aromatic ring and the oxygen atoms $O = 1$, $O =_2$, and $O =_3$ of the phosphates are connected by magnetic flux tubes to some molecules. These flux tubes represent genuinely new physics in accordance with the fact that "high energy phosphate bonds" are not really understood in the standard chemistry. Suppose that the flux tube associated with $O =_2$ connects it with $O =_3$ and defines the somewhat mysterious high energy phosphate bond. This bond would be formed during cellular breathing and the metabolic energy would go the formation of the magnetic flux tube between $O =_2$ and $O =_3$. Suppose that $O =_1$- the innermost $O$ has a flux tube connecting it to catalyst in this case $F_1$.

2. At Step 1 $F_1$ and $ATP$ molecule would find each other. This would be due to the shortening of the magnetic flux tube connecting them and associated with the innermost phosphate. This would liberate.42 eV of metabolic energy.

3. At Step 2 hydrolysis would induce $F_1 \cdot \mathrm{ADP} \cdot P_i \to F_1 \cdot ADP + P_i$. Since no energy is released at this step, there is temptation to conclude that a reconnection of $O_2 - O_2$ fluc tube and a flux tube associated with catalyst occurs. $ADP$ and $P_i$ fors now a high energy bond with catalyst. the reconnection of $(O =_2) - (O =_3)$ flux tube with the hydrogen bond connecting two water molecules leads to the disappearance of this flux tubes so that the incoming and outgoing the flux tubes are shortcut by $(O =_2) - -H - (OH)$ *resp.* $(O =_3) - -H - (OH)$ hydrogen bonds (connection to ground is the analog in circuit theory). This would correspond in the usual terminology the liberation of the third phosphate: $ATP \to ADP + P_i$. $P_i$ however remains at the end of flux tube to be attached later to another $ADP$. The resulting bonds to water molecules would have low energy and the liberated energy would be usable metabolic energy. In this case the function of the splitting would be purely energetic.

4. One can imagine also a function related to information processing. $P_i$ could be also attached to some other molecule in phosphorylation process so that the outcome would be a reconnection in the web of magnetic flux tubes. Phosphorylation is infeed known to play a key role in activation and deactivation of proteins and in the formation of signal pathways. In

the case of AMP associated with DNA there would be only single flux tube involved and it could connect DNA nucleotide to nuclear or cell membrane.

5. The process involves also hydration. $(OH)^-$ ion joins to the third $P$ to give $P_i^{-3}$ and $H^+$ to $O-P$ in second $P$ to give $H^+-O$ in $ADP^{-1}$. The exchange of electron would lead to the final state $ADP^{-2}+P_i^{-2}$.

A possible model for the dropping of protons would be following.

1. It is absolutely essential to realize that $F_1$ is an open system and that naive thermodynamic considerations can lead to misunderstandings. In particular, the notion of high energy phosphate bond does not make sense. The source of the metabolic energy is the chemical energy used to drive protons to the atomic space-time sheets of $F_1$. The function of the large negative charge of $ATP$ is to increase the rate for the binding of $ATP^{-4}$ to $F_1$. In the classical picture the binding to $F_1$ is followed by the dropping of two protons to larger space-time sheet. The value of the metabolic quantum could be reduced from .5 eV to about .21 eV by the Coulomb energy of proton with $PO^{4-}$. The Coulomb binding energy of the remaining protons at $F_1$ with $ADP+P_i$ is smaller and the dropped proton liberates larger energy about .31 eV. In quantum picture the division of the process to this kind of sequence might not be a good approximation.

2. One function of the $ATP \to ADP$ would be to induce the dropping of the third proton from $F_1$ space-time sheet. Second function would relate to the topological quantum computation like process since the decay would correspond to a splitting of a braid strand coming to the aromatic ring of $A$ and proceeding along string defined by the ring and three $O =:$ s of phosphates and continuing further. This would make possible TQC as a braiding for both halves of the split flux tubes. After the reconnection the total braid structure would be different. Quite generally, reconnection process would make possible to modify the hardware of topological quantum computer.

3. The reason for why $P_i$ leaves the catalyst site and proton is dropped (step 2) should be the in-stabilization of the bound state of positively charged proton with $ADP^{-2}+P_i^{-2}$ which does not have so strong Coulomb interaction energy with proton as $ATP^{-4}$ As a consequence, proton can drop to the larger space-time sheet.

4. What remains open are the details of the transformation of the chemical energy to zero point kinetic energy of protons. Remote metabolism suggests that protons send negative energy phase conjugate photons to the geometric past inducing a transition of an energy carrying molecule to a lower energy state (zero energy ontology gives justification for this picture). This would mean the failure of the standard description in terms of reaction kinetics. The catabolism of nutrients is the eventual provider of the metabolic energy and the coenzyme nicotinamid adenic dinucleotide $NAD^+$ [I19] receives electron and the energy liberated in the catabolic reaction. In the proposed framework it is not an surprising that $NAD^+$ is analogous to RNA dinucleotide (perhaps as remnant from RNA era when dinucleotides defined the 2-codon code) and consists of two phosphates and adenine and nicotinamide nucleosides. The oxidation reaction $NADH \to NAD^+$ in turn liberates this energy. Protons could gain their energy by sending negative energy photons to $NADH$. Negative energy photons would propagate along "topological light rays" parallel to the flux tubes connecting the system in a precisely targeted manner to NADH aromatic rings. Alfven waves propagating along magnetic field lines would be the standard electrodynamics counterpart for these topological light rays.

Many details of the process remain open but it would seem that the key ideas of TGD based quantum vision about living matter are fused together in rather detailed manner in this picture.

*3. Polymerization of DNA and RNA*

The polymerization of RNA and DNA by dehydration involves the fusion of $PO_4H_2^{2-}$ phosphate molecule with ribose. In this process the stub...-O-H of the phosphate ion combines with H-O-C-...

stub of ribose (here C is the carbon atom not belonging to the ribose cycle). This gives rise to..-O-(H-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 de-stabilizes long polymers unless there is a continual feed of protons to the atomic space-time sheets. This could be achieved by irradiation with photons with energy equal to the metabolic energy currency. Situation changes also if water is ordered/structured water, in liquid crystal form, or as ice, and therefore unable to provide the water molecules needed for the hydration. Stabilization of RNA and DNA polymers could be achieved in this manner in gel phase.

Clay structures are known to act as catalyzers of RNA polymerization. The general model of catalysis based on the recombination and $\hbar$ changing transition for magnetic flux tubes should explain also this.

### 3.3.6 Why DNA is stable inside cell nucleus?

Inside membrane bound surface both DNA and RNA nucleotides and polymers are stable. The un-stability of the DNA nucleotides and polymers outside membrane bound surfaces could involve many-sheeted physics.

1. What one expects that DNA transforms to RNA unless it is inside a membrane bound region. A possible reason is that water molecule is needed to transform DNA to RNA but not available inside membrane bound structure where water is structure water in gel phase.

2. In the case of A, G, and C nucleotides DNA$\rightarrow$ RNA transformation means simply an addition of one oxygen atom to the de-oxyribose ring, that is replacement of one C-H with C-O-H. If ordinary water is present this could be achieved by the dissociation of the water molecule to $OH^-$+$H^+$ followed by the replacement of C-H in the de-oxyribose cycle with C-$OH^-$ so that a negative1ly charged ribose results. The outcome is free hydrogen atom. If $H^+$ drops to a larger space-time sheet, the liberated zero point kinetic energy is of order .5 eV. This process is basically the same which should occur when single $ATP$ molecule is utilized in metabolism.

3. In the case of T nucleotide also $CH_3$ group differentiating T from U must be de-attached. This is achieved if the hydrogen atom from the water molecule is taken by the de-attached $CH_3$ group to give $CH_4$ molecule. As a result a negatively charged U results. Inside cell nucleus or in gel phase this process is not favored because the water is in liquid crystal form and it costs energy to take the needed $H_2O$ molecule from it.

## 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 (see **Fig.** `http://tgdtheory.fi/appfigures/cat.jpg` or **Fig. ??** in the appendix of this book) are in order.

1. Ordinary bound states are stable because they have positive binding energy. One can visualize this kind of binding as a jail: the second particle resides near the bottom of a potential well. Organized marriage is a social analogy for this situation. Negentropic entanglement makes possible bound states for which binding energy can have and perhaps even has always a wrong sign. The state is not prevented from decaying to free particles in state function reduction by energy conservation: Negentropy Maximization Principle (NMP) [K22] 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 [K1] 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 (see `http://tinyurl.com/yar7zv7j`) [I12] assigned with the two outer-most phosphates of ATP (see `http://tinyurl.com/clnu4`) [I2] is

fundamental for the basic processes in living matter. The $ATP \to ADP + P_i$ liberates metabolic energy loaded to ATP in the cellular respiration process (see `http://tinyurl.com/yyvrbp`) [I5] or its equivalent and occurs again and again and defines a kind of Karma's cycle in living matter. The phosphate bond is assumed to have a high energy content liberated as $ATP$ is hydrated to ADP (see `http://tinyurl.com/5w7cud`) [I1] and phosphate ion (see `http://tinyurl.com/2xbv3y`) $P_i = PO_4^{3-}$ [I25]. The notion of high energy phosphate bond has been however challenged as being meaningless [D8, D4], [I63].

1. One can of course consider a high energy bond for which the interaction potential looks like a well at the top of mountain and spin glass degeneracy of quantum TGD would certainly allow to consider this kind of notion. I do not know whether models realizing this idea concretely have been really constructed.

2. My earlier proposal for $ATP \to ADP + P_i$ process is inspired by the notion of many-sheeted space-time and p-adic length scale hypothesis making sense in the intersection of real and p-adic worlds and involves the dropping of protons (or electrons) to larger space-time sheets and driven back in oxidative metabolism. The energy liberated in this process corresponds to the zero point kinetic energy of protons (or electrons), which is smaller at the larger space-time sheet. The maximum value of zero point kinetic energy is predicted to be $E_0 \simeq .5$ eV for $k = 137$ in the case of proton and for $k = 148$ in the case of electron (for electron the energy would be by a factor $2^{-11}m_p/m_e \simeq .94$ smaller).

   In many-sheeted space-time particles topologically condense at all space-time sheets having projection to given region of space-time so that this option makes sense only near the boundaries of space-time sheet of a given system. Also p-adic phase transition increasing the size of the space-time sheet could take place and the liberated energy would correspond to the reduction of zero point kinetic energy. Particles could be transferred from a portion of magnetic flux tube portion to another one with different value of magnetic field and possibly also of Planck constant $h_{eff}$ so that cyclotron energy would be liberated. In the following only the "dropping" option is discussed.

3. With an inspiration coming from DNA as topological quantum computer model [K12] 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 [K12, K1]. 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 [K28] raises the question whether these high energy states could be made possible by the presence of negentropic bonds- most naturally associated with the flux tubes with large $\hbar$. This love marriage would stabilize $ATP$, $ADP$, and DNA and other charged biomolecules. The presence of phosphates would be a clear-cut signature of this stabilization mechanism. Also proteins involve phosphates playing a key role in the bio-control: typically phosphorylation activates or de-actives the protein and is also involved with the generation of signal pathways. Why this happens would be easy to understand in Indra's net model.

5. In $ATP \to ADP + P_i$ transformation the energy carried by the negentropic bonds would be liberated but leave the flux tube bonds negentropic. Cell respiration would take care of

the loading of the batteries with negentropic metabolic energy. This would involve also the kicking of protons back to the smaller space-time sheets. Also the molecular lovers $ADP$ and $P_i$ would find each other again as the Planck constant for the flux tube connecting them would be reduced during the cellular respiration transform $ADP$ and $P_i$ back to $ATP$.

### 3.4.3 Quantitative estimates

Consider now a more detailed model for $ATP \to ADP + P_i$. The binding of $ATP$ to the catalytic site involves several steps. I have described them in the previous section and in the following add to this template the interpretation suggested by the proposed picture.

1. **Step 1** : The binding $ATP + F_1 \to ATP \cdot F_1$ to the catalyst site is a complex process involving the break-up of the hydrogen bonds between cellular water and ATP molecule and cell water and catalyst site and generation of hydrogen bonds between catalyst site and $ATP$ molecule. In TGD framework this means that protons can be kicked to and dropped back from atomic space-time sheets. Only the net number of protons dropped however matters.

   This process involves a liberation of Gibbs free energy per single attachment, which is about $\Delta g_{ATP} = .42$ eV. It was earlier believed that this energy is liberated instantaneously but the findings about the behavior of the $F_1$ motor coupled to dissipative load, lead Oster and Wang to suggest that the process is more complex and starts from a loose binding and ending up to a strong binding [I72].

   *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 $\Delta e$. 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 $\Delta e$ is now smaller than $\Delta G$, 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: $F_1 \cdot ADP + P_i \to F_1 + ADP + P_i$. $\Delta G \sim 0$ 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 $P_i$s or $F_1$s. 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 [I34, I36, I46, I47] 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 [J5]. 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 [I46]. 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 [I47], [J5].

This picture might apply be the case also in the case of water memory.

1. The shaking might drop some fraction of antigene molecules to dark space-time sheets where they generate a dark color magnetic field. Because of the large value of Planck constant super-conductivity along color flux tubes running from molecular space-time sheets could still be present.

2. TGD based model of super conductivity involves double layered structures with same p-adic length scale scale as cell membrane [K4]. 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) [I47].

### 3.5.3 Why experimenter had to know which bottle contained the treated water?

Why experimenter had to know which bottle contained the treated water? The role of experimenter eliminates the possibility that the (magnetic bodies of) clusters of water molecules able to mimic the (magnetic bodies of) antigene molecules electromagnetically are present in the solution at geometric now and produce the effect. The earlier explanation for experimenter's role was based on the idea that memory storage requires metabolic energy and that experimenter provides it. The vision about living matter as topological quantum computer (TQC) suggests a variant of this model in which experimenter makes possible the recall of memories of water represented as braiding patterns and realized via TQC.

*1. Does experimenter provide the metabolic energy needed to store the memories of water?*

What could be then the explanation for the failure of the modified experiment? Each memory recall reduces the occupation of the states representing bit 1 and a continual metabolic energy feed is needed to preserve the bit sequence representations of antibodies using laser light systems as bit. This metabolic energy feed must come from some source.

By the universality of metabolic energy currencies population inverted many-sheeted lasers in living organisms define the most natural source of the metabolic energy. Living matter is however fighting for metabolic energy so that there must be some system willing to provide it. The biological bodies of experimenters are the best candidates in this respect. In this case experimenters had even excellent motivations to provide the metabolic energy. If this interpretation is correct then Benveniste's experiment would demonstrate besides water memory also psychokinesis and direct action of desires of experimenters on physics at microscopic level. Furthermore, the mere fact that we know something about some object or direct attention to it would mean a concrete interaction of our magnetic with the object.

*2. Does experimenter make possible long term memory recall?*

The alternative explanation is that experimenter makes possible long term memory recall which also requires metabolic energy.

1. If braiding pattern represents, the water memory the situation changes since the robustness of the braiding pattern suggests that this representation is still in the geometric past (which is replaced with a new one many times). If the dark variants of molecules created in the process are still in the water, the braid representation of water memories could be available even in the geometric now but it is better to not make this assumption. The challenge is to understand how this information can be made conscious.

2. What is certainly needed is that the system makes the TQC again. This would mean a fractal quantum jump involving unitary $U$ process and state function reduction leading to the generation of generalized EEG pattern. Only the sums and differences of cyclotron frequency and Josephson frequency would matter so that the details of the flow inducing braiding do not matter. The shaking process might be continuing all the subjective time in the geometric past so that the problem is how to receive information about its occurrence. Experimenter might actually help in this respect since the mechanism of intentional action initiates the action in the geometric past by a negative energy signal.

3. If the magnetic body of the water in the geometric now can entangle with the geometric past, TQC would regenerate the experience about the presence of antigene by sharing and fusion of mental images. One can however argue that water cannot have memory recall in this time scale since water is quite simple creature and levels with large enough $\hbar$ might not be present. It would seem that here the experimenter must come in rescue.

4. The function of experimenter's knowledge about which bottle contains the homeopathic solution could be simply to generate time-like entanglement in the required long time scale by serving as a relay station. The entanglement sequence would be *water now - experimenter now - water in the past* with "now" and "past" understood in the geometric sense. The crucial entanglement bridge between the magnetic body of water and experimenter would be created in the manufacturing of the homeopathic remedy.

   Note that this explanation does not exclude the first one. It is quite possible that experimenter provides also the metabolic energy to the bit representation of water memories possibly induced by the long term memory recall.

This picture is of course just one possible model and cannot be taken literally. The model however suggest that magnetic bodies of molecules indeed define the braiding; that the generalized EEG provides a very general representation for the outcome of TQC; that liquid flow provides the manner to build TQC programs - and also that shaking and sudden pulses is the concrete manner to induce visible-dark phase transitions. All this might be very valuable information if one some day in the distant future tries to build topological quantum computers in laboratory.

## 3.6 How Bio-Polymers Were Associated With Their Dark Counterparts?

The experiments of Pollack [L7] demonstrating what he calls fourth phase of water is characterized by negatively charged regions - exclusion zones (EZs). The stoichiometry of water inside EZ is

$H_{1.5}O$. TGD based model assumes that part of protons in these regions have been transferred to to magnetic flux tubes were they form sequences identifiable as dark nuclei. The surprising finding is that a simple model for dark proton allows to assign its states to multiplets for which numbers of states are those assignable to DNA, RNA, and tRNA codons, plus amino-acids. Also the vertebrate genetic code can be realized in a simple manner. This leads to a vision about prebiotic life as dark life evolved in water before the ordinary life. Dark life would be present also in ordinary life forms.

If one believes that dark proton sequences [K18] define the counterparts of DNA, RNA, tRNA, and amino-acids realized at magnetic flux tubes, the question is how this form of life was transformed to the bio-chemical life.

The article "Hydrogen cyanide polymers, comets and the origin of life" (`http://tinyurl.com/ybfuwneq`, thanks to Ulla for the link) helped me to discover a new big gap in my knowledge about biology and this in turn led to a more detailed vision about how the transition could have taken place. HCN is everywhere and Miller demonstrated in his classic experiments that 11 out of 20 amino-acids emerged in presence of HCN. It has been later found that well over 20 amino-acids were produced. (`http://tinyurl.com/y9at46fe` ). In my own belief system amino-acids could have appeared first as concrete something "real" and DNA as symbolic representations of this something "real". First at dark matter level and then biochemically.

In TGD Universe one can imagine - with inspiration coming partially from Pollack's experiments [L7] (`http://tinyurl.com/oyhstc2` ) - that dark variants DNA, RNA and amino-acids were realized first as dark proton sequences at flux tubes- dark nuclei - I call them just dark DNA, RNA and amino-acids although dark proton sequences are in question. The genetic machinery involving translation and transcription was realized as dark variant and dark DNA was a symbolic representation for dark amino-acids.

How did this dark life give rise to bio-chemical life as its image? This is the question! I can only imagine some further questions.

1. Was this process like master teaching to a student a skill? Master does it first, and then student mimics. If so, the emergence of amino-acids, mRNA and DNA polymers would *not* have been purely chemical process. Dark variants of these polymers would have served as templates for the formation of ordinary basic biopolymers, for transcription, and for translation. These templates might have been necessary in order to generate long RNA and DNA sequences: mere chemistry might have not been able to achieve this. Without dark polymers one obtains only bio-monomers, with dark polymers as template one obtains also bio-polymers. Dark polymers would have been the plan, biopolymers the stuff used to build.

2. Are dark DNA, RNA, amino-acids, etc indeed still there and form binary structures with their biochemical variants as I have indeed proposed?

3. Are dark translation and transcription processes still an essential part of ordinary translation and transcription? Master-student metaphor suggest that these dark processes actually induce them just like replication of magnetic body could induce the replication of DNA or cell. Visible chemistry would only make visible the deeper "dark chemistry". Apologies for all biochemists who have done heroic work in revealing chemical reaction paths!

How the process assigning biochemical life to dark life could have proceeded? The minimalistic guess is that the only thing that happened was that dark life made itself gradually visible! As a consciousness theoretician I have a temptation to see religious statements as hidden metaphors, at least they provide an excellent manner to irritate skeptics: Dark matter - the "God" made us- the biological life - to its own image.

1. First dark amino-acid sequences were accompanied by ordinary amino-acid sequences so that the dark translation process had now a visible outcome. At this step the presence of HCN was crucial and made the step unavoidable. Also the presence of template was necessary.

2. Dark mRNA got a visible counterpart in the same manner: the presence of template made possible long RNA polymers. The translation remained basically dark process but made visible by mRNA.

3. Dark DNA got a visible companion: again the presence of the template was - and still is - crucial.

What about generation of DNA and RNA? It is known that in reducing atmosphere DNA and RNA nucleobasis are obtained in an environment believed to mimick prebiotic situation: the presence of HCN and ammonia are necessary (http://tinyurl.com/y9at46fe ). Reducing atmosphere http://tinyurl.com/yc62g22f does not oxidize, in other worlds does not contain oxygen and other oxidizing agents and can contain also actively reducing agents such as hydrogen, carbon monoxide. There are however some problems.

1. There is evidence that early Earth atmosphere contained less reducing molecules than thought in times of Miller. If life emerged in the underground water reservoirs as TGD strongly suggests, the usual atmosphere was absent and there are good hopes about reducing atmosphere.

2. The experiments using reducing gases besides those used in Miller's experiments produce both left and right handed polymers so that chiral selection is missing. This is not a surprise since weak interactions generate extremely small parity breaking for visible matter. If dark proton strings or even dark nuclei are involved, the Compton length of weak gauge bosons can be of the order of atomic length scale or even longer and weak interactions would be as strong as electromagnetic interactions. Therefore chiral selection becomes possible. The simplest option is that chirality selection occurred already for the helical magnetic flux tubes and induced that of biopolymers.

## 3.7 Two steps towards understanding of the origins of life

Two highly interesting findings providing insights about the origins of life have emerged and it is interesting to see how they fit to the TGD inspired vision.

The group led by Thomas Carell has made an important step in the understanding the origins of life. They have identified a mechanism leading to the generation of purines A and G which besides pyrimidines A,T (U) are the basic building bricks of DNA and RNA. The crucial step is to make the solution involved slightly acidic by adding protons. For year later I learned that a variant of Urey-Miller experiment with simulation of shock waves perhaps generated by extraterrestrial impacts using laser pulses generates formamide and this in turn leads to the generation of all 4 RNA bases.

These findings represent a fascinating challenge for TGD inspired quantum biology. The proposal is that formamide is the unique amide, which can form stable bound states with dark protons and crucial for the development of life as dark matter-visible matter symbiosis. Pollack effect would generate electron rich exclusions zones and dark protons at magnetic flux tubes. Dark protons would bind stably with unique amine leaving its chemical properties intact. This would lead to the generation of purines and the 4 RNA bases. This would be starting point of life as symbiosis of ordinary matter and dark matter as large $h_{eff}/h = n$ phases of ordinary matter generated at quantum criticality induced by say extraterrestrial impacts. The TGD based model for cold fusion and the recent results about superdense phase of hydrogen identifiable in TGD framework as dark proton sequences giving rise to dark nuclear strings provides support for this picture.

There is however a problem: a reductive environment (with ability to donate electrons) is needed in these experiments: it seems that early atmosphere was not reductive. In TGD framework one can imagine two - not mutually exclusive - solutions of the problem. Either life evolved in underground oceans, where oxygen concentration was small or Pollack effect gave rise to negatively charged and thus reductive exclusion zones (EZs) as protons were transferred to dark protons at magnetic flux tubes. The function of UV radiation, catalytic action, and of shock waves would be generation of quantum criticality inducing the creation of EZs making possible dark $h_{eff}/h = n$ phases.

### 3.7.1 The first step: binding of dark protons to formamido-pyrimidine

I learned about very interesting discovery related to the problem of understanding how the basic building bricks of life might have emerged. RNA (DNA) has nucleotides A,G,C,U (T) as basic building bricks.

The first deep question is how the nucleotides A,G,C,U, and T emerged.

1. There are two types of nucleotides. Pyrimidines C and T/U (see http://tinyurl.com/k3vxl9b) have single carbon 6-cycle. Purines A and G (see http://tinyurl.com/odvqw2p)

in turn have single 6-single and 5-cycle fused attached together along one side. Purines are clearly more complex than pyrimidines.

2. U.K. chemist John Sutherland demonstrated a plausible sequence of steps leading to the emergence of pyrimidines. Purines turned out to be more problematic. Leslie Orgel and colleagues suggested a possible pathway but it produces purines in too tiny amounts.

Now a group led by Thomas Carell in Ludwig Maximilian University have found a more plausible mechanism [I48] (see `http://tinyurl.com/z65kpyo`).

1. Carell and colleagues studied the interaction of biomolecule formamido-pyrimidine (FaPy) with DNA and found that it also reacts to produce purines. Could FaPys have served as predecessors of purines? (For formamide see `http://preview.tinyurl.com/lwqyqnu` and for the class of chemical compounds known as amines see `http://tinyurl.com/mad6c2u`).

2. The first step would have been a copious production of amino-pyrimidines containing several chemical groups known as amines. The problem is that the are so many amines and they normally react indiscriminantly to produce many different compounds. One wants mostly purines so that only one critical amine is wanted.

3. When Carell and his team added some acid to the solution to decrease its pH, a miracle happened. The extra protons from acid attached to the amines of the amino-pyrimidine and made them non-reactive. There was however one exception: just the amine giving rise to purine in its reactions! The reactive amine also readily bonded with formic acid acid (see `http://tinyurl.com/lmstt7n`) or formamide. Hence it seems that one big problem has been solved.

The second challenge is to understand how the building bricks of RNA and DNA combined to form longer polymers and began to replicate.

1. One prevailing vision is that so called RNA world preceded the recent biology dominated by DNA. The goal has been to achieve generation of RNA sequence in laboratory. Unlike DNA RNA sequences are not stable and long sequences are difficult to generate. DNA in turn replicates only inside cell and the presence of what is known as ordered water seems to be essential for this.

2. This step might involve new physics and chemistry and I have considered the possibility that the new physics involves magnetic bodies and dark proton sequences as a representation of the genetic code at the level of dark nuclear physics. There is no need to add that the fact that dark proton states provide representations for RNA, DNA, tRNA, and amino-acids [K18, L2] looks like a miracle and I find still difficult to believe that it is true and for genetic code. Also the representation of vertebrate code emerges in terms of correspondences of dark proton states.

   This suggests that the replication of DNA and takes place at the level of dark proton sequencies - dark nuclear strings - serving as a dynamical template for the biological replication. Also transcription and translation would be induced by dark process. Actually all biochemical processes could have as template the dynamics of molecular magnetic bodies and biochemistry would be kind of shadow of deeper dynamics.

3. There is actually support for dark proton sequences. Quite recently I learned about the article of Leif Holmlid and Bernhard Kotzias [L13] (see `http://tinyurl.com/hxbvfc7`) about the superdense phase of hydrogen. In TGD superdense phase has interpretation as dark proton sequences at magnetic flux tubes with the Compton length of dark proton coded by $h_{eff}/h \simeq 2^{11}$ to electron's Compton length [L8]. Remarkably, it is reported that the superdense hydrogen is super-conductor and super-fluid at room temperatures and even above: this is just what TGD predicts.

   The dark protons in TGD inspired quantum biology [L9] should have much longer Compton length of order of the distance between nucleotides in DNA sequences in order to serve as templates for chemical DNA. This gives a dark Compton length of order $\simeq 3.3$ Angstroms from the fact that there are 10 codons per 10 nm. This gives $h_{eff}/h \simeq 2^{18}$.

One can return back to the first step in the genesis of DNA and RNA. The addition of protons to the solution used to model prebiotic environment to make it slightly acidic was the key step. Why?

1. Here cold fusion might help. Cold fusion is claimed to take place in electrolysis involving ionization and charge separation. The electric fields used in electrolysis induce ionization and thus charge separation. For me it has however remained a mystery how electric fields, which are extremely tiny using the typical strength of molecular electric field as standard are able to induce a charge separation. Of course, every chemist worth of his salt regards this as totally trivial problem. I am however foolish enough to consider the possibility that some new physics might be involved.

2. The mechanism causing charge separation could be analogous to or that discovered by Pollack as he irradiated water bounded by a gel phase [L7] [L7]: in the recent case the electric field would take the role of irradiation as a feeder of energy. Negatively charged exclusion zones (EZs) were formed and 1/4 of protons went somewhere.

   The TGD proposal is that part of protons went to magnetic flux tubes and formed dark proton sequences identifiable as dark nuclear strings. The scaled down nuclear binding energy favours the formation of dark nuclear strings perhaps proceeding as analog of nuclear chain reaction. This picture allows to ask whether dark proton sequences giving rise to a fundamental representation of the genetic code could have been present already in water [L9]!

3. How DNA/RNA could have then formed? Could the protons making the solution acidic be dark so that the proton attaching to the amine would be dark? Could it be that for all amines except the right one the proton transforms to ordinary proton and destroys the chemical reactivity. Could the attached dark proton remain dark just for the correct amine so that the amine would remain reactive and give rise to purine in further reactions? Could A,G,C,T and U be those purines and pyrimidines - or even more general biomolecules - for which the attachment to dark proton does not transform it to ordinary proton and in this manner affect dramatically the chemical properties of the molecule? What is the condition for the preservation of the darkness of the proton?

### 3.7.2 Second step: Could shock waves due to extraterrestrial impacts have produced RNA bases?

About year later I learned about a further interesting finding related to the prebiotic evolution (see the popular article at `http://tinyurl.com/m8npeor`). The conclusion of the research article (see [I51]) is that that the extraterrestrial impacts on Earth's early atmosphere might have generated all 4 RNA bases (see `http://tinyurl.com/kxxc7db`). Also now the formamide is involved and my layman guess is that the motivation for this comes from the experiment of Carell et al [I48] (see `http://tinyurl.com/z65kpyo`) discussed above. If formamide is generated then it becomes possible to generate formamido-pyridine and from this the RNA bases can be generated.

The experiment was a modern version of Urey-Miller experiment originally intended to simulate the situation at the surface of the early atmosphere modelled as a mixture a water $H_2O$, carbon-monoxide CO, and ammonium $NH_3$. The shock waves generated by the impacts were modelled in the experiment using terawatt laser pulses.

In the original Urey-Miller experiment amino-acids were generated. In the modern version of the experiment it was found that also formamide $CONH_3$ is formed, whose presence under suitable circumstances can lead to the generation of all 4 RNA bases. The presence of UV radiation, shock waves caused by extraterrestrial collisions, or of catalyst is the necessary condition.

In TGD Universe the additional condition could guarantee quantum criticality accompanied by dark $h_{eff}/h = n$ phases leading to the generation of dark protons and their stable binding with formamido-pyrimidine. The stable binding would not be possible for other amido-pyrimidines since dark protons would transform to ordinar protons for them. All 4 RNA bases would emerge from formamido-pyrimidine. All basic molecules of life could be produced in the reductive atmosphere.

The atmosphere was assumed to be reductive and this is a problem: the best that one can hope is that the early atmosphere was weakly reductive. Chemical compound is reductive (see `http://tinyurl.com/m9cqnob`) if it tends to donate electron. Reduction means receiving electron - and in

chemistry hydrogen atom. To obtain a reducing atmosphere (see http://tinyurl.com/lx4tat2) one should remove oxygen from it. It however seems that the early atmosphere has contained oxygen and was oxidative rather than reductive. How could one overcome the problem?

1. In the experiment of Carell et al protons were added to reduce the pH of water. The basic experimental rule is that this makes the environment more reductive. The TGD proposal is that it led to a formation of dark proton-amine pair for the amine leading to the formation of purine. Charge separation by Pollack effect [L7] [L9] leading to the generation of dark proton sequences (dark nuclei) at magnetic flux tubes could have been due to the IR radiation, and maybe also by UV radiation, catalytic action, or by shock waves. The presence of electrons in the exclusion zones (EZs) could have made them electron donors and therefore reductive.

   The addition of protons in the experiment of Carell reducing the pH of water could have induced a transformation of dark protons at magnetic flux tube to ordinary protons. Dark protons bound to the amines would have transformed to ordinary protons and inducing their chemical inactivity. Only for the amine formamide serving as a precursor of purine the dark proton-amine bound state was stable and remained chemically reactive since dark proton did not affect the properties of visible matter part of the compound. Symbiosis between dark and ordinary matter began. This view conforms also with the vision about the pairing of DNA/RNA and dark DNA/RNA formed by sequences of proton triplets representing DNA/RNA codons [L10]. DNA is indeed negatively charged and dark proton could neutralize it but allow it to remain chemically active.

2. Second possibility is suggested by the conjecture that prebiotic life evolved in the crust of Earth, perhaps in the underground oceans or regions related to volcanoes [K15, L9]. The content of oxygen of this environment could have been much lower than at the surface making it reductive: it would not be possible to even talk about atmosphere. But where did the metabolic energy come from? Could volcanic energy emitted as dark long wave photons with energies in the range of bio-photon energies help here? There are indeed a theories assuming that first life forms emerged from volcanoes. These problems are discussed in [K15, L9] from TGD viewpoint. Note that these two explanations do not exclude each other.

## 3.8 Could the replication of mirror DNA teach something about chiral selection?

I received a link to a very interesting popular article (see http://tinyurl.com/zqgutdv) from which I learned that short strands of mirror DNA and mirror RNA - known as aptamers - have been be produced commercially for decades - a total surprise to me. Aptamers bind to targets like proteins and block their activity and this ability can be utilized for medical purposes.

Now researchers at Tsinghua University of Beijing have been able to create a mirror variant of an enzyme - DNA polymeraze - catalyzing the transcription of mirror DNA to mirror RNA also replication of mirror DNA [I84]. What is needed are the DNA strand to be replicated or transcribed, the mirror DNA nucleotides, and short primer strand (see http://tinyurl.com/j3o8cyx)) since the DNA polymeraze starts to work only if the primer is present. This is like recalling a poem only after hearing the first few words.

The commonly used DNA polymerase containing about 600 amino-adics is too long to be built up as a right-handed version and researchers used a much shorter version: African swine fever virus having only 174 amino-acids. The replication turned out to be very slow. A primer of 12 nucleotides was extended to a strand of 18 nucleotides in about 4 hours: 3/2 nucleotides per hour. The extension to a strand of 56 nucleotides took 36 hours making 44/36= 11/9 nucleotides per hour. DNA and its mirror image co-existed peacefully in a solution. One explanation for the absence of mirror life is that the replication and transcription of mirror form was so slow that it lost the fight for survival. Second explanation is that the emergence of mirror forms of DNA polymerase and other enzymes was less probable.

Can one learn anything about this?

1. Chiral selection is one of the deep mysteries of biology. Amino-acids are left-handed and DNA and RNA double strands form a right-handed screw. One can assign handedness with

individual DNA nucleotides and with DNA double strand but web sources speak only about the chirality of double strand. If the chirality of the DNA nucleotides were not fixed, it would have been very probably discovered long time ago as an additional bit doubling the number of DNA letters.

2. What could be the origin of the chirality selection? Second helicity could have been loser in the fight for survival and the above finding supports this: fast ones eat the slow ones like in market economy. There must be however a breaking of mirror symmetry. Weak interactions break of mirror symmetry but the breaking is extremely small because the weak bosons mediating weak interaction are so massive that the length scale in which the breaking of mirror symmetry matters is of order 1/100 times proton size. This breaking is quite too small to explain chiral selection occurring in nano-scales: there is discrepancy of 8 orders of magnitude. The proposal has been that the breaking of mirror symmetry has been spontaneous and induced by a very small seed. As far as I know, no convincing candidate for the seed has been identified.

According to TGD inspired model chiral selection would be induced from that in dark matter sector identified in terms of phases of ordinary matter with non-standard value of Planck constant $h_{eff}/h = n$ [K36, K37]. In living matter dark matter would reside at magnetic flux tubes and control ordinary matter. TGD predicts standard model couplings, in particular weak parity breaking. For $h_{eff}/h = n$ the scale below which weak bosons behave as massless particles implying large parity breaking is scaled up by $n$. Large parity breaking for dark matter becomes possible in even biological length scales for large enough $h_{eff}$.

The crucial finding is that the states of dark proton regarded as part of dark nuclear string can be mapped naturally to DNA, RNA, tRNA, and amino-acid molecules and that vertebrate genetic code can be reproduced naturally [K18]. This suggests that genetic code is realized at the level of dark nuclear physics and induces its chemical variant. More generally, biochemistry would be kind of shadow of dark matter physics. A model for dark proton sequences and their helical pairing is proposed and estimates for the parity conserving and breaking parts of $Z^0$ interaction potential are deduced.

### 3.8.1 Dark matter and chirality selection

In TGD framework the hierarchy of Planck constants suggests an explanation for the chirality selection.

1. In TGD Universe the new physics of quantum biology involves magnetic bodies and dark proton sequences as a representation of the genetic code at the level of dark nuclear physics. The crucial observation is that dark proton states provide representations for RNA, DNA, tRNA, and amino-acids [K18, L2] and there is also natural map between DNA and amino-acid type states giving rise to vertebrate genetic code. This looks like a miracle and I find still difficult to believe that it is true. A The extreme slowness of the wrong-handed DNA replication as compared to the ordinary replication means large breaking of parity symmetry. This is possible to understand in terms of weak interactions only if they are dark in DNA length scales so that weak bosons are effectively massless and weak interactions are as strong as electromagnetic interactions.

   This suggests that the replication of DNA and takes place at the level of dark proton sequencies - dark nuclear strings - serving as a dynamical template for the biological replication. Also transcription and translation would be induced by dark processes. Actually all biochemical processes could have as template the dynamics of molecular magnetic bodies and biochemistry would be kind of shadow of dark matter physics.

   If this is the case, then chiral selection would take place the selection at the level of dark nuclear strings and induce that the level of biochemistry. If dark and ordinary chiralities fit together like hand and glove. Dark matter at magnetic bodies could control the behavior of ordinary matter. By parity breaking the dark weak binding energy between members of proton pairs in the dark DNA strand consisting of a pair of helical dark proton strings is higher for the second helical chirality and would favour this chirality. A very naive thermodynamical

estimate is that the ratio of the densities of two chiralities is proportional to the Boltzmann exponent $exp(-\Delta E_B/T)$. The transition to thermodynamical equilibrium can be however very slow so that thermodynamical argument need not make sense.

2. There is experimental support for dark proton sequences. Leif Holmlid and Berhard Kotzias [L13] (see `http://tinyurl.com/hxbvfc7`) have published an article about the superdense phase of hydrogen proposed to make possible to overcome the Coulomb wall making cold fusion impossible in the textbook Universe. In TGD superdense phase has interpretation as dark proton sequences at magnetic flux tubes with the Compton length of dark proton coded by $h_{eff}/h = n_{eff} \simeq 2^{11}$ to electron's Compton length [L8]. Remarkably, it is reported that the superdense hydrogen is super-conductor and super-fluid at room temperatures and even above: this is just what TGD predicts.

   The dark protons in TGD inspired quantum biology (see `http://tinyurl.com/lwxdl7y`) should have much longer Compton length of the order of the distance between nucleotides in DNA sequences in order to serve as templates for chemical DNA. This gives a dark Compton length of order $\simeq 3.3$ Angstroms from the fact that there are 10 codons per 10 nm. This would give $n_{eff,p} \simeq 2^{18}$. The safest manner to estimate the dark binding energy is by scaling the binding energy about $E_B \simeq 7$ MeV per nucleon by $1/n_{eff,p}$ to give $E_{B,d} = E_B/n_{eff,p} = 28$ eV.

3. Further evidence for the importance of dark protons in biology comes from the recent finding of the group led by Thomas Carell related to the understanding the origins of life [I48] (see `http://tinyurl.com/z65kpyo`). For TGD inspired model see [L12], [K14]. Carell et al have identified a mechanism leading to the generation of purines A and G, which besides pyrimidines A,T (U) are the basic building bricks of DNA and RNA. The crucial step is to make the solution involved slightly acidic by adding protons.

   In TGD inspired quantum biology this suggest that the protons in the acidic water are dark and that the attachment of the dark protons to the amines of the amino-pyrimidine transforms them to ordinary protons and makes the amino-pyrimidine non-reactive. There would be however one exception: the amine which reacts further to give purines as a reaction product. In this case the proton would remain dark and the chemical properties of the amine would remain intact. This suggests that DNA nucleotides and DNA strands can attach to dark protons or are accompanied by them.

### 3.8.2 Model for the replication of DNA

One can consider a detailed model for the replication as induced by the addition of dark protons to dark proton sequence representing dark DNA strand. The added dark protons would be accompanied or attached with the DNA nucleotides as suggested by the work of Carell et al.

1. In the replication and transcription of DNA the basic step would be the addition of dark proton to an increasing dark proton sequence. The need for primer means that there must already exist a dark proton sequence. In the presence of prime the attractive dark nuclear binding energy of the added dark proton with the prime would make the dark fusion rate higher. The addition of dark protons could proceed like a dark nuclear chain reaction. It would be made possible by the dark nuclear binding energy per proton scaling like $1/h_{eff,p}$.

   For the ordinary nuclei the binding energy per nucleon would be of the order of 7 MeV (note that charge independence of strong interactions holds in good approximation). The scaling down by $h_{eff}/h = 2^{18}$ would give $E_B \simeq 4$ eV, which corresponds to UV photon energy. Note that bio-photons assumed to correspond dark photons with same energy have energies in visible and UV range.

2. Dark nuclear energy cannot explain parity breaking. The axial part of dark weak energy between dark protons belonging to dark strand and its conjugate and having nuclei acids and its conjugate as a chemical "shadow" must be also involved. Two values of $h_{eff}$ are involved: $h_{eff,p}$ assignable to the flux tubes containing dark protons parallel to DNA strands and $h_{eff,W}$ assignable to the transversal flux tube connecting dark protons associated with different dark strands.

One of the assumptions of the TGD inspired model of cold fusion [L8, L13] is that the weak scale is scaled up from weak boson Compton length to about atomic length scale. This would require $h_{eff,W}/h = n_{eff,W}$ for weak bosons to be roughly

$$n_{eff,W} \simeq \frac{m_Z}{m_p} \times n_{eff,p} \simeq 91 \times n_{eff,p}$$

so that one would have $n_{eff,W} \simeq 2^{25}$. If this is the case weak interactions are of essentially same strength as em interaction below the scaled up Compton scale of order 3 Angstroms. This makes it possible to talk about classical $Z^0$ Coulomb potential and about spin dependent parity breaking $Z^0$ force. These two interaction energies sum up and this reduces the binding energy per proton in double strand for the other chirality.

3. The parity conserving $Z^0$ Coulomb interaction energy between two protons at different strands connected by a flux tube is given by the expression

$$\begin{aligned} & V_{PC}(r_{12}) = -kV(r_{12}) \ , \quad V(r_{12}) = \tfrac{\hbar}{r_{12}} \ , \\ & k = \alpha_Z Q_Z^2(p) \ , \qquad\qquad \alpha_Z = \tfrac{\alpha}{sin^2(\theta_W)cos^2(\theta_W)} \ , \quad Q_Z(p) = 1/4 - sin^2(\theta_W) \ . \end{aligned} \tag{3.2}$$

Here units $\hbar = 1$, $c = 1$ are used. $r_{12}$ refers to the distance between dark protons at magnetic flux tubes assignable to DNA strands. Base pair thickness is about .34 nm and thickness of DNA double strand is about 2 nm. $r_{12}$ could be between these two limits.

4. The spin dependent and parity non-conserving $Z^0$ interaction potential for Dirac spinors proportional to the gradient of the $Z^0$ Coulomb potential can be written as

$$V_{PNC} \quad = \quad \alpha_Z Q_Z^A(p) Q_Z^V(p) \gamma_5 V(r_{12}) \ . \tag{3.3}$$

Here $Q_Z^A = I_{3,A}/2 = 1/4$ is the axial weak charge of proton. The vectorial charge of proton is $Q_Z(p) = 1/4 - sin^2(\theta_W) \simeq 0.02$ so that it is much smaller than $Q_Z^A(p)$. Hence the axial force dominates by a factor $10^2/8 \sim 12.5$ for a given relative position. Usually the axial part becomes very small by symmetries as one estimates quantum averages but in the recent situation one cannot expect this since the positions of dark protons are in the first approximation fixed.

5. Using non-relativistic correspondence following from $\gamma_5 = \gamma_0\gamma_1\gamma_2\gamma_3$ and $(\gamma_5)^2 = -1$: this equation holds true also for $(\gamma^0\gamma^k p_k(m)$, and one has

$$\gamma_5 \to \frac{\overline{\sigma} \cdot p}{m_p} \ .$$

Here $\overline{\sigma}$ denotes Pauli sigma matrices expressible as $\gamma^0\gamma^i$). Using the replacement $p \leftrightarrow i\hbar_{eff,W}\nabla$ one can write $V_{PNC}$ as the sum of the axial energies of the two protons

$$\begin{aligned} V_{s_1,s_2} \quad &= \quad V_{s_1} + V_{s_2} \ , \\ V_{s_i} \quad &= \quad \frac{\hbar_{eff,W}}{m_p}\overline{\sigma}_i \cdot \nabla_i V_{PC}(r_{12}) = (-1)^i \frac{k n_{eff,W}\hbar}{m_p}\hbar\frac{\overline{\sigma}_i \cdot \overline{r}_{12}}{r_{12}^2} \ . \ i = 1,2 \ . \end{aligned} \tag{3.4}$$

The parity breaking part of $Z^0$ force is proportional to $n_{eff,W}$ from the expression of momentum operator in terms of gradient operator so that dark matter physics makes itself visible

and increases further the magnitude of parity breaking. The potential energy changes sign in reflection $\overline{r}_{12} \to -\overline{r}_{12}$. This gives

$$\begin{aligned} V_{s_1,s_2} &= -\frac{\alpha_Z}{4}(\frac{1}{4} - sin^2(\theta_W))\frac{n_{eff,W}\hbar}{m_p r_{12}}\frac{(\overline{\sigma}_1 - \overline{\sigma}_2)\cdot\overline{r}_{12}}{r_{12}}\frac{\hbar}{r_{12}} \\ &= \frac{1}{4}\frac{1}{(\frac{1}{4} - sin^2(\theta_W)}\frac{n_{eff,W}\hbar}{m_p r_{12}}\frac{(\overline{\sigma}_1 - \overline{\sigma}_2)\cdot\overline{r}_{12}}{r_{12}}V_{PC}(r_{12}) \ . \end{aligned} \tag{3.5}$$

6. For the vectorial part one has

$$V_{PC} = -\alpha_Z(\frac{1}{4} - sin^2(\theta_W))^2 V(r_{12}) \ . \tag{3.6}$$

   The order of magnitude is about $V_Z = .16/x$ eV.

7. The condition that $r_{12}$ corresponds to dark Compton length of proton implies in the first approximation $\frac{n_{eff,p}}{m_p r_{12}} = 1$ so that $n_{eff,W}$ proportionality gives factor $m_Z/m_p \simeq 91$. The order of magnitude parity breaking potential is the value potential at distance in the range $r_{12} \in [3.4, 2]$ nm. Let us expres the horizontal distance between the paired dark protons as $r_{12} = x$ Angstroms. This gives for the axial part

$$\begin{aligned} V_{s_1,s_2} &= \frac{1}{4}\frac{1}{(\frac{1}{4} - sin^2(\theta_W)}\frac{m_Z}{m_p}(\overline{\sigma}_1 - \overline{\sigma}_2)\cdot\frac{\overline{r}_{12}}{r_{12}}V_{PC}(r_{12}) \\ &\simeq .5\times 10^2 \times 91 \times \frac{V_{PC}(r_{12})}{x} \times (\overline{\sigma}_1 - \overline{\sigma}_2)\cdot\frac{\overline{r}_{12}}{r_{12}} \ . \end{aligned} \tag{3.7}$$

   The order or magnitude for the axial part is roughly $4550/x$ times larger than for the vectorial part. $V_{PNC}$ is proportional to $1/x^2$ and $V_{PC}$ to $1/x$. The condition that the states are spin eigenstates requires that spin quantization axes must be chosen along the flux tube connecting the dark protons. This is rather natural choice.

   This would give for the axial part order of magnitude $V_{PNC} \sim 728/x^2$. For 2 nm distance one would obtain $V_{PNC} \sim 1.82$ eV. For 1 nm distance one would have $x = 10$ and this would give $V_{PNC} \simeq 7.28$ eV. For this value $V_{PC} \simeq 16$ meV, which is of same order of magnitude as thermal energy $kT/2$ at room temperature.

8. The process of adding dark protons to the increasing DNA sequence must be possible irrespectively of the direction of spin. The spin eigenvalue in the direction of the horizontal axis connecting the members of dark proton pair is assumed to be opposite for the members of the dark proton pairs of dark double strand. This assumption comes from the model of the dark genetic code. This demands that $V_{NPC}$ is considerably smaller than strong binding energy $E_B$. For 1 nm distance one has $V_{PNC} \simeq 7.28$ eV considerably smaller than $E_B \simeq 28$ eV.

9. What is the relation of the fermionic chirality to the geometric chirality? The reflection for dark protons induces the reflection of the entire helix turning also its direction. The reflection permutes the dark protons of each pair since their positions are related by reflection in the plane orthogonal to z-axis $(x_2, y_2) = (-x_1, -y_1)$. One has $(x_1, y_1, z) \leftrightarrow (x_2, y_2, -z)$. A further rotation of $\pi$ in say $(x, z)$-plane around say y-axis is symmetry and gives $(x_2, y_2, -z) \to (-x_2, y_2, z) = (x_1, -y_1, z)$. Hence the net effect is $(x_1, y_1, z) \to (x_1, -y_1, z)$ and DNA strand with an opposite screw direction is generated.

The model of dark genetic code motivates the assumption that the dark protons of the pair are spin eigenstates for the spin projection along the axis connecting the members of the pair. The direction of the spin quantization axis changes in reflection from that given by $(x_1, y_1)$ to that given by $(x_1, -y_1)$ so that the states are not anymore eigenstates of the spin projection along this axis. Thus the fermionic chirality indeed correlates with the chirality of double strand and the two chiralities are in physically different position.

What happens at the level of classical fields? Kähler magnetic field transforms like angular momentum in reflections and rotations as is easy to see from its expression in terms of vector potential. Hence it does not change its direction in reflection but changes its direction in the rotation. Hence the magnetic flux along flux tube changes to opposite in the reflection. This also affects the physics and induces effects at the level of dark strong interactions. The magnetic energy is of form $s \cdot B$ and vanishes classically. Quantum mechanically it does not vanish since $s$ is operator and one can wonder what this implies physically.

### 3.8.3 Differences between standard model and TGD based description

The above estimate relies on standard model, which is quantum field theory in Minkowski space, and one can wonder what new elements TGD brings in. I do not try to estimate the effects in TGD framework but just list the differences.

1. In TGD framework space-time is 4-surface in $M^4 \times CP_2$ and this description must be replaced with a description using 8-D imbedding spinors. At space-time level massive $M^4$ Dirac equation $p_k\gamma^k\Psi = m\Psi$ is replaced by 8-D chiral symmetry implying separate conservation of quark and lepton numbers with the analog of massless Dirac equation for the Kähler-Dirac gamma matrices, which are superpositions of $M^4$ and $CP_2$ gamma matrices. K-D gamma matrices are contractions of canonical momentum current densities of Kähler action with the imbedding space gamma matrices. If the action is volume term, one obtains induced gamma matrices. The twistorialization of TGD by replacing the imbedding space with the product of twistor spaces of $M^4$ and $CP_2$ and lifting space-time surfaces to their twistor spaces with induced twistor structure leads to the addition of volume term to Kähler action [K39]. This term corresponds to cosmological constant and is extremely small in the recent cosmology.

2. One can decompose K-D gamma matrices to their $M^4$ and $CP_2$ parts: $\Gamma^\alpha = \Gamma^\alpha_{M^4} + \Gamma^\alpha_{CP_2}$ and write the K-D equation as $\Gamma^\alpha_{M^4} D_\alpha \Psi = -\Gamma^\alpha_{CP_2}\Psi$. The presence of $\Gamma^\alpha_{CP_2}$ parts breaks conservation of $M^4$ chirality and serves as a signal for massivation. This operator is kind of mass operator acting non-trivial in electroweak spin degrees of freedom assignable to $CP_2$ and the action of its square is analogous to the action of mass squared operator.

   The understanding of particle massivation at this level does not seem however possible and the proper approach relies of p-adic thermodynamics for super-Virasoro representations for which ground states are characterized by the modes of imbedding space spinors which are massless in 8-D sense and are eigenstates of $M^4$ mass squared operator with eigenvalues determined by $CP_2$ spinor Laplacian [K21]. Its action on $M^4$ chirality is same as action of mass in massive Dirac equation in $M^4$.

3. In the case of $M^4$ Dirac equation the multiplication of massive Dirac equation with $\gamma_5$ using anti-commutativity of $\gamma_5$ and $\gamma_k$ gives $\gamma^k p_k \gamma_5 \Psi = -m\gamma_5\Psi$ instead of$p_k\gamma^k\Psi = m\Psi$. TGD framework $\gamma_5$ anti-commutes with $\Gamma^\alpha_{M^4}$ but commutes with $\Gamma^\alpha_{CP_2}$ so that also now one has similar equation $\Gamma^\alpha_{M^4} D_\alpha \Psi = +\Gamma^\alpha_{CP_2}\Psi$.

# 4 Model For The Hierarchy Of Josephson Junctions

As far as hierarchy of EEGs and its generalizations is considered the hierarchy of Josephson junctions assignable to cell membrane itself is relevant. Dark matter hierarchy and p-adic fractality allow to imagine a fractal hierarchy of structures analogous to cell membrane with arbitrarily large thickness. One can even imagine scaled up variants of cell membrane with different p-adic length scale and value of Planck constant but possessing same membrane potential as ordinary cell membrane. The generalization of the imbedding space helps to understand what is involved and is discussed in Appendix.

## 4.1 The Most Recent Model For The Generation Of Nerve Pulse

For some time ago I learned [J1, J2, J7, J8, J9] (thanks to Ulla Mattfolk) that nerve pulse propagation seems to be an adiabatic process and thus does not dissipate: the authors propose that 2-D acoustic soliton is in question. Adiabaticity is what one expects if the ionic currents are dark currents (large $\hbar$ and low dissipation) or even supra currents. Furthermore, Josephson currents are oscillatory so that no pumping is needed. Combining this input with the model of DNA as topological quantum computer (TQC) [K12] leads to a rather precise model for the generation of nerve pulse.

1. The system would consist of two superconductors- microtubule space-time sheet and the space-time sheet in cell exterior- connected by Josephson junctions represented by magnetic flux tubes defining also braiding in the model of TQC. The phase difference between two super-conductors would obey Sine-Gordon equation allowing both standing and propagating soliton solutions. A sequence of rotating gravitational penduli coupled to each other would be the mechanical analog for the system. Soliton sequences having as a mechanical analog penduli rotating with constant velocity but with a constant phase difference between them would generate moving kHz synchronous oscillation. Periodic boundary conditions at the ends of the axon rather than chemistry determine the propagation velocities of kHz waves and kHz synchrony is an automatic consequence since the times taken by the pulses to travel along the axon are multiples of same time unit. Also moving oscillations in EEG range can be considered and would require larger value of Planck constant in accordance with vision about evolution as gradual increase of Planck constant.

2. During nerve pulse one pendulum would be kicked so that it would start to oscillate instead of rotating and this oscillation pattern would move with the velocity of kHz soliton sequence. The velocity of kHz wave and nerve pulse is fixed by periodic boundary conditions at the ends of the axon implying that the time spent by the nerve pulse in traveling along axon is always a multiple of the same unit: this implies kHz synchrony. The model predicts the value of Planck constant for the magnetic flux tubes associated with Josephson junctions and the predicted force caused by the ionic Josephson currents is of correct order of magnitude for reasonable values of the densities of ions. The model predicts kHz em radiation as Josephson radiation generated by moving soliton sequences. EEG would also correspond to Josephson radiation: it could be generated either by moving or standing soliton sequences (latter are naturally assignable to neuronal cell bodies for which $\hbar$ should be correspondingly larger): synchrony is predicted also now.

3. The previous view about microtubules in nerve pulse conduction can be sharpened. Microtubular electric field (always in the same direction) could explain why kHz and EEG waves and nerve pulse propagate always in same direction and might also feed energy to system so that soliton velocity could be interpreted as drift velocity. This also inspires a generalization of the model of DNA as TQC sine also microtubule-cell membrane systems are good candidates for performers of TQC. Cell replication during which DNA is out of game seems to require this and microtubule-cell membrane TQC would represent higher level TQC distinguishing between multi-cellulars and mono-cellulars.

4. New physics would enter in several manners. Ions should form Bose-Einstein cyclotron condensates. The new nuclear physics predicted by TGD [L2], [L2] predicts that ordinary fermionic ions (such as $K^+$, $Na^+$, $Cl^-$) have bosonic chemical equivalents with slightly differing mass number obtained by replacing one or more neutral color flux tubes connecting nucleons of neutral atom with a charged one. Anomalies of nuclear physics and cold fusion provide experimental support for the predicted new nuclear physics. Electronic supra current pulse from microtubules could induce the kick of pendulum inducing nerve pulse and induce a small heating and expansion of the axon. The return flux of ionic Josephson currents would induce convective cooling of the axonal membrane. A small transfer of small positive charge into the inner lipid layer could induce electronic supra current by attractive Coulomb interaction. The exchange of exotic $W$ bosons which are scaled up variants of ordinary $W^{\pm}$ bosons is a natural manner to achieve this if new nuclear physics is indeed present.

## 4.2 Quantum Model For Sensory Receptor

This original model of nerve pulse and EEG was still based on the implicit assumption that the space-time sheet carrying the Josephson currents is far from vacuum. The model for sensory receptor and sensory qualia however led to a the proposal that the space-time sheet in question is near vacuum extremal [K16, K26]. Near vacuum extremal property does not affect the general structure of the model in an essential manner.

1. The only change [K26, K27] is the replacement of charges $\pm 1$ of ions with effective charges given as

$$Q_{eff} = -\frac{Z-N}{2p} + 2Z + q_{em} \ . \tag{4.1}$$

   $Z$ and $N$ denote nuclear charge and neutron number. $p = sin^(\theta_W)$ corresponds to Weinberg angle. For $K^+$, $Cl^-$, $Na^+$, $Ca^{++}$ one has $Z = (19, 17, 11, 20)$, $Z - N = (-1, -1, -1, 0)$, and $q_{em} = (1, -1, 1, 2)$. **Table 1** gives the values of Josephson energies for some values of resting potential for $p = sin^(\theta_W) = .0295$ reproducing the frequencies of peak sensitivity for photoreceptors. Rather remarkably, they are in IR or visible range.

2. The energies are in UV and visible range. Hence one can consider also Josephson junctions with considerably lower membrane potentials of order mV are possibly without losing the thermal stability. For instance, one could consider $k = 151, 157, 163, 167$ Josephson junctions with a membrane potential scaling as $1/L(k)$. For $k = 167$ the energies would be scaled down by a factor $2^{-(167-151)/2} = 2^{-8}$ giving for $V_{eff} = .09$ V a photon energy somewhat below the thermal energy at room temperature. On the other hand, the fact that Josephson junctions with a vanishing $Z^0$ field are at the verge of thermal instability suggests that also they might be present in living matter.

3. From **Table 1** one can evaluate the value of Planck constant for a given Josephson frequency for various ions. For $f_J = 5$ Hz giving a first estimate for neuronal Josephson frequency and V=-55 mV corresponding to the critical voltage for the generation of action potential one obtains the values $r = \hbar/\hbar_0 = (1.51, 1.89, 2.11, 1.59) \times 2^{46}$ for $(Na^+, Cl^-, K^+, Ca^{++})$. For V=-70 mV corresponding to the resting potential of neuron and same Josephson frequency one obtains $r = (0.961.201.341.01) \times 2^{47}$. For $Ca^{++}$ ion $r$ is very near to a power of 2. A good mnemonic is that the Josephson energies of biologically important ions vary in an interval, which is in a reasonable approximation half octave $(E_J(K^+)/E_J(Na^+) = 1.3958 \simeq \sqrt{2} \simeq 1.4142)$.

It interesting to try to interpret the resting potentials of various cells in this framework in terms of the Josephson frequencies of various ions. **Table 1** gives the values of Josephson frequencies of basic biological ions for typical values of the membrane potential.

1. The maximum value of the action potential during nerve pulse is +40 mV so that Josephson frequencies are same as for the resting state of photoreceptor. Note that the time scale for nerve pulse is so slow as compared to the frequency of visible photons that one can consider that the neuronal membrane is in a state analogous to that of a photoreceptor.

2. For neurons the value of the resting potential is -70 mV. $Na^+$ and $Ca^{++}$ Josephson energies 2.80 eV and 2.94 eV are in the visible range in this case and correspond to blue light. This does not mean that $Ca^{++}$ Josephson currents are present and generate sensation of blue at neuronal level: the quale possibly generated should depend on sensory pathway. During the hyper-polarization period with -75 mV the situation is not considerably different.

3. The value of the resting potential is -95 mV for skeletal muscle cells. In this case $Ca^{++}$ Josephson frequency corresponds to 4 eV metabolic energy quantum.

4. For smooth muscle cells the value of resting potential is -50 mV. In this case $Na^+$ Josephson frequency corresponds to 2 eV metabolic energy quantum.

| Ion | $Na^+$ | $Cl^-$ | $K^+$ | $Ca^{+2}$ |
|---|---|---|---|---|
| $E_J(.04\ \ mV, p = .23)/eV$ | 1.01 | 1.40 | 1.51 | 1.76 |
| $E_J(.065\ \ V, p = .23)/eV$ | 1.64 | 2.29 | 2.69 | 2.73 |
| $E_J(40\ \ mV, p = .0295)/eV$ | 1.60 | 2.00 | 2.23 | 1.68 |
| $E_J(50\ \ mV, p = .0295)/eV$ | 2.00 | 2.49 | 2.79 | 2.10 |
| $E_J(55\ \ mV, p = .0295)/eV$ | 2.20 | 2.74 | 3.07 | 2.31 |
| $E_J(65\ \ mV, p = .0295)/eV$ | 2.60 | 3.25 | 3.64 | 2.73 |
| $E_J(70\ \ mV, p = .0295)/eV$ | 2.80 | 3.50 | 3.92 | 2.94 |
| $E_J(75\ \ mV, p = .0295)/eV$ | 3.00 | 3.75 | 4.20 | 3.15 |
| $E_J(80\ \ mV, p = .0295)/eV$ | 3.20 | 4.00 | 4.48 | 3.36 |
| $E_J(90\ \ mV, p = .0295)/eV$ | 3.60 | 4.50 | 5.04 | 3.78 |
| $E_J(95\ \ mV, p = .0295)/eV$ | 3.80 | 4.75 | 5.32 | 3.99 |
| Color | R | G | B | W |
| $E_{max}$ | 2.19 | 2.32 | 3.06 | 2.49 |
| energy-interval/eV | 1.77-2.48 | 1.97-2.76 | 2.48-3.10 | |

**Table 1:** Table gives the prediction of the model of photoreceptor for the Josephson energies for typical values of the membrane potential. For comparison purposes the energies $E_{max}$ corresponding to peak sensitivities of rods and cones, and absorption ranges for rods are also given. R, G, B, W refers to red, green, blue, white. The values of Weinberg angle parameter $p = sin^2(\theta_W)$ are assumed to be .23 and.0295. The latter value is forced by the fit of Josephson energies to the known peak energies.

5. For astroglia the value of the resting potential is -80/-90 mV for astroglia. For -80 mV the resting potential for $Cl^-$ corresponds to 4 eV metabolic energy quantum. This suggests that glial cells could also provide metabolic energy as Josephson radiation to neurons.

6. For all other neurons except photo-receptors and red blood cells Josephson photons are in visible and UV range and the natural interpretation would be as bio-photons. The bio-photons detected outside body could represent sensory leakage. An interesting question is whether the IR Josephson frequencies could make possible some kind of IR vision.

## 4.3 The Role Of Josephson Currents

The general vision is that Josephson currents of various ions generate Josephson photons having dual interpretations as bio-photons and EEG photons. Josephson photons can in principle regenerate the quale in the neurons of the sensory pathway. In the case of motor pathways the function would be different and the transfer of metabolic energy by quantum credit card mechanism using phase conjugate photons is suggested by the observation that basic metabolic quanta 2 eV *resp.* 4 eV are associated with smooth muscle cells *resp.* skeletal muscle cells.

As already found in the previous section, the energies of Josephson photons associated with the biologically important ions are in general in visible or UV range except when resting potential has the value of -40 mV which it has for photoreceptors. In this case also IR photons are present. Also the turning point value of membrane potential is +40 mV so that one expects the emission of IR photons.

Josephson photons could be used to communicate the qualia to the magnetic body.

1. If Josephson currents are present during the entire action potential, the entire range of Josephson photons down to frequencies of order 2 kHz range is emitted for the standard value of $\hbar$. The reason is that lower frequencies corresponds to cycles longer than the duration of the action potential. The continuum of Josephson frequencies during nerve pulse makes it possible to induce cyclotron transitions at the magnetic body of neuron or large structure. This would make possible to communicate information about spatial and temporal behavior of the nerve pulse pattern to the magnetic body and build by quantum entanglement a sensory map.

| fermion | $f_c(e)/MHz$ | $f_c(u)/MHz$ | $f_c(d)/MHz$ |
|---|---|---|---|
| standard | .564 | .094 | .019 |
| nearly vacuum extremal | 8.996 | 2.275 | .947 |

**Table 2:** Cyclotron frequencies of quarks and electron in magnetic field $B_{end} = .2$ Gauss for standard vacuum with very small $Z^0$ field and nearly vacuum extremal.

2. The frequencies below 2 kHz could be communicated as nerve pulse patterns. When the pulse rate is above $f = 28.57$ Hz the sequence of pulses is experienced as a continuous sound with pitch $f$. $f$ defines the minimum frequency for which nerve pulses could represent the pitch and there remains a 9 Hz long range to be covered by some other communication method.

3. The cyclotron frequencies of quarks and possibly also of electron would make possible a selective reception of the frequencies emitted during nerve pulse. Same applies also to the Josephson frequencies of hair cell (, which does not fire). If the value of Planck constant is large this makes possible to communicate the entire range of audible frequencies to the magnetic body. Frequency would be coded by the magnetic field strength of the flux tube. Two options are available corresponding to the standard ground state for which $Z^0$ field is very weak and to almost vacuum extremals. For the first option one as ordinary cyclotron frequencies. The cyclotron frequency scales for them differ by a factor

$$r(q) = \frac{Q_{eff}(q)}{Q_{em}(q)} = \frac{\epsilon(q)}{2pQ_{em}(q)} + 1 \ , \ \epsilon(u) = -1 \ , \epsilon(d) = 1 \tag{4.2}$$

from the standard one. For $p = .0295$ one obtains $(r(u), r(d), r(e) = (24.42, 49.85, 15.95)$. The cyclotron frequencies for quarks and electron with masses m(u)=2 MeV, m(d)=5 MeV, and m(e)=.5 MeV are given by **Table 2** for the two options. If one assumes that $B_{end}$ defines the upper bound for field strength then he standard option would require both d quark and electron. Gor $d$quark with kHz CD the upper bound for cyclotron frequencies would be 20 kHz which corresponds to the upper limit of audible frequencies.

4. Besides cyclotron frequencies also the harmonics of the fundamental frequencies assignable to quark and electron CDs could be used and in case of musical sounds this looks a highly attractive option. In this case it is now however possible to select single harmonics as in the case of cyclotron transitions so that only the rate of nerve pulses can communicate single frequency. Lorentz transform sub-CD scales up the frequency scale from the secondary p-adic time scale coming as octave of 10 Hz frequency. Also the scaling of $\hbar$ scales this frequency scale.

## 4.4 What Is The Role Of The Magnetic Body?

The basic vision is that magnetic body receives sensory data from the biological body- basically from cell membranes and possibly via genome - and controls biological body via genome. This leaves a huge amount of details open and the almost impossible challenge of theoretician is to guess the correct realization practically without any experimental input. The following considerations try to clarify what is involved.

### 4.4.1 Is magnetic body really needed?

Libet's findings and the model of memory based on time mirror (see **Fig.** `http://tgdtheory.fi/appfigures/timemirror.jpg` or **Fig. ??** in the appendix of this book) hypothesis suggests that magnetic body is indeed needed. What is the real function of magnetic body? Is it just a sensory canvas? The previous considerations suggest that it is also the seat of geometric qualia, in particular the pitch of sound should be coded by it. It would be relatively easy to understand magnetic body as a relatively passive sensory perceiver defining sensory map. If one assumes that

motor action is like time reversed sensory perception then sensory and motor pathways would be just sensory pathways proceeding in opposite time directions from receptors to the various layers of the magnetic body. Brain would perform the information processing.

Certainly there must exist a region in which the motor and sensory parts of the magnetic body interact. What comes in mind is that these space-time sheets (or actually pairs of space-time sheets) are parallel and generate wormhole contacts between them. This interaction would be assignable to the region of the magnetic body could receive positive energy signals from associative sensory areas and send negative energy signals to motor motor neurons at the ends of motor pathways wherefrom they would propagate to premotor cortex, supplementary motor cortex and to frontal lobes where the abstract plans about motor actions are generated.

### 4.4.2 Is motor action time reversal of sensory perception in zero energy ontology?

One could argue that the free will aspect of motor actions does not conform with the interpretation as sensory perception in reversed direction of time. On the other hand, also percepts are selected -say in binocular rivalry [J6]. Only single alternative percept need to be realized in a given branch of the multiverse. This makes possible metabolic economy: for instance, the synchronous firing at kHz frequency serving as a correlate for the conscious percept requires a lot of energy since dark photons at kHz frequency have energies above thermal threshold. Similar selection of percepts could occur also at the level of sensory receptors but quantum statistical determinism would guarantee reliable perception. The passivity of sensory perception and activity of motor activity would reflect the breaking of the arrow of time if this interpretation is correct.

### 4.4.3 What magnetic body looks like?

What magnetic body looks like has been a question that I have intentionally avoided as a question making sense only when more general questions have been answered. This question seems however unavoidable now. Some of the related questions are following. The magnetic flux lines along various parts of magnetic body must close: how does this happen? Magnetic body must have parts of size at least that defined by EEG wavelengths: how do these parts form closed structures? How the magnetic bodies assignable to biomolecules relate to the Earth sized parts of the magnetic body? How the personal magnetic body relates to the magnetic body of Earth?

1. The vision about genome as the brain of cell would suggest that active and passive DNA strands are analogous to motor and sensor areas of brain. This would suggests that sensory data should be communicated from the cell membrane along the passive DNA strand. The simplest hypotesis is that there is a pair of flux sheet going through the DNA strands. The flux sheet through the passive strand would be specialized to communicate sensory information to the magnetic body and the flux sheet through the active strand would generate motor action as DNA expression with transcription of RNA defining only one particular aspect of gene expression. Topological quantum computation assignable to introns and also electromagnetic gene expression would be possible.

2. The model for sensory receptor in terms of Josephson radiation suggests however that flux tubes assignable to axonal membranes carry Josephson radiation. Maybe the flux tube structures assigned to DNA define the magnetic analog of motor areas and flux tubes assigned with the axons that of sensory areas.

3. A complex structure of flux tubes and sheets is suggestive at the cellular level. The flux tubes assignable to the axons would be parallel to the sensory and motor pathways. Also microtubules would be accompanied by magnetic flux tubes. DNA as topological quantum computer model assumes and the proposed model of sensory perception and cell membrane level suggests transversal flux tubes between lipids and nucleotides. The general vision about DNA as brain of cell suggest flux sheets through DNA strands.

   During sensory perception of cell and nerve pulse the wormhole flux tube connecting the passive DNA strand of the first cell to the inner lipid layer would recombine with the flux tube connecting outer lipid layer to some other cell to form single flux tube connecting two cells. In the case of sensory organs these other cells would be naturally other sensory receptors.

This would give rise to a dynamical network of flux tubes and sheets and axonal sequences of genomes would be like lines of text at the page of book. This structure could have a fractal generalization and would give rise to an integration of genome to super-genome at the level of organelles, organs and organism and even hypergenome at the level of population. This would make possible a coherent gene expression.

4. This vision gives some idea about magnetic body in the scale of cell but does not say much about it in longer scales. The CDs of electrons and quarks could provide insights about the size scale for the most relevant parts of the magnetic body. Certainly the flux tubes should close even when they have the length scale defined by the size of Earth.

Additional ideas about the structure follow follow if one assumes that magnetic body acts a sensory canvas and that motor action can be regarded as time reversed sensory perception.

1. If the external world is represented at part of the magnetic body which is stationary, the rotation of head or body would not affect the sensory representation. This part of the magnetic body would be obviously analogous to the outer magnetosphere, which does not rotate with Earth.

2. The part of the magnetic body at which the sensory data about body (posture, head orientations and position, positions of body parts) is represented, should be fixed to body and change its orientation with it so that bodily motions would be represented as motions of the magnetic , which would be therefore analogous to the inner magnetosphere of rotating Earth.

3. The outer part of the personal magnetic body is fixed to the inner magnetosphere, which defines the reference frame. The outer part might be even identifiable as the inner magnetosphere receiving sensory input from the biosphere. This magnetic super-organism would have various life forms as its sensory receptors and muscle neurons. This would give quantitative ideas about cyclotron frequencies involved. The wavelengths assignable to the frequencies above 10 Hz would correspond to the size scale of the inner magnetosphere and those below to the outer magnetosphere. During sleep only the EEG communications with outer magnetic body would remain intact.

4. Flux quantization for large value of $\hbar$ poses an additional constraint on the model.

   (a) If Josephson photons are transformed to a bunch of ordinary small $\hbar$ photons magnetic flux tubes can correspond to the ordinary value of Planck constant. If one assumes the quantization of the magnetic flux in the form

   $$\int BdA = n\hbar$$

   used in super-conductivity, the radius of the flux tube must increase as $\sqrt{\hbar}$ and if the Josephson frequency is reduced to the sound frequency, the value of $\hbar$ codes for the sound frequency. This leads to problems since the transversal thickness of flux tubes becomes too large. This does not however mean that the condition might not make sense: for instance, in the case of flux sheets going through DNA strands the condition might apply.

   (b) The quantization of magnetic flux could be replaced by a more general condition

   $$\oint (p - ZeA)dl = n\hbar \ , \tag{4.3}$$

   where $p$ represents momentum of particle of super-conducting phase at the boundary of flux tube. In this case also $n = 0$ is possible and poses no conditions on the thickness of the flux tube as a function of $\hbar$. This option looks reasonable since the charged particles at the boundary of flux tube would act as sources of the magnetic field.

(c) Together with the Maxwell's equation giving $B = ZeNv$ in the case that there is only one kind of charge carrier this gives the expression

$$N = \frac{2m}{RZ^2e^2} \tag{4.4}$$

for the surface density $N$ of charge carrier with charge $Z$. $R$ denotes the radius of the flux tube. If several charge carriers are present one has $B = \sum_k N_k Z_k e v_k$, and the condition generalizes to

$$N_i = \frac{2m_i v_i}{RZ_i \sum_k Z_k v_k e^2} \ . \tag{4.5}$$

It seems that this condition is the most realistic one for the large $\hbar$ flux sheets at which Josephson radiation induces cyclotron transitions.

### 4.4.4 What are the roles of Josephson and cyclotron photons?

The dual interpretation of Josephson radiation in terms of bio-photons and EEG photons seems to be very natural and also the role of Josephson radiation seems now relatively clear. The role of cyclotron radiation and its interaction with Josephson radiation are not so well understood.

1. At least cell membrane defines a Josephson junction (actually a collection of them idealizable as single junctions). DNA double strand could define a series of Josephson junctions possibly assignable with hydrogen bonds. This however requires that the strands carry some non-standard charge densities and currents- I do not know whether this possibility is excluded experimentally. Quarks and antiquarks assignable to the nucleotide and its conjugate have opposite charges at the two sheets of the wormhole flux tube connective nucleotide to a lipid. Hence one could consider the possibility that a connection generated between them by reconnection mechanism could create Josephson junction.

2. The model for the photoreceptors leads to the identification of bio-photons as Josephson radiation and suggests that Josephson radiation propagates along flux tubes assignable to the cell membranes along sensory pathways up to sensory cortex and from there to motor cortex and back to the muscles and regenerates induced neuronal sensory experiences.

3. Josephson radiation could be used quite generally to communicate sensory data to/along the magnetic body: this would occur in the case of cell membrane magnetic body at least. The different resting voltages for various kinds of cells would select specific Josephson frequencies as communication channels.

4. If motor action indeed involves negative energy signals backwards in geometric time as Libet's findings suggest, then motor action would be very much like sensory perception in time reversed direction. The membrane resting potentials are different for various types of neurons and cells so that one could speak about pathways characterized by Josephson frequencies determined by the membrane potential. Each ion would have its own Josephson frequency characteristizing the sensory or motor pathway.

The basic questions concern the function of cyclotron radiation and whether Josephson radiation induces resonantly cyclotron radiation or vice versa.

1. Cyclotron radiation would be naturally associated with the flux sheets and flux tubes. The simplest hypothesis is that at least the magnetic field $B_{end} = .2$ Gauss can be assigned with the some magnetic flux quanta at least. The model for hearing suggests that $B_{end}$ is in this case quantized so that cyclotron frequencies provide a magnetic representation for audible frequencies. Flux quantization does not pose any conditions on the magnetic field strength if the above discussed general flux quantization condition involving charged currents at the boundary of the flux quantum are assumed. If these currents are not present, $1/\hbar$ scaling of $B_{end}$ for flux tubes follows.

2. The assumption that cyclotron radiation is associated with the motor control via genome is not consistent with the vision that motor action is time reversed sensory perception. It would also create the unpleasant question about information processing of the magnetic body performed between the receival of sensory data and motor action.

3. The notion of magnetic sensory canvas suggests a different picture. Josephson radiation induces resonant cyclotron transitions at the magnetic body and induces entanglement of the mental images in brain with the points of the magnetic body and in this manner creates sensory maps giving a third person perspective about the biological body. There would be two kind of sensory maps. Those assignable to the external world and those assignable to the body itself. The Josephson radiation would propagate along the flux tubes to the magnetic body.

4. There could be also flux tube connections to the outer magnetosphere of Earth. It would seem that the reconnections could be flux tubes traversing through inner magnetosphere to poles and from there to the outer magnetosphere. These could correspond to rather low cyclotron frequencies. Especially interesting structure in this respect is the magnetic flux sheet at the Equator.

## 4.5 Dark Matter Hierarchies Of Josephson Junctions

The hierarchy of Josephson junctions assignable to cell membrane and characterized by values of Planck constant provides a rather nice model for cell membrane but one can consider also more general dark hierarchies of Josephson junctions. This model conforms with the general vision that living matter processes information by locating it to various pages of the "Big Book".

### 4.5.1 Maximization of Planck constant in quantum control and communication in living matter

The sectors of the imbedding space for which CD and $CP_2$ are replaced with their $n_a$- *resp.* $n_b$-fold coverings define the most promising candidates concerning the understanding of living matter, at least the quantum control of living matter. The reason is that the value of the Planck constant is maximized and given by $r = \hbar/\hbar_0 = n_a n_b$. Also the number of pages with same Planck constant would be finite unlike for the more general option allowing rational values of Planck constant. In particular, infinite number of pages with the standard value of Planck constant would be possible and this might lead to mathematical difficulties.

Experimental constraints allow to consider also the possibility that only covering spaces are possible. One must be however very cautious in making hasty conclusions. If also factor spaces are allowed one can have $G_a$ or $G_b$ as discrete and exact symmetry groups at the level of dark matter and these symmetries would be manifested as approximate symmetries of the visible matter topologically condensed around the dark matter.

1. In $M^4$ degrees of freedom since the restriction to the orbifold $\hat{M}^4/G_a$ is equivalent to the exact $G_a$-invariance of dark matter quantum states. Molecular rotational symmetries correspond typically to small groups $G_a$ and might relate to this symmetry. Small values of $n_a$ would not affect dramatically the value of Planck constant if $n_b$ is large.

2. $G_a = Z_n$, $n = 5, 6$ are favored for molecules containing aromatic cycles. Also genuinely 3-dimensional tetrahedral, octahedral, and icosahedral symmetries appear in living matter.

In the sequel only integer values of Planck constant will be considered. An especially interesting hierarchy corresponds to ruler and compass integers expressible as a product of power of two and distinct Fermat primes (see Appendix). The reason is that these integers correspond to number theoretically very simple quantum phases. This hierarchy includes as a special case powers of two and one can imagined a resonant interaction between p-adic length scale hierarchy and hierarchy of Planck constants.

### 4.5.2 Dark hierarchy of Josephson junctions with a constant thickness

The model for EEG relies on fractal hierarchy of cell membrane like structures with a fixed thickness and membrane potential. Therefore cell membrane thickness is not scaled by $\hbar$ as one might naively expect. Same applies to magnetic flux tubes: this is possible since the condition for the quantization of magnetic flux can be replaced with a more general one if one allows charged currents at the boundaries of flux quanta [K26]. In this model the value of $\hbar$ becomes a measure for the evolutionary level of cell and neurons in hippocampus, associative regions of cortex and their motor counterparts, and frontal lobes are expected to correspond to the largest values of $\hbar$ measuring also the time scale of long term memory and planned action. Note that cell membrane corresponds to twin primes $k = 149$ and $k = 151$ with $k = 151$ defining a Gaussian Mersenne so that it is indeed very special.

Page of a book is rather precise metaphor for the magnetic flux sheet going through a linear array of strings of nuclei and also for a collection flux tubes parallel to axons. This raises several questions. Do the lines of the text of this book correspond to axons in neural circuits? Do the pages correspond to larger structures formed by the axons?

The quantum model for qualia [K26] implies that Josephson radiation travels through flux tubes parallel to sensory pathways and there could be also a horizontal organization of the neurons- at least at the level of sensory receptors in the sense that magnetic flux tubes connecting DNA nucleotides to lipids of cell membrane fuse to form longer flux tubes between DNA nucleotides of different cells when sensory receptor is active. Axons could thus be seen as the analogs of text lines which however can interact with each other. Similar organization would appear at the level of flux sheets traversing through DNA strands.

Books are made for reading and one can thus ask whether the book metaphor extends. Could the observed moving brain waves scanning cortex relate to the "reading" of the information associated with these sheets of book by the magnetic body and does our internal speech correspond to this "reading" ? One is also forced to ask whether these brain waves are induced by waves propagating along magnetic flux quanta of the magnetic body of Earth or personal magnetic body in the case that it has components other than magnetic flux sheets serving as Josephson junctions.

### 4.5.3 An objection against a fractal hierarchy of Josephson junctions with thickness scaling as $\hbar$

One can consider also a hierarchy of Josephson junctions with a scaled up thickness proportional to $\hbar$ instead of constant thickness. If these junctions have same voltage at all levels of the hierarchy a resonant interaction between various levels of the hierarchy would become possible.

One can represent common sense objections against this idea. The electric field involved with the higher levels of Josephson junction hierarchy is very weak: something like $10^{-7}$ V/m for lito-ionospheric Josephson junctions (of thickness about 176 km from the scaling of the cell membrane thickness by $\lambda^4 = 2^{44}$) which might be responsible for EEG. The electric field of the Earth at space-time sheets corresponding to ordinary matter is much stronger: about $10^2 - 10^4$ V/m at the surface of Earth but decreasing rapidly as ionosphere is approached being about.3 V/m at 30 km height. The estimate for the voltage between ionosphere and Earth surface is about 200 kV [F13].

The many-sheeted variant of Faraday law implies that on order to have a voltage of order.08 V over lito-ionospheric Josephson junction at dark matter space-time sheet, the voltage over ionospheric cavity must be almost completely compensated by an opposite voltage over litosphere so that lito-ionospheric double layer could be seen as a pair of capacitor plates in a radial electric field of order $10^{-7}$ V/m generated by the charge density in sub-litospheric part of Earth. This condition requires fine-tuning and therefore looks unrealistic.

A natural distance scale in which the electric field is reduced would correspond to 10-20 km thick layer in which whether phenomena are present. The mirror image of this layer would be Earth's crust. The cell membrane counterpart would be a dipole layer like charge density between the lipid layers of the cell membrane. Note that the electric field at dark matter space-time can be constant. However, as far as Josephson junction is considered, it is only the net voltage what matters.

| $(k, k+2)$ | $(137, 139)$ | $(149, 151)$ | $(167, 169 = 13^2)$ | $(179, 181)$ |
|---|---|---|---|---|
| $L_e(k)$ | .78 $A$ | 5 $nm$ | $2.5\mu m$ | .32 $mm$ |
| $(k, k+2)$ | $(191, 193)$, | $(197, 199)$ | | |
| $L_e(k)$ | 1 $cm$ | 8 $cm$ | | |

**Table 3:** Twin primes define especially interesting candidates for double membrane like structures defining Josephson junctions. Also included the pair $(137, 13^2 = 169)$ although $k = 169$ is not prime. The two largest scales could relate to structures appearing in brain.

## 4.6 P-Adic Fractal Hierarchy Of Josephson Junctions

p-Adic length scale hypothesis allows to imagine a hierarchy of Josephson junctions at least in length scales regarded usually as biologically relevant. The voltage through the junction need not however be same as for the ordinary cell membrane anymore. Twin primes are especially interesting since they would naturally correspond to pairs of structures analogous to a pair of lipid layers defining cell membrane.

In particular, twin primes abundant in the p-adic length scale range assignable to living matter could define double layered structures acting as Josephson junctions.

Also Gaussian Mersennes define highly interesting p-adic length scales and the length scale range between cell membrane thickness and the size of cell contains as many as four Gaussian Mersennes corresponding to $k = 151, 157, 163, 167$. Only the smallest one is associated with a twin prime but p-adic length scale hypothesis allows also non-prime values of $k$.

### 4.6.1 The possibility of a p-adic hierarchy of membrane like structures accompanied by Josephson junctions

One can imagine the existence of fractally scaled up variants of cell membrane defining hierarchy of Josephson junctions possibly realized as magnetic flux tubes. The possible existence of this hierarchy is however not relevant for the model of EEG in its recent form.

The first hierarchy correspond to the p-adic length scales varying in the range of biologically relevant p-adic length scales $L(k)$ involving membrane like structures. Twin primes $(k, k+2)$ are good candidates here (Table 3). Second hierarchy corresponds to dark matter hierarchy for which length scales come as $\sqrt{r}L(k)$), $r = \hbar/\hbar_0$. Later the question which values of $r$ are favored will be discussed.

The size of cell nucleus varies in the range $(L(169) = 5\ \mu m, 2L(169) = 10\ \mu m)$. This is consistent with the assumption that cell nucleus provides the fundamental representation for this block. This would mean that at least the multiply coiled magnetic flux quantum structures associated with DNA appear as fractally scaled up copies.

Each dark matter level corresponds to a block of p-adic length scales $L(k)$, $k = 151, ..., 169$. Also new length scales emerge at given level and correspond to $L(k)$, $k > 169$. The dark copies of all these length scales are also present. Hence something genuinely new would emerge at each level.

### 4.6.2 Fractal hierarchy of magnetic bodies assignable to cell

Second hierarchy corresponds to a dark matter hierarchy involving values of Planck constant. The original hypothesis was that the values of Planck constant comes as $r \equiv \hbar/\hbar_0 = 2^{11k}$ of given p-adic length scale assignable to biological membrane like structure. A possible justification for the hypothesis is that the ratio of electron and proton masses is rather near to $2^{11}$ and that this number appears in quantum TGD in the role of fundamental constant. This hypothesis is however un-necessarily restrictive and it is better to consider at least the values of $r$ given as products of two ruler and compass integers $n_F$ expressible as a product of distinct Fermat primes and some power of two. The justification comes from the number theoretic vision about evolution and number theoretical simplicity of the phases $q = exp(i2\pi/n_F)$ (Appendix).

The emergence of a genuinely new structure or function in evolution would correspond to the emergence of new level in this fractal hierarchy. Quantum criticality would be essential: phases

corresponding different values of Planck constant would compete at quantum criticality.

The flux sheet or tubes through cell membranes should integrate to larger structures at the higher levels of dark matter hierarchy implying the integration of sensory inputs from a large number of cells to single coherent input at higher levels of dark matter hierarchy. One can think two options: the sensory inputs from cell membranes are communicated directly to the magnetic body or via the DNA. The second option would require that the flux sheets or tubes starting from cell membrane traverse also the DNA.

# 5 Physical Model For Genetic Code And Its Evolution

The original number theoretic models for genetic realized on the idea that genetic code has deeper number theoretical significance. The neglect of some obvious physical inputs however generated some pseudo problems. These models however led to what I believe is the correct track concerning the understanding of the prebiotic evolution. The original model for the evolution of genetic code as a fusion of singlet and doublet codes to triplet code has been discussed in [K14]. The model to be discussed here is obtained from this model by some dramatic simplifications.

The basic questions are following.

1. What were the physical counterparts of the pre-amino-acids and pre-tRNAs for singlet and doublet codes?

2. How the triplet code emerged from the singlet and doublet codes? How the tRNA molecules evolved and how the amino-acids replaced pre-amino-acids?

3. Can one identify singlet and doublet life-forms or at least some predecessors of triplet life forms as existing life-forms?

In an attempt to answer these questions p-adic length scale hypothesis and the vision about the molecular evolution as a sequence of spontaneous symmetry breakings induced by the generation of new space-time sheets serve as valuable guide lines. The following biological input is needed.

1. RNA world [I83] as a model for pre-biotic evolution allows to identify pre-amino-acids as RNA sequences ($RNA_1$ for short) differing somehow from the ordinary RNA sequences ($RNA_2$ for short). 1-code was associated with the transformation of $RNA_2 \to RNA_1$ and 2-code in the simplest case with the transcription of $RNA_2$ to its conjugate.

2. The cross like structure of tRNA molecule identifiable as a composite of its singlet and doublet predecessors allows to read directly the main steps in the evolution of the triplet code as a fusion of singlet and doublet codes and also gives detailed and highly non-trivial information about $RNA_1$.

3. The reverse transcriptase, appearing in retro-viruses like HIV and acting also as a transcriptase [J3], provides the mechanism transforming RNA sequences to DNA sequences inside pre-nucleus so that DNA→RNA code emerged and also evolved rapidly since reverse transcriptase makes a lot of errors.

4. The basic idea is that the fusion of $tRNA_1$ and $tRNA_2$ to to $tRNA_3$, the recent tRNA, made $RNA_2 \to RNA_1$ and $RNA_2 \to RNA_2$ transformations impossible and the amino-acids originally catalyzing the attachment of $RNA_2$ doublet in $RNA_2$ transcription began to be attached to a growing amino-acid sequence and mRNA→ amino-acid part of genetic machinery was established. The emergence of reverse transcriptase brought in DNA. DNA as topological quantum computer idea generalized to RNA context provides tight additional conditions on the course of events: in particular, membrane like structures, most naturally consisting of $RNA_1$ should have been present already at RNA era.

5. Nanno-bacteria claimed to be even the dark bio-matter are excellent candidates for singlet and doublet life-forms or at least, predecessors of the recent life-forms. There are reasons to believe that RNA era is still continuing inside cell nucleus.

Second group of questions relates to the quantum control of the translation process. There are many questions also now.

1. What makes a codon stopping codon?
2. What is behind the symmetries of the code with respect to the third codon.
3. What is the origin of breaking of the canonical A-T, C-G rules for mRNA-tRNA association?

The model for the transition from RNA era to RNA-amino-acid era allows to answer these questions and te DNA as TQC picture leads to a physical interpretation of these symmetries and their breaking.

## 5.1 RNA World

The hypothesis that pre-biotic life before the emergence of the cell membrane structures was RNA dominated (the notion of RNA world) is based on a strong empirical evidence summarized in detail in [I43]. For instance, only RNA can be generated spontaneously in the absence of cell membrane bounded structures. There is also a lot of support for the ability of RNA to take care of functions like replication, translation, and transfer (see the [I43] and references therein). Ribozymes could even replace enzymes as RNA based catalyzing agents so that even amino-acids might be unnecessary in RNA world and the system could consist of RNA only. This of course does not mean that this system could yet realize genetic code and evolve.

An important implication is that pre-amino-acids might be identifiable as $2',5'$ RNA, which was produced in the classical experiments of Leslie Orgel at 1980s mimicking primordial ocean. There are however also other candidates and the structure of tRNA more or less fixes identification to a high degree.

Ontogeny recapitulates phylogeny principle suggests that if RNA coded RNA during primordial period, the remnants of these RNAs could still exist and be coded by specific genes. This is indeed the case [I69] (for an article about RNA genes and RNA world see [I79] ). RNA genes were discovered already 1990 in the genome of Caenorhabditis elegans, the small nematode worm but it took years to realize that they do not code proteins but small RNA molecules that somehow turn off other genes that play a role in worm development. Later these small RNA coding genes were found in flies, mollusks, fish, and even humans. As many as 200 microRNA genes in C. elegans were known at time of the writing of the article, which would represent about 1 percent of the genes of its genes. There is also evidence that centrosomes possess their own genome based on RNA rather than DNA [I6].

## 5.2 Programming Of Bio-Molecular Self Assembly Pathways From TGD Point Of View

The beautiful results (for a popular summary see [I73] ) about programming of bio-molecular self assembly - described above - when combined with the earlier model for the pre-biotic evolution - inspire interesting insights about the role of braiding in translation. The basic observation is that the structure of tRNA- although more complex than that of hairpin- has much common with that of hairpins. Therefore it is interesting to look this structure from the point of view of TGD. For instance, one can find whether the notions of braiding, anomalous em charge and quark color could provide additional insights about the structure and function of tRNA.

The brief summary of the resulting picture is as follows. According to the TGD based model of pre-biotic evolution, 3-code should have resulted as a fusion of 1- and 2- codes to 3-codes involving fusion of $tRNA_1$ and $tRNA_2$ to $tRNA_3 \equiv tRNA$. Second hypothesis is that during RNA era the function of $tRNA_2$ was to generate $RNA_2$ double helix from single RNA strand and that amino-acids catalyzed this process. The considerations that follow strongly suggest that $tRNA_1$ was involved with a non-deterministic generation of new RNA sequences essential for the evolution. After the establishment of 3-code these two process fused to a deterministic process generating amino-acid sequences. RNA era could still continue inside cell and play an important role in evolution.

There is an interesting work about programming bio-molecular self assembly pathways [I27]. The catalytic self assembly of complexes of nuclei acids is carried out automatically by a program represented implicitly as a mixture of linear DNA strand acting as catalyst and so called hairpin DNA: s containing three nucleation sites $a_t$, $b_t$, $c_t$ - so called toeholds.

### 5.2.1 Key ideas

The basic idea is that a set of bio-molecular reactions can be programmed to occur in a desired order by using a generalization of lock and key mechanism. The simplest self assembly pathway can be specified by a collection of keys and locks. In the beginning there is only one key and the this key fits to only one door, which leads into a room with several doors. The lock eats the key but gives one or more keys. If the room contains several doors to which the keys fits, the reaction corresponds to addition of several branches to the already existing reaction product. By continuing in this manner one eventually ends up to the last room and at the last step the lock gives back the original key so that it can act as a catalyst.

The translation of this idea to a program defining self assembly pathway is following.

1. DNA hairpin define key structural element of the self-assembly program. Hairpin is a single-stranded DNA strand in meta-stable configuration having form A+B+C [I64] such that $B$ forms a loop and $C$ is a palindrome [I24] . The formal expression for palindromy is $C = A_t^*$: this means that $C$ read backwards ($C_t$) is conjugate $A^*$ of $A$ implying that $A$ and $C$ running in opposite direction can form a double helix (duplex) by hydrogen bonding. As catalytic $a^*$ acting as key forms a double helix with $a$, the hairpin molecule opens to a linear DNA molecule and energy is liberated. In this process original key is lost but the two other toeholds $b_t$ and $c_t$ contained by the hairpin become available as keys. Each hairpin in the mixture of catalyst and hairpin molecules has its own lock and two keys.

2. The process of opening new doors continues until all hairpin molecules are used. The key given by the last lock must be catalyst strand $a^*$. The outcome is a molecule consisting of pieces of DNA strands and can possess a very complex topology. For instance, the formation trees and star like structures can be easily programmed.

3. To run this program one needs only an optimal mixture of catalyst molecule and hairpin DNA molecules. In the applications discussed in [I27] hairpins have length of order 10 nm which corresponds to $L_e(151) = \sqrt{5}L(151)$ defining also cell membrane thickness. That $L_e(151)$ corresponds also to the length of 30-nucleotide sequence defining the codon of the code associated with Mersenne prime $M_{61} = 2^{61} - 1$ might not be an accident. The simplest applications are autocatalytic formation of DNA dublex molecules and of branched junctions, nucleated dendritic growth, and autonomous locomotion of a bipedal walker.

The basic idea in the realization of the autonomous motion of bipedal walker is to cheat the walker to follow a track marked by food. The walker literally eats the food and receives in this manner the metabolic energy needed to make the step to the next piece of food. The menu contains two kinds of hairpins (see **Fig. 1** ): hairpins $A$ attached regularly along the desired path of the walker (second DNA strand) and hairpins $B$ but not attached to the strand. The front leg $l$ of the walker attaches to $A$ and this catalyzes the formation of the duplex $A \cdot B$ as a waste and the liberated metabolic energy allows to make a step in which hind leg becomes the front leg.

### 5.2.2 TGD view about the situation

The possibility to program the self-assembly relies on the almost deterministic realization of the lock and key mechanism. The presence of braid strands could make this possible.

1. Consider first the hypothesis about the cancelation of anomalous DNA charge. The palindromic character of $A$ means that the neck of the hairpin has vanishing anomalous em charge and also vanishing color charge is possible. Hence palindromes are favored in TGD Universe. The circular piece $B$ is not in general color singlet. It could have braid strands connecting it to it to some other DNA or nuclear membrane but this is not necessary. Same applies to the toehold $a_t$ at the end of the other strand of neck.

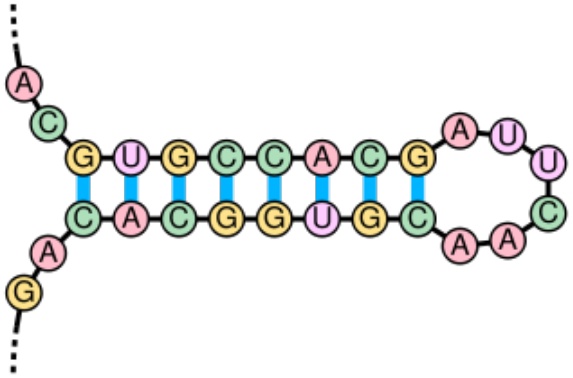


**Figure 1:** The structure of DNA hairpin (stem loop)

2. The attachment of the lock to key could be seen as a process in which a braid consisting of magnetic flux tubes connecting lock and key strands (DNA and its conjugate) is formed spontaneously and followed by a phase transition reducing $\hbar$ contracting the flux tubes and in this manner guiding the key to the lock.

If one assumes that only paired nucleotides of single DNA strand possess braid strands, one must assume the same for mRNA. As a consequence one would loose the nice interpretation for the formation of AAA... tail of mRNA as a manner to guarantee integer valuedness and small value (or even vanishing) of the anomalous em charge. If there is braid strands associated with entire mRNA, it could end at the nuclear membrane. In this case the transfer of tRNA to mRNA during translation by a phase transition reducing $\hbar$ of braid strands could be initiated by the fusion of the braid strand ends coming from mRNA codon and from its conjugate codon at tRNA at nuclear membrane.

## 5.3 The Archeology Of TRNA Molecules As A Guideline

The study of the structure of the ordinary tRNA molecule is of considerable help in the attempts to guess what might have been its predecessor.

### 5.3.1 The structure of the tRNA molecule

The shape of the tRNA molecule [I31] in 2-D representation is that of cruciform.

1. tRNA molecule has a cross like appearance, and decomposes into a body coded by tRNA gene and an acceptor stem which is same for all amino-acids and added separately and can be replaced during the lifetime of the tRNA molecule. Acceptor stem, to which the amino-acid is attached with the mediation of amino-acyl-tRNA synthase, can be said to be a passive component and is same for all tRNAs so that its structure does not determine which amino-acid is attached to it. The stem is not coded by genes and contains 4 nucleotides.

2. tRNA molecule can be seen as single RNA strand just as hairpin. The five stems are double helices analogous to the necks of the hairpin. Strand begins at $5'$ end of the acceptor stem directed upwards. The second strand of acceptor stem continues as a toehold ending to $3'$ end of tRNA. The toehold has at its end ACC to which the amino-acid (rather than conjugate DNA) attaches.

3. tRNA molecule (see **Fig. 2** ) contains three arms with hairpin structure. $A$ arm containing the anticodon is directed downwards. $D$ and $T$ arms are horizontal and directed to left and right. Between $T$ arm and $A$ arm there is additional variable hairpin like structure but with highly degenerate loop is degenerate. It has emerged during evolution.

4. The structure of tRNA minus anticodon depends on anti-codon which conforms with the fact $T$ and $D$ arms are related to the binding of amino-acid so that their nucleotide composition correlates with that of anticodon.

5. Anticodon arm contains the anticodon of mRNA codon and thus corresponds to RNA. For doublet part of the mRNA codon the correspondence is 1-1 but for the third nucleotide the correspondence is more complex due to wobble base pairing to be discussed below. Wobble base pairing indeed leads to the recent simplified model for the evolution of the triplet code as a fusion of 1-code and 2-code.

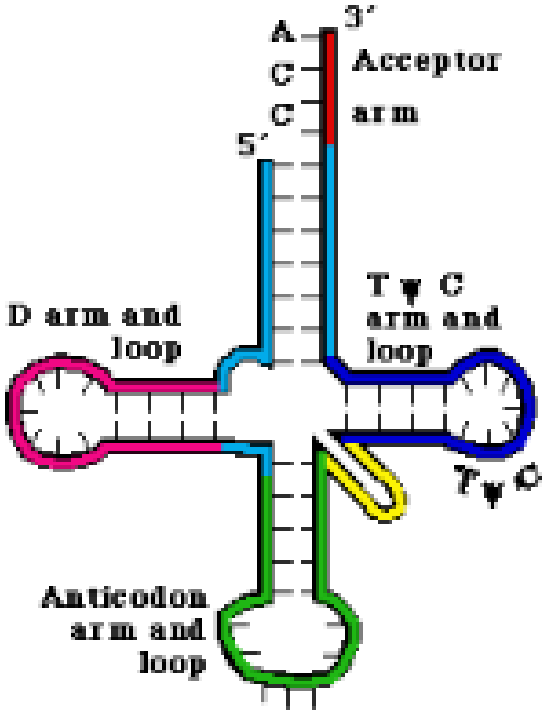


**Figure 2:** The structure of tRNA

### 5.3.2 Wobble base pairing

The phenomenon of wobble base pairing [I35] is very important. There are only about 40 tRNA molecules instead of 61 which means that one-to-one map between mRNA nucleotides and tRNA conjugate nucleotides is not possible. Crick suggests that so called wobble base pairing resolves the problem. What happens that the first nucleotide of anticodon is either $A$, $G$, $U$, or $I$(nosine) [I14]. The base-pairings for third nucleotide are $\{A-U, G-C, U-\{A,G\}, I-\{U,A,C\}\}$. The explanation for the non unique base pairing in the case of $U$ is that its geometric configuration is quite not the same as in ordinary RNA strand. $I$ is known to have 3-fold base pairing.

Minimization of the number of tRNAs requiring that only three mRNA codons act as stopping signs predicts that the number of tRNAs is 40.

1. It is convenient to classify the 4-columns of code table according to whether all four codons code for the same amino-acid ($(T,C,A,G) \to X$, whether 4-column decomposes into two doublets: $[(T,C),(A,G)] \to [X,Y]$, or whether it decomposes to triplet and singlet ($[(T,C,A),G] \to [ile, met]$). There are also the 4-columns containing stop codon: $[(U,C),(A,G)] \to [(tyr,tyr),(stop,stop)]$ and $[(U,C),A,G] \to [(cys,sys),stop,trp]$. Mitochondrial code has full A-G and T-C symmetries whereas for vertebrate nuclear code 3 4-columns break this symmetry.

2. Consider first 4-columns for which the doublet symmetry is broken. $[tyr, tyr, top, stop]$ column must correspond to first tRNA nucleotide which is $A$ or $G$ (tyr). The absence of anti-codons containing $U$ implies stop codon property. For $[cys, sys, stop, trp]$ one must have $A$, $G$ and $C$ but $U$ is not allowed. ile-met column can correspond to tRNAs with $I$ and $C$ as the first nucleotide.

3. For 4-columns coding for two doublet amino-acids the minimal set of first tRNA codons is $\{A, G, U\}$. For completely symmetric 4-columns the minimal set of tRNA codons is $\{I, U\}$. Thus $\{A, G, U, I\}$ would replace $\{A, G, U, C\}$.

4. There are 9 completely symmetric 4-columns making 18 tRNAs, 5 doublet pairs making 15 tRNAs, ile-met giving 2 tRNAs, and the columns containing stopping codons giving 5 tRNAs. Altogether this gives 18+15+2+5= 40. Also the deviations from the standard code can be understood in terms of the properties of tRNA.

Consider the interpretation of wobble base pairing in TGD framework assuming the braiding picture and the mapping of nucleotides to quarks. The completely symmetric 4-columns correspond to unbroken isospin and matter-antimatter asymmetries. 4-columns decomposing into doublets result from the breaking of matter-antimatter asymmetry at quark level. ile-met column corresponds to the breaking of both symmetries. The base pairings of $I$ obviously break both symmetries.

The non-unique based pairing of $U$ and $I$ means that they cannot correspond to a unique quark or anti-quark in braiding $U$ pairs with both $A$ and $G$ so that the braid strands starting from these RNA nucleotides must both be able to end to tRNA $U$. Hence tRNA $U$ is not sensitive to the isospin of the quark. This non-uniqueness could relate to the assumed anomalous geometric character of the binding of $U$ codon to tRNA sequence. The braid strands beginning from $U$, $A$, and $C$ must be able to end up to $I$ so that $I$ can discriminate only between $\{U, C, A\}$ and $G$.

### 5.3.3 Anomalous em charge and color singletness hypothesis for tRNA

One can test also whether the vanishing of anomalous em charge of tRNA leads to testable predictions. One can also try understand translation process in terms of the braiding dynamics. One must distinguish between the states of tRNA alone and tRNA + amino-acid for which braidings are expected to be different.

Before continuing it must be made clear that braiding hypothesis is far from being precisely formulated. One question is whether the presence of the braiding could distinguish between matter in vivo and vitro. For instance, the condition that anomalous em charge is integer valued or vanishing for DNA hairpins in vivo gives strong condition on the loop of the hairpin but or hairpins in vitro there would be no such conditions. Second point is that amino-acids and $I$ and $U$ in $\mathrm{tRNA}_1$ could carry variable anomalous em charge allowing rather general compensation mechanism.

*1. tRNA without amino-acid*

1. The minimal assumption is that braiding hypothesis applies only to the stem regions of tRNA in this case. In this case the strands can indeed begin from strand and end up to conjugate strand. The possibility of color singletness and vanishing of total anomalous em charge are automatically satisfied for the stem regions as a whole in absence of non-standard base pairings. In general the acceptor stem contains however $G*U$ base pair which is matter-antimatter asymmetric but breaks isospin symmetry and gives unit anomalous charge for the acceptor stem. Also other stems can contain $G*U$, $U*G$ pairings as also $P*G$ and $L*U$ pairings ($P$ and $L$ denote amino-acids Pro and Leu). The study of concrete examples [I28] shows that single G*U bond is possible so that anomalous em charge can be non-vanishing but integer valued for double strand part of tRNA. Suppose that a given amino-acid can have anomalous of any codon coding for it. If $P$ in $G*P$ pair has the anomalous em charge of the codon CCG, $G*P$ pair has vanishing anomalous em charge. If $L$ corresponds to CUA the value of anomalous em charge is integer.

2. The anomalous em charge in general fails to vanish for the loops of hairpins. For the braids possibly associated with the loops of tRNA the strands can only end up to tRNA itself or nuclear membrane. If there are no braid strands associated with these regions, there is no

color or anomalous em charge to be canceled so that the situation trivializes. On the other hand, in the case of tRNA $I$ and $U$ associated with the first nucleotide of the anticodon of tRNA can have a varying value of anomalous em charge. Therefore integer valued em charge and color singletness become possible for tRNA. tRNA can also contain amino-acids. If the amino-acids can carry a varying anomalous em charge with a spectrum corresponding to its values for DNA codons coding it, also they could help to stabilize tRNA by cancelling the anomalous em charge.

*2. tRNA plus amino-acid*

1. Amino-acyl tRNA synthetase, which is the catalyst inducing the fusion of amino-acid with ACC stem [I32], could have braid strands to both amino-acid and tRNA and have regions with opposite anomalous em charges compensating separately that of amino-acid and of the active part of tRNA. The required correlation of amino-acid with anticodon would suggest that both $D$ and $T$ loops and $A$-loop are included. The simplest option is however that the anticodon is connected by braid to amino-acid so that braiding would define the genetic code at the fundamental level and the many-to-one character of genetic code would reflect the 1-to-many character of amino-acid-quark triplet correspondence. This hypothesis is easy to kill: for the portion of catalyst attaching to a given portion of DNA strand amino-acids and codons should have opposite anomalous em charges: $Q_a(amino) = -Q_a(codon)$.

2. After the catalysis involving reduction of $\hbar$ amino-acid and tRNA would form a system with a vanishing net anomalous em charge but with a braiding structure more complex than that before the fusion.

3. In the translation process the braiding structure of tRNA- amino-acid system should reorganize: the braid strands connecting anticodon with amino-acid are transformed to braid strands connecting it to mRNA codon with a subsequent reduction of $\hbar$ of braid strands bringing tRNA into the vicinity of mRNA. In the transcription the anticodon-codon braiding would be replaced with amino-acid-mRNA braiding forcing formation of the amino-acid sequence. It will be later found that the simpler option without this step corresponds to the earlier hypothesis according to which amino-acids acted originally as catalysts for the formation of RNA double helix.

4. tRNA is basically coded by genes which suggests that the general symmetries of the genetic code apply to to the variants of tRNA associated with same anticodon. Hence the variants should result from each other by isospin splits and modifications such as permutations of subsequent nucleotides and addition of $AT$ and $CG$ pairs not changing overall color and isospin properties. Also anomalous base pairs $X*Y$ can be added provide their net anomalous em charge vanishes.

5. tRNA has a complex tertiary (3-D) structure [I30] involving base pairing of distant nucleotides associated with the roots of the stem regions where tRNA twists sharply. This pairing could involve formation of braid strands connecting the nucleotides involved. The reduction of Planck constant for these strands could be an essential element of the formation of the tertiary structure.

### 5.3.4 The fossilized components of tRNA as record about the evolution of the recent form of the genetic code

The ordinary tRNA indeed seems to contain in its structure fossilized components providing a record about how the molecular evolution proceeded. $tRNA_1$ and $tRNA_2$ correspond naturally to the horizontal and vertical segment in the recent tRNA formed as a fusion of $tRNA_1$ and $tRNA_2$ to form a cross like structure (see figure above). Hence $tRNA_1$ and $trNA_2$ should represent in their structures the respective genetic codes.

1. $tRNA_2$ should contain both the conjugate of the coding RNA nucleotide attaching to $RNA_2$ plus the conjugate of the coded nucleotide to which RNA nucleotide was attached and then

transferred to $RNA_2$ and added to the growing RNA sequence. This means that the structure of tRNA should help to deduce the doublet code experimentally. The pairs formed by the RNA triplet $XYZ$ at the end of the anticodon arm of the ordinary tRNA and the pair formed by the triplet $X'Y'Z'$ and its conjugate on right and left sides of $XYZ$ should provide detailed information about the doublet code. The pairs $XY - X'Y'$ should represent the doublet code apart from possible symmetry breaking effects. These effects might be induced at the level of $X'Y'Z'$-amino-acid correspondence level and thus not visible in the structure of tRNA.

2. The transition to the triplet code added one RNA nucleotide to both the exotic doublet $(XY)_2$ and the doublet $X'Y'$ and its conjugate coded by it. The exotic $2', 5'$ doublet plus the added singlet transformed to ordinary triplet. The simplest assumption is that these RNAs came from D arm and T$\psi$C arm. This is possible since all loops are physically near to each other. The structure of D and T$\psi$ loops conforms with the assumption that the predecessor of the first *resp.* second loop has lost the coding *resp.* coded RNA. The structure of these loops forces also to conclude that all tRNA loops have been stem like structures before their deactivation just as the acceptor stem is. Deactivation of $RNA_1$ translation process must have meant the completion of these stems to loops by addition of a conjugate of the conjugate of the coded RNA.

### 5.3.5 The components of tRNA as ribozymes which have acted originally as RNA polymerases

The mechanism of ribozyme catalyzed polymerization for both the exotic RNA with mono- *resp.* disphosphate backbones, and their their double strand can be guessed from the fact that the process can be seen as an unfaithful replication. Hence the tRNAs involved would play a role analogous to DNA polymeraze in the polymerization of DNA. The only difference is that, instead of the conjugate of the template strand, a copy of strand is reproduced and the copy can be un-faithful.

DNA replication utilizes the conjugate strand as a template and occurs with the mediation of DNA polymerase enzyme, which brings dXTP, $X = A, T, C, G$ rather than dXMP, to the vicinity of the DNA conjugate strand [I40]. The di-phosphate is cleaved out from dXTP and the liberated energy makes it possible to add the resulting dXMP to the growing DNA strand.

The prediction is that $tRNA_1$ and $tRNA_2$ have originally been ribozymes acting as exotic RNA polymerases. In the case of DNA strand dXMP pairs with its conjugate in the template strand by hydrogen bonds and $3', 5'$ bond is formed between monophosphate deoxiribose of previous nucleoside. In the case of exotic RNA strand the XMP associated with the tRNA pairs with its conjugate in the template RNA strand, $2', 5'$ bond with the ribose of the previous RNA unit is formed. tRNA is not so selective as a polymerase as DNA polymerase and this ultimately gives rise to the many-to-one correspondence crucial for the non-triviality of the genetic code.

1. $RNA_2$ consists of exotic RNA doublets with nucleotides connected by $2', 5'$ monophosphate bonds. $tRNA_2$ brings $2', 5'$ doublet $XMP_2 \circ YTP_2$ to the growing strand and glues it to the $5'$ position of the ribose in the already existing polymer. The YTP suffers the cleavage $YTP_2 \to YMP_2$ as in the case of DNA polymerization and the amount of metabolic energy provided by the cleavage is the same. The formation of $XMP_2 \circ YTP_2$ proceeds by gluing of $XTP_2$ to $YTP_2$ by a similar process so that the net metabolic energy used per nucleotide is essentially the same as in the ordinary DNA polymerization.

2. $RNA_1$ consists of exotic RNA singlets connected by $2', 5'$ diphosphate bonds. $tRNA_1$ brings $XTP_2$ near the growing strand, the cleavage $XTP_2 \to XDP_2$ occurs, and $XDP_2$ is glued to the $5'$ position of the ribose of the previous RNA nucleotide. The amount of metabolic energy provided by the cleavage is roughly one half of that in the case of $RNA_2$ polymerization, and this might partially explain why diphosphate exotic RNA strands are rare whereas monophosphate exotic DNA strands can be found inside cells. On the other hand, it is $ATP \to ADP$ cleavage, which usually occurs in the ordinary metabolism instead of $ATP \to$ AMP cleavage: only during a very intense metabolism $ATP \to$ AMP cleavage occurs. Since $ATP$ metabolism is a functional fossil from a very early period of evolution, one might expect that $ATP \to$ ADP cleavage has in fact occurred naturally, if not even more naturally, also in the polymerization of $2', 5'$ RNA during (exotic) RNA era.

3. In the case of double exotic RNA strand of ordinary and exotic RNA the predecessor of the recent tRNA formed by $tRNA_1$+$tRNA_2$ would be a ribozyme bringing energized singlet and doublet RNAs to the double strand acting as a template with $tRNA_1$ component catalyzing the cleavage of the monophosphate and $tRNA_2$ component catalyzing the cleavage of the diphosphate.

The crucial and testable prediction is that the ribozymes responsible for the exotic mono- and diphosphate $2',5'$ RNA polymerization should have a strong resemblance with the two structural components of the recent tRNA. Furthermore, the replication catalyzed by these ribozymes should be unfaithful, perhaps in a manner consistent with the genetic code before the breaking of its symmetries. Ribozymes responsible for the ordinary RNA polymerization are known but I am not aware about how much is known about the corresponding ribozymes in the case of $2',5'$ RNA. The building blocks of recent tRNA would however provide a good starting point for innovative RNA engineers. In any case, the very fact that this form of RNA does not even allow DNA, makes it a more natural candidate for the basic building block of RNA life than $3',5'$ RNA.

### 5.3.6 From RNA world to RNA-tRNA world to RNA-DNA-tRNA world to DNA-RNA-protein world: how it went?

I encountered a highly interesting work [I49] (see `http://tinyurl.com/y9ps2efz`) related to the emergence of RNA world and I warmly recommend it to the reader (for a popular article see `http://tinyurl.com/y7m3absu`).

First a summary of basic terms for the possible reader of the article. There are three key enzymes involved in the process which is believed to lead to a formation of longer RNA sequences able to replicate.

1. Ribozyme is a piece of RNA acting as catalyst. In RNA world RNA had to serve also as a catalyst. In DNA world proteins took this task but their production requires DNA and transcription-translation machinery.

2. RNA ligase promotes a fusion of RNA fragments to a longer one in presence of ATP transforming to AMP and diphospate and giving metabolic energy presumably going to the fusion. In TGD fUniverse this would involve generation of an atom (presumably hydrogen) with non-standard value of $h_{eff} = n \times h$ having smaller binding energy scales so that ATP is needed. These dark bonds would be involved with all bio-catalytic processes.

3. RNA polymerase promotes a polymerization of RNA from building bricks. It looks to me like a special kind of ligase adding only single nucleotide to an existing sequence. In TGD Universe $h_{eff} = n \times h$ atoms would be involved as also magnetic flux tubes carrying dark analog of DNA with codons replaced with dark proton triplets.

4. RNA recombinase promotes RNA strands to exchange pieces of same length. Topologically this corresponds to two reconnections occurring at points defining the ends of piece. In TGD Universe these reconnections would occur for magnetic flux tubes containing dark variant of DNA and induce the chemical processes at the level of chemistry.

Self ligation should take place. RNA strands would serve as ligases for the generation of longer RNA strands. The smallest RNA sequences exhibiting self-ligation activity was found to be 40-nucleotide RNA and shorter than expected. It had lowest efficiency but highest functional flexibility to ligate substrates to itself. R18 - established RNA polymerase model - had highest efficiency and highest selectivity. What I can say about the results is that they give support for the notion of RNA world.

The work is related to the vision about RNA world proposed to precede DNA-RNA-protein world. Why I found it so interesting is that it relates to on particular TGD inspired glimpse to what happened in primordial biology.

In TGD Universe it is natural to imagine 3 or even 4 worlds.There are two scenarios: RNA world, RNA-tRNA world, and DNA-RNA-protein world and RNA world, RNA-tRNA world, DNA-RNA-tRNA world and DNA-RNA-tRNA-protein world.

Years ago I developed a rather detailed version of the idea about transition from RNA world to DNA-RNA-protein world [K14] but I did not realize the tRNA-RNA world as intermediate step (see `http://tinyurl.com/y8ho27rq`).

1. RNA world would contain only RNA. Protein enzymes would not be present in RNA world and RNA itself should catalyze the processes needed to for polymerization, replication, and recombination of RNA. Ribozymes are the RNA counterparts of enzymes. In the beginning RNA would itself act as ribozymes catalyzing these processes.

2. One can also try to imagine RNA-tRNA world. The predecessors of tRNA molecules containing just single amino-acid could have catalyzed the fusion of RNA nucleotide to a growing RNA sequence in accordance with the genetic code. The function of tRNA would thus been different: since the roles of RNA codon and amino-acid would have been changed from the usual. Amino-acid sequences would not have been present at this stage since there would be no machinery for their polymerisation.

3. One can consider a transition from this world to DNA-RNA-tRNA world. This would storage of genetic information to DNA from which it would have been transcribed by using polymerase consisting of RNA. This phase would have required the presence of cell membrane like structure since DNA is stabilized inside membranes or at them. Transition to this world should have involved reverse transcription catalyzed by RNA based reverse-transcriptase. Being a big evolutionary step, this transition should involve a phase transition increasing the value of $h_{eff} = n \times h$.

4. My earlier proposal has been that a transition from RNA world to DNA-RNA-protein world took place. The transition could have also taken place from DNA-RNA-tRNA world to world containing also amino-acid sequences and have led to rapid evolution of catalysis based on amino-acid sequences.

   The amino-acid sequences originating from tRNA originally catalyzing RNA replication stole the place of RNA sequences as the end products from RNA replication. The ribosome started to function as a translator of RNA sequences to amino-acid sequences rather than replication of them to RNAs! The roles of protein and RNA changed! Instead of RNA in tRNA the amino-acid in tRNA joined to the sequence! The existing machinery started to produce amino-acid sequences!

   Presumably the modification of ribosome or tRNA involved addition of protein parts to ribosome, which led to a quantum critical situation in which the roles of proteins and RNA polymers could change temporarily. When protein production became possible even temporarily, the produced proteins began to modify ribosome further to become even more favorable for the production of proteins.

   But how to produce the RNA sequences? The RNA replication machinery was stolen in the revolution. DNA had to do that via transcription to mRNA! DNA had to emerge before the revolution or at the same time and make possible the production of RNA via transcription of DNA to mRNA. The most natural options corresponds to "before", that is DNA-RNA-tRNA world. DNA could have emerged during RNA-tRNA era together with reverse transcription of RNA to DNA with RNA sequences defining ribozymes acting as reverse transcriptase. This would have become possible after the emergence of predecessor of cell membrane. After that step DNA sequences and amino-acid sequences would have been able to make the revolution together so that RNA as the master of the world was forced to become a mere servant!

   The really science fictive option would be the identification of the reverse transcription as time reversal of transcription. In zero energy ontology (ZEO) this option can be considered at least at the level of dark DNA and RNA providing the template of dynamics for ordinary matter.

How the copying of RNA strand to its conjugate strand catalysed by amino-acid of tRNA could have transformed to translation of RNA to amino-acid sequence? Something certainly changed.

1. The change must have occurred most naturally to tRNA or - less plausibly - to the predecessor of the ribosome machinery. The change in the chemical structure of tRNA is not

a plausible option. Something more than chemistry is required and in TGD Universe dark matter localized at magnetic flux tubes is the natural candidate.

2. Evolution corresponds in TGD Universe gradual increase of $h_{eff} = n \times h$. A dramatic evolutionary step indeed took place. The increase of the value of $h_{eff} = n \times h$ for some structural element of tRNA could have occurred so that the catalysis for amino-acid sequence instead of that for RNA sequence started to occur.

3. The general model for bio-catalysis in TGD Universe involves a contraction of magnetic flux tubes by a reduction of $h_{eff}$ and bringing together the reacting molecules associated with flux tubes: this explains the magic looking ability of biomolecules to find each other in the dense molecular soup. The reduction of $h_{eff}$ for some dark atom(s) of some reacting molecules(s) to a smaller value liberates temporarily energy allowing to kick the reactants over a potential wall so that the reaction can occur (atomic binding energies scale as $1/h_{eff}^2$). After than the liberated energy is absorbed and ordinary atom transforms back to dark atom.

   In the recent case $h_{eff}$ associated with a dark atom (or atoms) of tRNA could have increased so that the binding energy liberated would have increased and allowed to overcome a higher potential wall than before. If the potential wall needed to overcome in the fusion of additional amino-acid to a growing protein is higher than that in the fusion of additional RNA to a growing RNA sequence, this model could work.

4. The activation energy for the addition of amino-acid should be larger than that for RNA nucleotide. A calculated estimate for the activation energy for the addition of amino-acid is 63.2 eV (see `http://tinyurl.com/yab6dmrm`). An estimate for the activation energy for the addition of RNA nucleotide at the temperature range 37-13 C is in the range 35.6 -70.2 eV (see `http://tinyurl.com/y8xwpvvg`). An estimate for the activation energy for the addition of DNA nucleotide is 58.7 eV (see `http://tinyurl.com/yc8nr4kh`) The value in the case RNA would be considerably smaller than that in the case of amino-acids at physiological temperature. For DNA and amino-acid the activation energy would be somewhat smaller than for amino-acid. This is consistent with the proposed scenario. I am not able to decide how reliable these estimates are.

The natural first guess is that the dark atoms are hydrogen atoms. It is however not at all clear whether "ordinary" hydrogen atoms correspond to $n = h_{eff}/h = n = 1$.

1. Randell Mills [D2] has proposed his notion of hydrino atom to explain anomalous energy production and EUV radiation in 10-20 nm range taking place in certain electrolytic system and having no chemical explanation. The proposal of Mills is that hydrogen atom can make in presence of a catalyst a transition to a lower energy state with a reduced size. I have already earlier considered some TGD inspired models for hydrino. The resemblance with the claimed cold fusion suggests that the energy production involved in the two cases might involve the same mechanism.

   I have considered two models for the findings [L11]. The first model is a variant of cold fusion model that might explain the energy production and the observed radiation at EUV energy range. Second model is a variant of hydrino atom assuming that ordinary hydrogen atom corresponds to $h_{eff}/h = n_H > 1$ and that catalyst containing hydrogen atoms with lower value of $n_h < n_H$ could induce a phase transition transforming hydrogen atoms to hydrinos with binding energy spectrum scaled up by scaling factor $(n_H/n_h)^2$ and radii scaled down by $(n_h/n_H)^2$. The findings of Mills favour the value $n_H = 6$.

2. Suppose the transition corresponds to a transition analogous to photon emission so that it occurs between $\Delta J = 1$ transitions of hydrogen atom. There are two simple options: either the direction of electron spin change but orbital angular momentum remains unaffected or the angular momentum of electron changes by $\Delta L = 1$ but spin direction does not change.

   The simplest assumption is that the principal quantum numbers in the initial and final state are $n_i = 1$ and $n_f \geq n_i$. Assume first that initial state with $(n_{Hi}, n_i = 1)$ having $L_i = 0$ and final state with $(n_{Hf}, n_f \geq n_i)$.

| $(n_{Hi}, n_i)$ | $(n_{Hf}, n_f)$ | $\Delta E/eV$ |
|---|---|---|
| $(3,1)$ | $(1,2)$ | 17.0 |
| $(4,1)$ | $(1,2)$ | 40.8 |
| $(4,1)$ | $(2,2)$ | 0.0 |
| $(5,1)$ | $(1,2)$ | 71.4 |
| $(5,1)$ | $(2,2)$ | 7.7 |
| $(6,1)$ | $(1,2)$ | 109.0 |
| $(6,1)$ | $(2,2)$ | 17.0 |

**Table 4:** The liberated energy in transition $(n_{Hi}, n_i = 1) \to (n_{Hf}, n_f = 2)$ in some cases.

3. The energy difference between the initial state with $(n_{Hi}, n_i = 1)$ and final state with $(n_{Hf}, n_f)$. The initial binding energy is the ordinary binding of thought-to-be hydrogen atom in the ground state: $E_i = E_f(n_{Hf}/n_{Hi})^2 \simeq 13.6$ eV. Here $E_f$ denotes the final ground state binding energy. The final state binding energy is $E_{fn_f} = E_f/n_f^2$.

   The liberated energy defining the order of magnitude for the activation energy (thermodynamical quantity) is given by

$$\Delta E = E_{fn_f} - E_i = \frac{E_f}{n_f^2} - E_f(\frac{n_{Hf}}{n_{Hi}})^2 = E_i\left[(\frac{n_{Hi}}{n_{Hf}})^2 n_f^{-2} - 1\right] \quad . \tag{5.1}$$

   The condition $\Delta E > 0$ gives

$$\frac{n_{Hi}}{n_{Hf}} > n_f \quad .$$

   For $n_{Hi}/n_{Hf} = n_f$ one has $\Delta E = 0$. For instance, this occurs for $(n_{Hi}, n_{Hf}) \in \{(2,1), (6,3), (6,2)\}$ $\Delta E > 0$ condition gives $n_{Hi} > 2$.

4. Consider first $n_i = n_f = 1$ for which the spin direction of electron changes if the transition is analogous to photon emission. By putting $n_f = 1$ in Eq. 5.1 one obtains a formula for the transition energy in this case. For instance, $(n_{Hi}, n_i) = (6,1) \to (n_{Hf}, n_f) = (3,1)$ would correspond to $\Delta E = 40.8$ eV perhaps assignable to RNA polymerization and the transition $(n_{Hi}, n_i) = (7,1) \to (n_{Hf}, n_f) = (3,1)$ to $\Delta E = 60.4$ eV perhaps assignable to amino-acid polymerization and DNA polymerization. Note that $n_H = 6$ is supported by the findings of Mills.

5. Table 4 gives the liberated energies $\Delta E$ for transitions with $(n_i, n_f) = (1,2)$ in some cases.

   The transitions $(4,1) \to (1,2)$ resp. $(5,1) \to (1,2)$ might give rise to the activation energies associated with RNA resp. amino-acid polymerization.

6. If ordinary hydrogen atom and atoms in general correspond to $h_{eff}/h = n = 1$, the liberated energies would be below the ground state energy $E_0 = 13.6$ eV of hydrogen atom and considerably below the above estimates. For heavier atoms the binding energy scale would be $Z^2$-fold and already for carbon with $Z = 6$ by a factor 36 higher. It is difficult to obtain $\Delta E$ in the scale suggested by the estimates for the activation energies.

One could try to test whether tRNA could be modified to a state in which RNA is translates to RNA sequences rather than proteins. This would require a reduction of $h_{eff} = n \times h$ for the dark atom in question.

## 5.4 Recent Genetic Code As A Fusion Of Singlet And Doublet Codes?

There are several guidelines helping to answer the question how DNA-amino-acid translation might have emerged from singlet and doublet codes producing only RNA from RNA.

The following vision about evolution leading from RNA era to the recent DNA-RNA-amino-acid era inspired by a combination of RNA world vision [I83] with the detailed study of the structure of tRNA suggesting the presence of 1- and 2-codes during RNA era with the DNA as TQC vision suggesting the presence of cell membrane like structures as a necessary ingredient making possible topological quantum computation like processes already during RNA era. The recent model is considerably simpler than the earlier models [K14].

### 5.4.1 RNA era and the transition to RNA-amino-acid era

1. Translation of mRNA to amino-acid sequences separates from the transcription of DNA to mRNA. One expects that during RNA two different kinds of RNAs, call them $\mathrm{RNA}_2$ and $\mathrm{RNA}_1$, analogous to mRNA and proteins existed. $RNA_2$ can be identified as the ordinary $3', 5'$ RNA acting in the role of mRNA. A natural candidate for $RNA_1$ playing the role of proteins is $2', 5'$ RNA since it is generated in the experiments of Orgel and appears also in genomes. Of course, also other candidates can be considered and the structure of tRNA gives valuable information about the character of this RNA. The copying of $\mathrm{RNA}_2$ to its conjugate was the counterpart of RNA replication. The transcription of $\mathrm{RNA}_2$ to $\mathrm{RNA}_1$ was the counterpart of translation.

2. The structure of tRNA, call it $\mathrm{tRNA}_3$, gives valuable information about the course of events leading to the translation of mRNA to amino-acids. The cross like structure of $\mathrm{tRNA}_3$ and the decomposition of RNA triplet appearing in it to 2-codon and 1-codon suggests that it resulted as a fusion of two hairpin like molecules $\mathrm{tRNA}_1$ and $\mathrm{tRNA}_2$. $\mathrm{tRNA}_2$ brought pairs of nucleotides forming the 2-codon part of RNA triplet to the growing $\mathrm{RNA}_2$ sequence during replication and 2-code was simply RNA conjugation. $\mathrm{tRNA}_1$ was involved with transcription of $\mathrm{RNA}_2$ to $\mathrm{RNA}_1$ bringing $\mathrm{RNA}_1$ nucleotides one-by own to the growing sequence. In $\mathrm{tRNA}_3$ the third nucleotide does not quite correspond to ordinary RNA but to to $A, G, U$ or $I$(nositol) and is believed to differ geometrically from ordinary nucleotide, and one can assume that these nucleotides were the building blocks of $\mathrm{RNA}_1$ possibly appearing in $2', 5'$ form. The phenomenon of the wobble pairing can be assumed to have been present already during RNA era so that correspondence 1-code was not not 1-to-1 nor deterministic but given by the correspondence $\{U \to A, C \to G, \{A, G\} \to U, \{U, A, C\} \to I\}$ deduced from the number 40 of tRNAs and assigning unique 1-codon to only $G$ could be interpreted as a many-to-one and non-deterministic correspondence generating new RNA sequences from existing ones. If there was $\mathrm{RNA}_2$ sequence coding for $\mathrm{tRNA}_1$, this sequence appearing in hairpin structure could have coded the inverse of the translation. As a consequence, the occurrence of transcription and its reversal generated a rapid evolution by creating new kinds of $\mathrm{RNA}_2$ sequences.

3. From the fact that amino-acids are attached to the ACC stem of $\mathrm{tRNA}_2$, one can guess that the role of amino-acids during RNA era was to catalyze the replication. If single amino-acid would have catalyzed the attachment of given RNA doublet to the growing sequence, there would be at most 16 amino-acids and genetic coded would not depend at all on the third nucleotide. This is indeed the case for roughly half of the code table (both matter antimatter symmetry and isospin symmetry with respect to third codon). For those mRNA codons for which A, G and T, C correspond to different amino-acids (breaking of matter antimatter asymmetry but isospin symmetry) two amino-acids catalyzed the attachment. Same amino-acid could also catalyzed two different attachments (ser, arg, leu for standard genetic code).

4. The crucial step was the fusion of the 1-code and 2-code to 3-code took place via fusion of $\mathrm{tRNA}_1$ and $\mathrm{tRNA}_2$ to $\mathrm{tRNA}_3$ along their ends containing $\mathrm{RNA}_1$ nucleotide and $\mathrm{RNA}_2$ doublet which thus combined to RNA triplet. Presumably $\mathrm{tRNA}_3$ in its original form was translated from a linear mRNA molecule and transformed spontaneously to the cross like shape because of the presence of palindrome structures in both. The original functions of tRNAs were not possible anymore since the triplet was not at the end of the molecule. The catalyzing amino-acid however was at the ACC end of and the function of $\mathrm{tRNA}_3$ became to assist the translation of mRNA to amino-acid sequence. For those 3-codons for which single amino-acid catalyzed the fusion of 2-codon, a full matter antimatter and isospin symmetry

resulted. For those 3-codons for which two amino-acids catalyzed the fusion, a breaking of matter antimatter symmetry took place in the sense that for given mRNA codon only the $tRNA_3$ corresponding to single amino-acid was stable. Isospin symmetry was broken only weakly or not at all (human mitochondrial code). Thus codons with A, G as third nucleotide almost always coded the first amino-acid and those with T, C as the third nucleotide the second one. Stopping codons resulted when all $tRNA_3$ corresponding to mRNA triplet were unstable. That same RNA can code for both amino-acid and act as a stop codon in certain situations, can be understood if the stability of corresponding $tRNA_3$ depends on the chemical environment.

### 5.4.2 Symbiosis with membrane bounded structures

In DNA as TQC picture nuclear and cell membranes make possible topological quantum computation. The magnetic flux tubes connecting DNA nucleotides to lipids of the cell membrane could also explain why DNA is stabile inside cell. The emergence of cell membranes consisting of lipids and generated via self-organization rather being coded by genes would have stabilized DNA generated in this manner during DNA-RNA-amino-acid era. Membrane bounded structures emerged when the space-time sheets corresponding to the p-adic length scale $k = 151$ emerged in the condensate.

Topological quantum computation should have taken place already during RNA era. This suggest that the counterpart of the cell membrane was present already at that time. Quite recently it was reported [I58] that DNA duplexes of length 6 to 20 base pairs can join to longer cylinders which in turn form liquid crystals and that the liquid crystal phase separates from the phase formed by single DNA strands. Long strands had been already earlier known to form liquid crystals. This encourages to think that also RNA duplexes are able to self-organize in this manner so that the analog of cell nucleus containing RNA double helices as genetic material could have existed already during RNA era.

The latter option would allow to distinguish between $RNA_2$ and $RNA_1$ used as building block of various structures. This suggests that $RNA_1$, which disappeared in the transition to RNA-amino-acid era, might have formed liquid membranes containing inside then $RNA_2$ such that $RNA_2$ nucleotides were connected by magnetic flux tubes to $RNA_1$ nucleotides. The minimal function of $RNA_1$ would have been to make possible the buildup of cell membrane. In this case the lengths of $RNA_1$ needed to be only of order $L_e(151) = 10$ nm. The sequences consisting of 30 $RNA_1$ base pairs would correspond roughly to the thickness of cell membrane and to the codon of $M_{61}$ code. Lipid layer of thickness 5 nm would correspond to roughly 16 base pairs and to the codon assignable to $M_{17}$. If magnetic flux tubes indeed stabilize DNA, the presence of $RNA_1$ membrane might have been enough to stabilize also DNA so that RNA era could have been followed by DNA-RNA era and eventually by DNA-RNA-amino-acid era with $RNA_1$ membrane being replaced by double lipid layer membrane.

### 5.4.3 Reverse transcription of RNA to DNA

The basic problem was how to build DNA sequences which would later take the command. If one, in conflict with the Central Dogma, assumes the presence of the predecessor of the so called reverse RNA transcriptase [J3] associated with retro-viruses (in particular HIV virus), one can understand how this step occurred. Reverse RNA transcriptase allowed to transform ordinary RNA sequences to DNA sequences inside newly emerged pre-nuclei. The reverse transcriptase catalyzes also the transcription of DNA back to RNA so that DNA began to produce new RNA.

Reverse transcriptase requires amino-acids sequences. Amino-acids appeared as catalysts in $tRNA_2$ already during RNA era but the spontaneous emergence of reverse transcriptase before RNA$\rightarrow$ amino-acids translation look improbable. After the fusion of $tRNA_1$ and $tRNA_2$ $RNA_2$ could replicate only if $tRNA_1$, $tRNA_2$ and $tRNA_3$ continued to live in symbiosis for some time. This could have led naturally to the generation of reverse transcriptase and DNA. After that DNA could have taken care of the production of RNA and $tRNA_1$ and $tRNA_2$ might have lost in the fight for molecular survival or at least their importance could have diminished. The emergence of DNA could have been associated with the replacement of $RNA_1$ membrane with ordinary cell

membrane. For instance, it might be that DNA was able to form only magnetic flux tubes only with lipid bilayer membrane.

The reverse transcription is not reliable (one error per about 1000 nucleotides), and this led to a rapid evolution of DNA analogous to that of HIV virus. This meant an escape from the fixed point situation, and a genuine DNA $\rightarrow$ RNA predecessor of the genetic code emerged. Together with the emergence of membrane bounded structures this meant genuine evolution at DNA level. Reverse transcription is possible only for the ordinary RNA and explains why exotic doublet RNA has disappeared from cell.

### 5.4.4 What were the first self replicators?

The TGD inspired model of pre-biotic evolution suggests a reasonable guess for the first self-replicating molecular entities. Both $tRNA_1$ and $tRNA_2$ molecules must have resulted as more or less copies of corresponding $RNA_2$ sequences (amino-acid was added after transcription to $tRNA_2$) and the minimal self-reproducing system could have consisted of $tRNA_1$, $tRNA_2$ and corresponding $RNA_2$ molecules. Since $tRNA_1$ and $tRNA_2$ are hairpins in the usual configuration and the mechanism making possible biochemical reaction series suggests that these hairpin molecules catalyzed the opening of the corresponding $RNA_2$ pieces and their coding to $tRNA_1$ or $tRNA_2$.

Note that double strands in the sense they occur for DNA are not necessary since the double strand part of hairpin is analogous to DNA double strand and the opening of hairpin structure is analogous to the opening of DNA double strand during transcription and replication. The non-determinism of 1-code could have rapidly led to a genuine evolution and one can also imagine a spontaneous generation of $RNA_2$ sequences as oligonucleotides consisting of copies of pieces of $RNA_2$ coding for $tRNA_2$.

Also more general hairpin might be used to construct a self-catalyzing system. Since exotic and normal RNA do not differ too much, a reasonable amount of guess work might allow to identify $tRNA_1$ and $tRNA_2$, and perhaps even create simple pre-biotic life-forms in the laboratory.

## 5.5 Is RNA Era Continuing Inside Cell Nuclei?

The last issue of [I38] contains an article about the discovery that only roughly one half of DNA expresses itself as amino-acid sequences. A detailed summary of the results has been published in Nature [I13]. The Encyclopedia of DNA Elements (ENCODE) project has quantified RNA transcription patterns and found that while the "standard" RNA copy of a gene gets translated into a protein as expected, for each copy of a gene cells also make RNA copies of many other sections of DNA. In particular, intron portions ("junk DNA", the portion of which increases as one climbs up in evolutionary hierarchy) are transcribed to RNA in large amounts. What is also interesting that the RNA fragments correspond to pieces from several genes which raises the question whether there is some fundamental unit smaller than gene.

None of the extra RNA fragments gets translated into proteins, so the race is on to discover just what their function is. TGD proposal is that the RNA gets braided and performs a lot of topological quantum computation [K31]. Topologically quantum computing RNA fits nicely with replicating number theoretic braids associated with light-like orbits of partonic 2-surfaces and with their spatial "printed text" representations as linked and knotted partonic 2-surfaces giving braids. An interesting question is how printing and reading could take place. Is it something comparable to what occurs when we read consciously? Is the biological portion of our conscious life identifiable with this reading process accompanied by copying by cell replication and as secondary printing using amino-acid sequences?

This picture conforms with TGD view about pre-biotic evolution. Plasmoids [I70], which are known to share many basic characteristics assigned with life, came first: high temperatures are not a problem in TGD Universe since given frequency corresponds to energy above thermal energy for large enough value of $\hbar$ [K13]. Plasmoids were followed by RNA, and DNA and amino-acid sequences emerged only after the fusion of 1- and 2-letter codes fusing to the recent 3-letter code. The cross like structure of tRNA molecules carries clear signatures supporting this vision. RNA would be still responsible for roughly half of intracellular life and perhaps for the core of "intelligent life".

I have also proposed that this expression uses memetic code which would correspond to Mersenne $M_{127} = 2^{127} - 1$ with $2^{126}$ codons whereas ordinary genetic code would correspond to $M_7 = 2^7 - 1$ with $2^6$ codons. Memetic codons in DNA representations would consist of sequences of 21 ordinary codons. Also representations in terms of field patterns with duration of.1 seconds (secondary p-adic time scale associated with $M_{127}$ defining a fundamental bio-rhythm) can be considered.

A hypothesis worth of killing would be that the DNA coding for RNA has memetic codons scattered around genome as basic units. It is interesting to see whether the structure of DNA could give any hints that memetic codon appears as a basic unit.

1. In a "relaxed" double-helical segment of DNA, the two strands twist [I29] around the helical axis once every 10.4 base pairs of sequence. 21 genetic codons correspond 63 base pairs whereas 6 full twists would correspond to 62.4 base pairs.

2. Nucleosomes [I21] are fundamental repeating units in eukaryotic chromatin [I7] possessing what is known as 10 nm beads-on-string structure. They repeat roughly every 200 base pairs: integer number of genetic codons would suggest 201 base pairs. 3 memetic codons makes 189 base pairs. Could this mean that only a fraction $p \sim 12/201$, which happens to be of the same order of magnitude as the portion of introns in human genome, consists of ordinary codons? Inside nucleosomes the distance between neighboring contacts between histone and DNA is about 10 nm, the electron Compton scale $L_e(151)$ associated with the Gaussian Mersenne $(1+i)^{151} - 1$ characterizing also cell membrane thickness and the size of nucleosomes. This length corresponds to 10 codons so that there would be two contacts per single memetic codon in a reasonable approximation. In the example of Wikipedia [I21] nucleosome corresponds to about 146=126+20 base pairs: 147 base pairs would make 2 memetic codons and 7 genetic codons. The remaining 54 base pairs between histone units + 3 ordinary codons from histone unit would make single memetic codon. That only single memetic codon is between histone units and part of the memetic codon overlaps with histone containing unit conforms with the finding that chromatin accessibility and histone modification patterns are highly predictive of both the presence and activity of transcription start sites. This would leave 4 genetic codons and 201 base pairs could decompose as memetic codon+2 genetic codons+memetic codon+2 genetic codons. The simplest possibility is however that memetic codons are between histone units and histone units consist of genetic codons. Note that memetic codons could be transcribed without the straightening of histone unit occurring during the transcription leading to protein coding.

## 5.6 Could Nanno-Bacteria Correspond To Predecessors Of TheTriplet Life-Forms?

The experiments of Leslie Orgel (at 1980) imitating the primordial ocean demonstrate the emergence of the exotic RNA for which doublet effectively replaces the triplet. The so called nanno-bacteria represent a mystery at the borderline between living and non-living matter. The web article of Robert L. Folk [I76], who is one of the pioneers in the field besides Y. Morita [I77] and E. O. Kajander [I56], provides a brief summary about nanno-bacteria and contains also references. A priori one cannot exclude the possibility that nanno-bacteria might represent a predecessor of the triplet code, perhaps even singlet or doublet life-form or their symbiosis.

### 5.6.1 Basic facts about nanno-bacteria

Nanno-bacteria (often called also nanobacteria) are considerably smaller than ordinary bacteria. The sizes of the nanno-bacteria vary from about 20 nm to.2 micro-meters. Thus the smallest nanno-bacteria have size scale not much above $L_e(151)$ so that optical microscope does not allow to study them. Indeed, geologists discovered nanno-bacteria by using scanning electron microscope.

Nanno-bacteria can originate a precipitation in calcite and argonite crystals by providing the seed of the crystal. Nanno-bacteria act also as catalysts by attracting cations to their negatively charged cell walls. They appear as dense clumps in various minerals and rocks such as limestones, dolomites, native sulphur crystals, and metallic sulfide minerals [I76]. Nanno-bacteria produce complex silicates such as clays, where their sizes can be as small as 30 nanometers. They are involved even with the construction of bird's eggs! Nanno-bacteria of size about.1 micro-meters

were found in the Martian meteorite ALH84001 [E4], and there is evidence that carbonaceous chondrite meteorite Allende [I76] contains them. According to Folk, the nanno-bacteria might the biological counterpart of the dark matter perhaps dominating over the ordinary bio-matter in the entire universe. An interesting question is how deep in the rock nanno-bacteria based life forms can survive. The hypothesis about intra-terrestrial life suggests that there is no limit here!

Although nanno-bacteria have been demonstrated to replicate [I76], the prevailing belief has been that nanno-bacteria cannot be real life forms since by their small size they cannot contain the usual genetic apparatus. A Finnish biologist Kajander and his collaborators have done a lot of self-funded pioneering work in the study of the nanno-bacteria [I56]. It has not been demonstrated that nanno-bacteria possess DNA-mRNA-amino-acid translation machinery, the existence of which is often taken almost as a definition for what it is to be a living system (a size larger than.2 micro-meters has been the second prevailing definition of a living system!). This failure could be understood if nanno-bacteria contain only replicating DNA or if only the RNA-to-RNA translation machinery exists possibly accompanied by RNA-DNA transcriptase transforming the code to DNA-RNA code. Due to the hard cell wall of nanno-bacteria, the study of DNA/RNA is very difficult but according to the Kajander's private communication to Folk [I76], the nanno-bacterial DNA exists and consists of very short strands.

### 5.6.2 Nanno-bacteria as RNA life?

Nanno-bacteria could correspond to some predecessor of the recent genetic code. One can consider several options.

1. Nanno-bacteria represent an RNA life form involving two kinds of RNA sequences and closed inside $RNA_1$ membrane. This does not require DNA.

2. If the claim of Kajander about about nanno-bacterial DNA is correct, then two options remain.

   i) Nanno-bacteria are able to just replicate DNA and do not possess genetic code. Thus nanno-bacteria would be at a higher level than viruses.

   ii) RNA-DNA reverse transcription is utilized so that nanno-bacteria could realize DNA-RNA code and would probably be at a higher developmental level than RNA life-forms but had not yet realized DNA-amino-acid code. The objection against this is that the reverse transcriptase enzyme probably requires RNA-amino-acid translational machinery.

One can ask what what RNA life-forms (option 1) would look if they still exist.

1. Singlet RNA would express itself as RNA sequences containing only U (or C) and A (or G) nucleotides. The tRNAs used by these life-forms should appear as fossil remnants in the ordinary tRNA.

2. In the case of a singlet life-form the layer could correspond to the length scale $L_e(2,73)\backslash = "L_e(146)$ and be formed by doublet atomic layer corresponding to the twin pair of p-adic length scales formed by $L_e(16,9)\backslash = "L_e(144)$ and $L_e(2,73)\backslash = "L_e(146)$.

3. In the case of doublet life-forms the length scale $L_e(2,29)\backslash = "L_e(145)$ and the tertiary p-adic length scale $L_e(3,7^2)\backslash = "L_e(147)$ form a twin pair and could define a double-layered structure. The reported hard cell wall could correspond to this double layered structure. A cell wall consisting of minerals (also nanno-bacteria induce also the precipitation of mineral crystals) might however be most appropriate for life-forms living in the pores of rock, and possibly utilizing tectonic energy in some form to satisfy their metabolic needs.

The generation of the triplet code would have been accompanied by the generation of double lipid layers and possibly a transition to water environment. The most natural location for the primitive RNA-RNA translation machinery is at the inner surface of a lipid membrane if present inside nanno-bacteria.

The singlet or doublet RNA life-forms and their fusions could correspond to what I have christened plasmoids. Intelligent looking plasma balls occur repeatedly in UFO reports and they are

also reported to occur around crop formations. There is even a report about a plasma ball in the act of constructing the crop formation. The plasmoid like life forms serving as couriers of ITs could be also seen as multi-cellulars consisting of nanno-bacterial cells or, more probably, of their predecessors. The immune response against nanno-bacteria and their predecessors generated during very early evolution would make possible encounters with crops and even humans (abduction experiences) without fatal consequences. The reported immune response against exotic doublet RNA suggests that plasmoids contain exotic doublet RNA. The visible light from plasmoids suggests that the metabolism indeed involves also the hot $k = 131$ space-time sheet so that ITs or IPs might be in question.

### 5.6.3 Was the encounter of nanno-bacteria and plasmoids the moment of Gaian fertilization?

Earth consists mostly of ancient meteorites known as chondrites. Carbonaceous chondrites are shown to contain not only basic bio-monomers but even nanno-bacteria. The meteoritic material can end up to the interior of Earth along magnetic flux tubes even today. Recall that this mechanism actually explains the magnetized iron from meteors found in crop circles [K8] ).

Thus IT life might have developed nanno-bacteria contained by meteorites in the womb of Mother Gaia. The bio-molecules/nanno-bacteria contained by the meteorites from outer space would thus take the role of the sperm as in panspermia theory.

There is a temptation to develop the fertilization metaphor to a more concrete level in order to understand what happened when the symbiosis of pre-nucleus containing DNAandpre-cell containing RNA was established and led to the development of the genetic code and established a genuine evolution.

1. The simple nanno-bacteria in the meteorites having only replicating DNA or perhaps only the ability to produce DNA nucleotides would have been the sperm. Cell nucleus is much smaller than cell and might itself be regarded as having originated from ancient nanno-bacteria. The much more complex pre-cells containing RNA, amino-acids, and reverse transcriptase as well as the potentiality for the realization of the genetic code plus the needed metabolic machinery, were located in the interior of Earth and played the role of the egg. Since the hot $k = 131$ space-time sheets essential for the metabolic machinery were also involved, primitive plasmoid is an excellent candidate for the egg.

2. The encounter of nanno-bacteria and plasmoids led to the fertilization of Mother Gaia. What is fascinating that balls of light reported to appear near the crop circles and reported to even fabricate them migh be there in order to get fertilized by nanno-bacteria contained by meteors! Alternatively, the simultaneous appearance of pre-biotic egg and sperm might be interpreted as a symbolic hint about what happened in the key event of the pre-biotic evolution.

# 6 Did Life Evolve In The Womb Of Mother Gaia?

The idea that Earth interior, even the hot regions at the boundary of core and mantle, could serve as a seat for life, sounds totally outlandish in the standard physics framework. The many-sheeted space-time and hierarchy of Planck constants however allow to consider at least half seriously this idea although I hasten to admit that during these years I have very often had the feeling that this is one of those painfully stubborn fix idees that like to tease imaginative theoretician. This idea has variants characterized by a varying degree of craziness. It is a fact that rocks contain simple life forms down to surprising depths. A crazier idea is that underground lakes could have served as seats for evolving life. The really crazy variant of the idea is that the boundary between mantle and Earth's core as a regions containing strong gradients has been a seat of self organization leading to the emergence of life in some form.

Recently however completely unexpected support for this idea came as I learned that the geological evolution of Earth involves an anomaly. The continents would fit nicely to form a single super continent (Wegener's theory does not predict complete fit) if the radius of Earth would have been at the time of Cambrian explosion by factor of 1/2 smaller than now. The fact that

Cambrian explosion is one of the biggies mysteries of biology puts bells ringing. For long time ago this anomaly has inspired what have been called Expanding Earth Theory but the physical mechanism giving rise to expansion has been lacking.

Quantum TGD provides this mechanism. TGD predicts that cosmic expansion does not take place smoothly but via quantum jumps induces by the growth of the Planck constant by a factor of 2 for space-time sheet considered. This holds true also in planetary scales and TGD variant of Expanding Earth theory predicts relatively fast expansion of Earth's radius with a factor 2. The sudden appearance of completely new life forms in Cambrian explosion could be understood as a burst of various multicellular life forms which have developed in the womb of Mother Gaia sheltered from UV light and meteoric bombardment. What remains open is how deep in Earth's interior life is possible. This of course depends also on the definition of life: probably biological life would not be possible at core mantle boundary but one can consider much more general forms of molecular life.

In the following I will proceed in stepwise manner from not totally crazy (I hope so) to really crazy and discuss first the quantum version of Expanding Earth theory and its possible connection with Cambrian explosion and only after consider the really crazy possibilities.

## 6.1 Quantum Version Of Expanding Earth Theory And Cambrian Explosion

TGD predicts that cosmic expansion at the level of individual astrophysical systems does not take place continuously as in classical gravitation but through discrete quantum phase transitions increasing gravitational Planck constant and thus various quantum length and time scales. The reason would be that stationary quantum states for dark matter in astrophysical length scales cannot expand. One would have the analog of atomic physics in cosmic scales. Increases of $\hbar$ by a power of two are favored in these transitions but also other scalings are possible.

This has quite far reaching implications.

1. These periods have a highly unique description in terms of a critical cosmology for the expanding space-time sheet. The expansion is accelerating. The accelerating cosmic expansion can be assigned to this kind of phase transition in some length scale (TGD Universe is fractal). There is no need to introduce cosmological constant and dark energy would be actually dark matter.

2. The recently observed void which has same size of about $10^8$ light years as large voids having galaxies near their boundaries but having an age which is much higher than that of the large voids, would represent one example of jerk-wise expansion.

3. This picture applies also to solar system and planets might be perhaps seen as having once been parts of a more or less connected system, the primordial Sun. The Bohr orbits for inner and outer planets correspond to gravitational Planck constant which is 5 times larger for outer planets. This suggests that the space-time sheet of outer planets has suffered a phase transition increasing the size scale by a factor of 5. Earth can be regarded either as n=1 orbit for Planck constant associated with outer planets or n= 5 orbit for inner planetary system. This might have something to do with the very special position of Earth in planetary system. One could even consider the possibility that both orbits are present as dark matter structures. The phase transition would also explain why n=1 and n=2 Bohr orbits are absent and one only n=3, 4, and 5 are present.

4. Also planets should have experienced this kind of phase transitions increasing the radius: the increase by a factor two would be the simplest situation.

The obvious question - that I did not ask - is whether this kind of phase transition might have occurred for Earth and led from a completely granite covered Earth - Pangeia without seas - to the recent Earth. Neither it did not occur to me to check whether there is any support for a rapid expansion of Earth during some period of its history.

Situation changed when my son visited me and told me about a Youtube video [F15] by Neal Adams, an American comic book and commercial artist who has also produced animations for

geologists. We looked the amazing video a couple of times and I looked it again yesterday. The video is very impressive artwork but in the lack of references skeptic probably cannot avoid the feeling that Neal Adams might use his highly developed animation skills to cheat you. I found also a polemic article [F1] of Adams but again the references were lacking. Perhaps the reason of polemic tone was that the concrete animation models make the expanding Earth hypothesis very convincing but geologists refuse to consider seriously arguments by a layman without a formal academic background.

### 6.1.1 The claims of Adams

The basic claims of Adams were following.

1. The radius of Earth has increased during last 185 million years (dinosaurs [I9] appeared for about 230 million years ago) by about factor 2. If this is assumed all continents have formed at that time a single super-continent, Pangeia, filling the entire Earth surface rather than only 1/4 of it since the total area would have grown by a factor of 4. The basic argument was that it is very difficult to imagine Earth with 1/4 of surface containing granite and 3/4 covered by basalt. If the initial situation was covering by mere granite -as would look natural- it is very difficult for a believer in thermodynamics to imagine how the granite would have gathered to a single connected continent.

2. Adams claims that Earth has grown by keeping its density constant, rather than expanded, so that the mass of Earth has grown linearly with radius. Gravitational acceleration would have thus doubled and could provide a partial explanation for the disappearance of dinosaurs: it is difficult to cope in evolving environment when you get slower all the time.

3. Most of the sea floor is very young and the areas covered by the youngest basalt are the largest ones. This Adams interprets this by saying that the expansion of Earth is accelerating. The alternative interpretation is that the flow rate of the magma slows down as it recedes from the ridge where it erupts. The upper bound of 185 million years for the age of sea floor requires that the expansion period - if it is already over - lasted about 185 million years after which the flow increasing the area of the sea floor transformed to a convective flow with subduction so that the area is not increasing anymore.

4. The fact that the continents fit together - not only at the Atlantic side - but also at the Pacific side gives strong support for the idea that the entire planet was once covered by the super-continent. After the emergence of subduction theory this evidence as been dismissed.

5. I am not sure whether Adams mentions the following objections [F3]. Subduction only occurs on the other side of the subduction zone so that the other side should show evidence of being much older in the case that oceanic subduction zones are in question. This is definitely not the case. This is explained in plate tectonics as a change of the subduction direction. My explanation would be that by the symmetry of the situation both oceanic plates bend down so that this would represent new type of boundary not assumed in the tectonic plate theory.

6. As a master visualizer Adams notices that Africa and South-America do not actually fit together in absence of expansion unless one assumes that these continents have suffered a deformation. Continents are not easily deformable stuff. The assumption of expansion implies a perfect fit of *all* continents without deformation.

Knowing that the devil is in the details, I must admit that these arguments look rather convincing to me and what I learned from Wikipedia articles supports this picture.

### 6.1.2 The critic of Adams of the subduction mechanism

The prevailing tectonic plate theory [F6] has been compared to the Copernican revolution in geology. The theory explains the young age of the seafloor in terms of the decomposition of the litosphere to tectonic plates and the convective flow of magma to which oceanic tectonic plates participate. The magma emerges from the crests of the mid ocean ridges representing a boundary of two plates and leads to the expansion of sea floor. The variations of the polarity of Earth's

magnetic field coded in sea floor provide a strong support for the hypothesis that magma emerges from the crests.

The flow back to would take place at so called oceanic trenches [F4] near continents which represent the deepest parts of ocean. This process is known as subduction. In subduction oceanic tectonic plate bends and penetrates below the continental tectonic plate, the material in the oceanic plate gets denser and sinks into the magma. In this manner the oceanic tectonic plate suffers a metamorphosis returning back to the magma: everything which comes from Earth's interior returns back. Subduction mechanism explains elegantly formation of mountains [F5] (orogeny), earth quake zones, and associated zones of volcanic activity [F8] .

Adams is very polemic about the notion of subduction, in particular about the assumption that it generates steady convective cycle. The basic objections of Adams against subduction are following.

1. There are not enough subduction zones to allow a steady situation. According to Adams, the situation resembles that for a flow in a tube which becomes narrower. In a steady situation the flow should accelerate as it approaches subduction zones rather than slow down. Subduction zones should be surrounded by large areas of sea floor with constant age. Just the opposite is suggested by the fact that the youngest portion of sea-floor near the ridges is largest. The presence of zones at which both ocean plates bend down could improve the situation. Also jamming of the flow could occur so that the thickness of oceanic plate increases with the distance from the eruption ridge. Jamming could increase also the density of the oceanic plate and thus the effectiveness of subduction.

2. There is no clear evidence that subduction has occurred at other planets. The usual defense is that the presence of sea is essential for the subduction mechanism.

3. One can also wonder what is the mechanism that led to the formation of single super continent Pangeia covering 1/4 of Earth's surface. How probable the gathering of all separate continents to form single cluster is? The later events would suggest that just the opposite should have occurred from the beginning.

### 6.1.3 Expanding Earth theories are not new

After I had decided to check the claims of Adams, the first thing that I learned is that Expanding Earth theory [F3], whose existence Adams actually mentions, is by no means new. There are actually many of them.

The general reason why these theories were rejected by the main stream community was the absence of a convincing physical mechanism of expansion or of growth in which the density of Earth remains constant.

1. 1888 Yarkovski postulated some sort of aether absorbed by Earth and transforming to chemical elements (TGD version of aether could be dark matter). 1909 Mantovani postulated thermal expansion but no growth of the Earth's mass.

2. Paul Dirac's idea about changing Planck constant led Pascual Jordan in 1964 to a modification of general relativity predicting slow expansion of planets. The recent measurement of the gravitational constant imply that the upper bound for the relative change of gravitational constant is 10 time too small to produce large enough rate of expansion. Also many other theories have been proposed but they are in general conflict with modern physics.

3. The most modern version of Expanding Earth theory is by Australian geologist Samuel W. Carey. He calculated that in Cambrian period (about 500 million years ago) all continents were stuck together and covered the entire Earth. Deep seas began to evolve then.

### 6.1.4 Summary of TGD based theory of Expanding Earth

TGD based model differs from the tectonic plate model but allows subduction which cannot imply considerable back-flow of magma. Let us sum up the basic assumptions and implications.

1. The expansion is or was due to a quantum phase transition increasing the value of gravitational Planck constant and forced by the cosmic expansion in the average sense.

2. Tectonic plates do not participate to the expansion and therefore new plate must be formed and the flow of magma from the crests of mid ocean ridges is needed. The decomposition of a single plate covering the entire planet to plates to create the mid ocean ridges is necessary for the generation of new tectonic plate. The decomposition into tectonic plates is thus prediction rather than assumption.

3. The expansion forced the decomposition of Pangeia super-continent covering entire Earth for about 530 million years ago to split into tectonic plates which began to recede as new non-expanding tectonic plate was generated at the ridges creating expanding sea floor. The initiation of the phase transition generated formation of deep seas.

4. The eruption of plasma from the crests of ocean ridges generated oceanic tectonic plates which did not participate to the expansion by density reduction but by growing in size. This led to a reduction of density in the interior of the Earth roughly by a factor 1/8. From the upper bound for the age of the seafloor one can conclude that the period lasted for about 185 million years after which it transformed to convective flow in which the material returned back to the Earth interior. Subduction at continent-ocean floor boundaries and downwards double bending of tectonic plates at the boundaries between two ocean floors were the mechanisms. Thus tectonic plate theory would be more or less the correct description for the recent situation.

5. One can consider the possibility that the subducted tectonic plate does not transform to magma but is fused to the tectonic layer below continent so that it grows to an iceberg like structure. This need not lead to a loss of the successful predictions of plate tectonics explaining the generation of mountains, earthquake zones, zones of volcanic activity, etc...

6. From the video of Adams it becomes clear that the tectonic flow is East-West asymmetric in the sense that the western side is more irregular at large distances from the ocean ridge at the western side. If the magma rotates with slightly lower velocity than the surface of Earth (like liquid in a rotating vessel), the erupting magma would rotate slightly slower than the tectonic plate and asymmetry would be generated.

7. If the planet has not experienced a phase transition increasing the value of Planck constant, there is no need for the decomposition to tectonic plates and one can understand why there is no clear evidence for tectonic plates and subduction in other planets. The conductive flow of magma could occur below this plate and remain invisible.

The biological implications might provide a possibility to test the hypothesis.

1. Great steps of progress in biological evolution are associated with catastrophic geological events generating new evolutionary pressures forcing new solutions to cope in the new situation. Cambrian explosion indeed occurred about 530 years ago (the book "Wonderful Life" of Stephen Gould [I78] explains this revolution in detail) and led to the emergence of multicellular creatures, and generated huge number of new life forms living in seas. Later most of them suffered extinction: large number of phylae and groups emerged which are not present nowadays.

   Thus Cambrian explosion is completely exceptional as compared to all other dramatic events in the evolution in the sense that it created something totally new rather than only making more complex something which already existed. Gould also emphasizes the failure to identify any great change in the environment as a fundamental puzzle of Cambrian explosion. Cambrian explosion is also regarded in many quantum theories of consciousness (including TGD) as a revolution in the evolution of consciousness: for instance, micro-tubuli emerged at this time. The periods of expansion might be necessary for the emergence of multicellular life forms on planets and the fact that they unavoidably occur sooner or later suggests that also life develops unavoidably.

2. TGD predicts a decrease of the surface gravity by a factor 1/4 during this period. The reduction of the surface gravity would have naturally led to the emergence of dinosaurs 230 million years ago as a response coming 45 million years after the accelerated expansion ceased. Other reasons led then to the decline and eventual catastrophic disappearance of the dinosaurs. The reduction of gravity might have had some gradually increasing effects on the shape of organisms also at microscopic level and manifest itself in the evolution of genome during expansion period.

3. A possibly testable prediction following from angular momentum conservation ($\omega R^2 = constant$) is that the duration of day has increased gradually and was four times shorter during the Cambrian era. For instance, genetically coded bio-clocks of simple organisms during the expansion period could have followed the increase of the length of day with certain lag or failed to follow it completely. The simplest known circadian clock is that of the prokaryotic cyanobacteria. Recent research has demonstrated that the circadian clock of Synechococcus elongatus can be reconstituted in vitro with just the three proteins of their central oscillator. This clock has been shown to sustain a 22 hour rhythm over several days upon the addition of $ATP$: the rhythm is indeed faster than the circadian rhythm. For humans the average innate circadian rhythm is however 24 hours 11 minutes and thus conforms with the fact that human genome has evolved much later than the expansion ceased.

4. Scientists have found a fossil of a sea scorpion with size of 2.5 meters [I41], which has lived for about 10 million years for 400 million years ago in Germany. The gigantic size would conform nicely with the much smaller value of surface gravity at that time. The finding would conform nicely with the much smaller value of surface gravity at that time. Also the emergence of trees could be understood in terms of a gradual growth of the maximum plant size as the surface gravity was reduced. The fact that the oldest known tree fossil is 385 million years old [I68] conforms with this picture.

### 6.1.5 Did intra-terrestrial life burst to the surface of Earth during Cambrian expansion?

Intra-terrestrial hypothesis is one of the craziest TGD inspired ideas about the evolution of life and it is quite possible that in its strongest form the hypothesis is unrealistic. One can however try to find what one obtains from the combination of the IT hypothesis with the idea of pre-Cambrian granite Earth. Could the harsh pre-Cambrian conditions have allowed only intra-terrestrial multicellular life? Could the Cambrian explosion correspond to the moment of birth for this life in the very concrete sense that the magma flow brought it into the day-light?

1. Gould emphasizes the mysterious fact that very many life forms of Cambrian explosion looked like final products of a long evolutionary process. Could the eruption of magma from the Earth interior have induced a burst of intra-terrestrial life forms to the Earth's surface? This might make sense: the life forms living at the bottom of sea do not need direct solar light so that they could have had intra-terrestrial origin. It is quite possible that Earth's mantle contained low temperature water pockets, where the complex life forms might have evolved in an environment shielded from meteoric bombardment and UV radiation.

2. Sea water is salty. It is often claimed that the average salt concentration inside cell is that of the primordial sea: I do not know whether this claim can be really justified. If the claim is true, the cellular salt concentration should reflect the salt concentration of the water inside the pockets. The water inside water pockets could have been salty due to the diffusion of the salt from ground but need not have been same as that for the ocean water (higher than for cell interior and for obvious reasons). Indeed, the water in the underground reservoirs in arid regions such as Sahara is salty, which is the reason for why agriculture is absent in these regions. Note also that the cells of marine invertebrates are osmoconformers able to cope with the changing salinity of the environment so that the Cambrian revolutionaries could have survived the change in the salt concentration of environment.

3. What applies to Earth should apply also to other similar planets and Mars [E2] is very similar to Earth. The radius is .533 times that for Earth so that after quantum leap doubling the

radius and thus Schumann frequency scale (7.8 Hz would be the lowest Schumann frequency) would be essentially same as for Earth now. Mass is.131 times that for Earth so that surface gravity would be.532 of that for Earth now and would be reduced to.131 meaning quite big dinosaurs! have learned that Mars probably contains large water reservoirs in it's interior and that there is an un-identified source of methane gas usually assigned with the presence of life. Could it be that Mother Mars is pregnant and just waiting for the great quantum leap when it starts to expand and gives rise to a birth of multicellular life forms. Or expressing freely how Bible describes the moment of birth: in the beginning there was only darkness and water and then God saidLet the light come!

To sum up, TGD would provide only the long sought mechanism of expansion and a possible connection with the biological evolution. It would be indeed fascinating if Planck constant changing quantum phase transitions in planetary scale would have profoundly affected the biosphere.

## 6.2 Did Pre-Biotic Life Evolve In Mantle-Core Boundary?

In the sequel this question is taken to mean simple prebiotic life forms preceding the life that possibly developed in underground seas near to the surface of Earth. One can imagine that prebiotic life moved from high temperature environment in the Earth's interior to the underground seas and charged molecules polymerized in this process and generated gel like phase around them.

### 6.2.1 Some arguments supporting IT life

The following arguments favor IT hypothesis.

1. Life would have originated already in interstellar space via evolution of primitive metabolic cycles involving temporary chemical storage of metabolic energy. The decay of molecules would have been induced by incoming radiation in UV and visible range and fusion would have occurred spontaneously liberating energy quantum. As stars and planetary systems formed these primordial predecessors of life would have naturally ended into the planetary and even interiors and received their metabolic energy from the hot environment.

   The dropping of particles, in particular protons and electrons, to large space-time sheets could have provided fundamental metabolic energy quanta, and the anomalies lines in the IR, visible, and UV radiation from interstellar space indeed contains this kind of lines with energies which can be understood in terms of the spectrum of these quanta [K3].

   In many-sheeted space-time particles topologically condense at all space-time sheets having projection to given region of space-time so that this option makes sense only near the boundaries of space-time sheet of a given system. Also p-adic phase transition increasing the size of the space-time sheet could take place and the liberated energy would correspond to the reduction of zero point kinetic energy. Particles could be transferred from a portion of magnetic flux tube portion to another one with different value of magnetic field and possibly also of Planck constant $h_{eff}$ so that cyclotron energy would be liberated. In the following only the "dropping" option is discussed.

2. Boundary layers are ideal places for self-organization since they contain gradients which give rise to energy currents feeding self-organization. Liquid state is certainly crucial for life since this makes it possible quantum control the atomic space-time sheets very effectively. Ordinary life relies actually on the liquid crystal property of water which suggests that the same is the case quite generally. Thus those parts of the planetary core which correspond to boundary regions between solid and liquid phases and thus analogous to ordered water, could be ideal places for IT life forms to flourish, and it is actually difficult to imagine any other state of matter making possible life able to control the surrounding world effectively.

3. This picture is consistent with and would realize concretely the general vision about magnetosphere as a living system. In Earth's interior the mantle-core and core-inner core boundaries are especially interesting in this respect since these boundaries represent solid liquid boundaries.

4. Mg, Fe, Al, Si, and O are the dominant elements in mantle. Also Ca is present. These are the basic minerals involved with life. Also the minerals believed to be important for the evolution of polymer structures (like kaolinites consisting of Al, Si, and O) could form both at the hot space-time sheets and atomic space-time sheets. Below mantle-core boundary Fe and S are the prevailing elements. Fe-S centers play a key role in high temperature and pressure models for photosynthesis pathways [I43]. The establishment of the photosynthesis has been proposed to occur first in a sulphur containing environment with S replacing O. Inner core contains mainly Fe at hot space-time sheets.

5. A further possibly important aspect is the transparency of the liquid glass state at mantle-core boundary implying that visible light propagates over long distances without absorption. This might be absolutely essential for the possibility of visible photons to propagate through sufficiently long distances. For dark photons situation changes, and the transparency of liquid glass might be due the fact that some fraction of photons propagate as dark photons through it. Hence quartz is transparent in liquid state, and thus an optimal candidate for a medium whose behavior is quantum controlled from larger space-time sheets.

6. Magnetic body means the presence of both magnetic nervous system and the analog of blood circulation which could bring in sufficient amounts of elements needed for the synthesis of bio-polymers. The low concentrations of the elements needed to build up bio-monomers need not be a problem anymore since magnetic Mother Gaia could control them.

### 6.2.2 Structure of the Earth's interior and IT life

Combining the above described general ideas with the knowledge about Earth interior, one ends up with a more detailed picture.

1. Earth's interior decomposes into a relatively thin crust of thickness 30-60 km; a plastic mantle consisting mainly of Si, O, Mg, Fe, and Al mostly in form of silicates FeO-$SiO_2$ and MgO-$SiO_2$; a liquid core containing mainly Fe and S; and the inner core consisting mainly of solid Fe. There are thus two solid-liquid boundary regions. The upper boundary region could contain at least glass in liquid crystal form and the lower boundary region Fe in liquid crystal form.

2. Theoretically, the thickness for the mantle-core layer is expected to be of order few meters. The reflection of tectonic waves from mantle-core boundary has given evidence for a rich structure at this boundary and suggests that this expectation is not quite correct [F16]. Structures of thickness about 150 meters and with of several kilometers and between liquid and solid state have been identified at the top of the liquid core. One explanation is that lighter elements in the core-inner core boundary saturate and condense to solid form and being lighter than iron, raise up and form kind of puddles at the highest points of core.

   A more radical explanation is that these structures relate to a highly developed self-organization patterns which have given rise to some kind of life-forms. In the mantle-core layer the velocity of tectonic waves gets ultra-low. The velocity of sound in solid phase is quite generally higher than in liquid phase: this reflects directly the fact that the approximately harmonic forces between atoms are stronger. If liquid crystal phase is present the velocity in transversal liquid directions should be low. What is fascinating that sooner or later the analysis of reflected tectonic waves could give detailed information about mantle-core boundary.

3. Earth contains a previously unidentified core region with size of 300 km [F9]. Assuming that the magnetic field behaves like a dipole field down to the distances of order 300 km, the electronic cyclotron frequency at this distance is 5 GHz which corresponds to the wave length of about 6 cm, the size scale of BOLs for the dark companion $B_{end} = 2B_E/5$ of $B_E$. If the magnetization density below this distance is constant (so that the core would be like ordinary magnet), the magnetic field would be constant below this length scale.

Also some other experimental findings support this picture. It has been found that the times for of the compressional waves to travel through Earth in magnetic north-south direction and equatorial direction differ by 2-3 seconds [F14]. This suggests a gigantic crystal structure with symmetry

axis parallel to magnetic field. If the join along boundaries/flux tube condensate associated with atomic space-time sheets is hollow with a hole of radius 300 km, and if only $k = 151$ space-time sheet consisting of cold and magnetized iron is at this space-time sheet one can understand the crystal structure and how Earth's magnetic field results by magnetization. The estimated velocity of propagation for compressional waves in the crystal is about 3 km/s which is rather near to the 5 km/s for steel at room temperature. The appearance of a relatively small hole at the atomic space-time sheet is not so surprising since typically the field equations of TGD imply hole like singularities at given space-time sheet, and the hole could be analogous to black hole like singularity carrying inertial and gravitational masses at its boundary.

The simplest hypothesis is that the magnetic field associated with the plasmoids is the Earth's magnetic field in the core region of Earth. This would mean that some kind of plasmoid like life forms could reside also at the boundary layer associated with the new core. If the $k = 151$ space-time sheet is not ferromagnet above the radius $r = 300$ km, the boundary region could be in spin glass type magnetic phase and the bio-control from magnetic flux tubes would operate on the local direction of magnetization of the magnetized regions in the boundary region.

## 6.3 What Conditions Can One Pose On Life At Mantle-Core Boundary?

In the following some conditions on life at high temperatures at pressures are discussed as a mere intellectual exercise certainly not to meant taken deadly seriously. The speculations rely on the ideas which should be already familiar such as presence of strong gradients driving self-organization as indeed found in mantle-core boundary, magnetic bodies as controllers of biological bodies, dark matter as phases with large value of Planck constant able to form macroscopic quantum phases even at high temperatures, and the notion of universal metabolic currencies. Gel-sol phase transitions are also key element in the model of life. The condition that topological quantum computation like information processing based on braids requires existence of some kind of polymers defining braids and consisting of some basic building blocks stable under the conditions in question. The presence of analogs of lipids and cell membranes might be argued to be also necessary.

### 6.3.1 Plasmoid life as minimum option

The least non-realistic assumption is that IT life corresponds to plasmoid like life forms having magnetic body containing dark matter with large Planck constant controlling visible matter at high temperatures and in plasma phase. Fractality suggests that the high frequency analog of EEG is present and allows magnetic body to use the visible body as a sensory receptor and motor instrument. Frequencies and the values of Planck constant should be such that the energies of dark photons are above thermal energy. General vision about evolution suggests that the values of Planck constant are not very high so that frequency scale should be rather high.

1. Only biologically important ions and relatively simple molecules are expected to be present. Primitive metabolic cycles based on the fusion and decay of molecules induced by the radiation coming from environment can be considered. Cyclotron Bose-Einstein condensates of ions at magnetic flux tubes correspond to energies above thermal threshold only if the magnetic field is strong enough.

2. At temperature of about 4000 K at mantle core interior hydrogen bonds are still stable and metabolic energy quantum of $E_0 = .5$ eV is near thermal energy. There exists of course other metabolic quanta comings as power of two multiples of this quantum. Hence one can assumes that the dropping of protons and possibly of electrons from larger space-time sheets is responsible for metabolic energy quanta also now. One might argue that the typical p-adic length scale associated with the space-time sheets corresponds to the de-Broglie wave length a $\lambda_{dB} = \sqrt{3}\hbar/\sqrt{2mT}$ associated with electron. For electron this wavelength is around 35 slightly below $L(149) = 50$ A defining the thickness of the lipid layer of ordinary cell membrane. This scale increases with increasing $\hbar$.

3. Dark micro-waves amplified by quartz crystals might be crucial for the metabolism of plasmoid life-forms and replace visible light serving as the "food" of the terrestrial life forms. Tectonic activity might be as important for these life-forms as solar radiation is for us. The

crust and mantle could serve as amplifiers of em waves is a wide wave length range and make possible communications between IT and us.

### 6.3.2 Could topological quantum computation like activities be considered?

Could even more advanced life forms have evolved in the environment provided by mantle-core boundary? The presence of magnetic body makes possible braidings and simple versions for the mechanisms of memory, of topological quantum computation like information processing, and of catalysis. The presence of braids could be taken almost as a basic prerequisite of life. The presence of polymers of some basic molecules seems necessary if one wants something resembling DNA as TQC.

1. The presence of polymers consisting of some thermally stable basic units is the basic requirement. Hydrocarbons, lipids, amino-acids, and nucleotide polymers are not chemically stable at temperatures considered and mantle contains carbon only in trace amounts. The dominating elements in mantle are $O$, $Si$, and Mg whereas $C$ is present only in trace amounts. $S$ is present in core and thus also in mantle-core boundary. $P$ is so called siderophilic element meaning that it tends to avoid $Si$. It is theorized that during the formation of Earth from magma ocean siderophilic elements including $P$ separated from the mantle and went to core. In [F10] ratio of concentrations of $P$ in core and mantle was estimated to be $D(P) = 30$ but the article does not report the concentration of $P$ on mantle. In [F11] the phosphorus content of upper mantle is reported to be in the range 130-220 ppm which would give 3-7 percent in core. One can also imagine a formation of phosphate deposits in mantle core boundary: in absence of oxygen these kind of deposits are formed at sea floor. This kind of deposits might have formed at the top of the solid structures reported to exist at mantle core boundary [F16]. These structures could themselves have formed as light elements from inner core has gradually diffused to the mantle core boundary and could include phosphate deposits. If so then mantle-core boundary could contain considerable amounts of $P$ and the replacement $C, N, O$ with $Si, P, O$ or $Si, P, S$ might make sense.

2. Water flow is not the only flow which could generate the self-organization patterns defining braidings as the analogs of TQC programs. Since $O$ dominates in mantle water is however the first guess. It is known that lower mantle can contain water at least up to.2 weight per cent [F12]. Water molecules are stable at the temperatures considered. The phase diagram of water [D1] shows that water is in overcritical phase in the temperatures and pressures considered4000 K and 1.4 million atm and at the bottom of the mantle.

3. The replacement of $O$ with $S$ might be considered in the mantle-core boundary since $S$ is present in liquid core. Water would be replaced with hydrogen sulfide $H_2S$ (responsible for the smell of rotten eggs!) if it appears in liquid form $H_2S$ at temperatures and pressures considered. $H_2S$ could be also used as food. $H_2S$ is used by some bacteria living in deep ocean volcanic vents as a nutrient and also in our own gut: chemically this means that $H_2S$ acts as electron donor in primitive photosynthesis like process to give $ATP$. That sulphur is essential for growth and physical functioning of plants might be due to the fact that it preceded oxygen based life [F2]. For instance, Cys and met containing sulphur are very important amino-acids.

4. The polymers should contain atoms acting as plugs for flux tubes acceptors flux tubes ($O =$ or $S =$) and terminal points of flux tubes identifiable as donors of hydrogen bonds. $S-H$ shows only very weak tendency for hydrogen bonding so that $Si, P, O$ option looks more promising and is of course especially natural if IT life forms are considered. For instance, silicic acids [F7] satisfying the formula $[SiO_x(OH)_{4-2x}]_n$ are candidates for polymers containing both $O =$: s and $OH$: s. The presence of $PO_4$ could have made possible the formation simple analogs of nucleotides and AMP, $ADP$, and $ATP$ molecules. It might be possible to abstract nucleotides with a polymer consisting of four different simple molecules which are phosphorylized and attached to the backbone made of sugars.

5. One can continue the analogy with carbon life even further. The backbone could consist of the variants of riboses with carbon cycles replaced with Si cycles, the variants of aromatic

rings with $C$ and $N$ replaced with $P$, and base pairing between $N-H$ and $O=$ replaced with $P-H$ and $O=$. In the case of amino-acids one can also consider the replacement of $C, N \to Si, P$. It is of course far from obvious that the possibly existing silicon analogs of organic polymers are stable enough against rapid burning to $SiO_2$ and water. One might hope that the higher mass of $Si$ stabilizes them chemically at temperatures involved. Professional chemist could probably kill this kind of ideas without big effort.

Could one consider analogs of cell membrane and gel phase crucial for cellular life?

1. The first guess would be that gel like phase might have emerged only after these plasmoid like life-forms came in contact with water and induced the generation of structure water in presence of metabolic energy feed. On the other hand, it could well be that structured dater might form around charged polymers also at high temperatures and pressures as in the case of ordinary cell. Also silica ($SiO_2$) is known to form a gel. Also glass consists of $SiO_2$: the transparency of glass to visible light might be also relevant. A group of algae polymerize silicic acid to so called biogenic silica used to construct their cell walls.

2. Lipids forming cell membrane would be replaced with structures consisting of hydrosilicons with the silicon analog of carbon residue as its hydrophilic head and silicon analog of the hydrophobic fat forming the tail of the lipid. The formation of these double layers would be an outcome of self-organization. The analogs of phospholipids having $PO_4$ at their hydrophilic tail would be needed for TQC.

3. Super-conductivity plays an essential role in the TGD based model for cell membrane. Large enough values of Planck constant in principle allow to have super-conductivity at magnetic flux tubes.

4. The requirement that the energy $E = ZeV$ associated with Josephson junctions over the cell membrane like structure is above thermal energy requires very strong electric field over the membrane unless the membrane is thick. In the case of ordinary cell membrane the energy is rather near to thermal energy at room temperature. Now the energy would be roughly ten times higher and correspond to about.5 eV. Whether this kind of strong electric field is realizable is not clear. One might hope that the densities of ions could be high enough in the dense environment.

### 6.3.3 Do metabolism and photosynthesis possess signatures telling about intra-terrestrial evolution?

Also the intra-terrestrial metabolism should rely on atomic/molecular "Karma's cycles". Assume that the protons and electrons can be modeled as free particles in box. This assumption might not be correct as the model for $ATP$- $ADP$ involving Coulomb binding energy of proton with negatively charge $ATP$ molecule reducing the size of metabolic energy quantum already demonstrated. In this case the wavelength would be roughly by a factor 1/2 longer than predicted meaning Coulombic binding energy of order.25 eV.

In any case, with this assumption the quanta saturating to $E_{max}(k) = [.5, 1, 2, 4, 8, 16]$ eV and wavelengths $\lambda_{min} = [1240, 620, 310, 155]$ nm could have been important. The maximal quanta $E_0(k)$ correspond to the dropping from space-time sheet labeled by $k = 137 - \Delta k$ (in the case of proton) to a very large space-time sheet. The size of the space-time sheets would be given by $L(k) = r \times 2^{(k-151)/2} \times L(151)$, $L(151) = 10$ nm and $r = \hbar/\hbar_0$ the ratio of the Planck constant in question to its standard value. Actually and entire spectrum of quanta given by the formula $E_n = (1 - 2^- n)E_0(k)$ saturating to $E_0(k)$ for large values of $n$. In [K3] the presence of unidentified lines in the spectrum of UV, visible, and IR radiation from interstellar space has been shown to have a satisfactory explanation in terms of universal metabolic energy quanta.

The spectrum of diffuse interstellar medium exhibits three poorly understood structures [I15]: Unidentified Infrared Bands (UIBs), Diffuse Interstellar Bands (DIBs) [I8], and Extended Red Emission (ERE) [I82] allowing an interpretation in terms of dropping of protons or electrons (or their Cooper pairs) to larger space-time sheets. The model also suggests the interpretation of bio-photons in terms of generalizes EREs.

1. Unidentified infrared bands (UIBs) contain strong bands at $\lambda = 3300, 6200, 11, 300$ nm. Th

2. There are diffuse interstellar bands (DIBs) at wavelengths 578.0 and 579.7 nanometers and also at 628.4, 661.4 and 443.0 nm. The 443.0 nm DIB is particularly broad at about 1.2 nm across - typical intrinsic stellar absorption features are 0.1 nm [I15].

3. The Extended Red Emission (ERE) [I15, I82] is a broad unstructured emission band with width about 80 nm and located between 540 and 900 nm. The large variety of peak wavelength of the band is its characteristic feature. In majority of cases the peak is observed in the range 650-750 nm but also the range 610-750 nm appears. This general vision can be compared with experimental facts.

The generalization ontogeny recapitulates phylogeny principle would suggest that the recent metabolism should have some features serving as telltale signatures of the IT past. The IT past could in turn reflect the primordial evolution in interstellar dust. The signatures of this period would be maxima of the action spectrum for wavelengths which correspond to both the universal metabolic energy quanta and transition energies for transitions of simple molecules present in the molecular dust. Visible and UV range are the most promising regions to consider.

1. There are two wave lengths of maximal effectiveness in the photosynthesis of plants and these correspond to what are called photo-system I and II (see p. 287 of [I40] ). Photo-system I is maximally activated at $\lambda = 680$ nm, corresponds to the chlorophyll a, and is not involved with the oxygen evolution. $k = 136$ corresponds to wavelength saturating to $\lambda_{min} = 620$ nm (1 eV). The model of $ATP$- $ADP$ process suggests that Coulombic binding energy is increases the wavelength.

2. Photo-system II is activated by shorter wave lengths and maximum effectiveness is between 500-600 nm. Photo-system II utilizes second type of chlorophyll (b, c or d) plus some accessory pigments. All photosynthetic cells producing oxygen possess both photo-systems whereas bacteria which do not produce oxygen have only the photo-system I. Hence at least the photo-system I might derive from a very early intra-terrestrial period. The spectrum of metabolic energy quanta for $k = 135$ corresponds to the wave length range [620, 413, 354, .., 310] nm. Coulombic binding energy could increase the wavelength from the 413 nm for $k = 135$ and $n = 2$.

3. The action and absorption spectra of green alga Ulva Taeniata, see p. 284 of [I40], have besides 680 nm maximum also a broad maximum in the range 400-500 nm peaked around 430 nm. The action spectrum has also a shoulder like structure around 600 nm. For $k = 135$ the first peak could correspond to $n = 1$ (620 nm) and second peak $n = 2$ (412 nm).

4. For some bacteria encountered in hot springs [I26] the effective wave length range is in the near infrared range 700-1000 nm rather than in the range of visible frequencies dominating the sunlight. This looks strange since in general the evolution favors maximal metabolic economy. This leads to ask whether these bacteria might be kind of living fossils evolved in an intra-terrestrial environment. This range of wavelength corresponds in a reasonable approximation to that obtained by scaling the wave length range 400-500 nm in previous case and thus to $k = 136$.

5. DNA bases (A, G, T, C) strongly absorb UV light at around 260 nm. For $k = 16$ the nearest metabolic energy quanta correspond to $n = 2$ and $n = 3$ giving wavelengths 310 nm and 207 nm. For proton the p-adic length scale is below atomic size for $\hbar/\hbar_0 \geq 16$.

## 6.4 What About Analogs Of EEG?

It looks strange to mention EEG if one speaks about primordial life forms. These analogs of EEG have of course nothing to do with brains. The prediction is that the fractally scaled counterparts of EEG (in loose sense of course) provide the fundamental communication and control tool for the magnetic body. This analog of EEG is determined by the cyclotron energy spectrum $nE_c$ of biologically important ions scaling like $\hbar$ and by the characteristic energy $E_J = ZeV$ associated

with Josephson junctions assignable to membrane like structures and having no dependence on $\hbar$. The energies $nE_c$ and the differences $nE_c \pm E_J$ define the harmonics of bands and their satellites. alpha band corresponds to $E_c$ and beta and theta bands to differences in the case of ordinary EEG.

### 6.4.1 Conditions from the thermal stability of the analog of EEG

The analogs of EEG and its scaled up variants are in a fundamental role in the control of biological body by magnetic body and this should hold true also for ITs. According to the model of EEG resulting as a special case of the model for the fractal hierarchy of EEGs and its generalizations [K10], the analog of EEG involves two components.

*1. Cyclotron component*

The first component corresponds to the harmonics of cyclotron frequencies of biologically important ions: many of them belong to the alpha band in the case of ordinary ions.

Since 10 Hz corresponds to a secondary p-adic time scale assignable to electron defining an inherent time scale of elementary particle in zero energy ontology, one can ask whether this frequency means breakdown of the fractality hypothesis and raises the frequency scale of ordinary EEG in special role. One can also wonder whether 10 Hz frequency could define a universal biorhythm.

Dark ions reside at magnetic flux sheets traversing DNA and cyclotron radiation affects directly DNA. Cyclotron frequencies are associated with motor control affecting directly DNA and inducing gene expression among other things. The models leads naturally to the introduction of the notions of super genome and hyper genome [K10].

*2. Josephson junction component*

Josephson junctions assumed to be associated with cell membrane define second contribution to EEG as frequencies associated with coherent state of photons emitted by Josephson current. This component is present only if Josephson junctions, naturally assignable with a membrane like structure separating the plasmoid from environment, are present.

The frequencies are expressible as $f_{n,\pm} = nf_c \pm f_J$ and in the case of ordinary EEG alpha band and its harmonics split into counterparts of beta and theta band. alpha band has scaled variant also in more general case and corresponds to ions which define alpha band for ordinary ions.

1. The essential condition is that cyclotron energy scale is above the thermal energy $E_{th} = 2.88T$ ($k_B = 1$ in the units used). This fixes the minimal value of the integer $k_d$ characterizing the level of dark matter hierarchy involved. Note that the hypothesis is $h_{eff} = nh$, where $n$ is product of distinct Fermat primes and power $2^{k_d}$. For ordinary EEG frequency of order 1 Hz the minimal value of $k_d$ is roughly $k_d = 44$. DNA cyclotron frequencies assuming that the charge of DNA is solely due to the phosphate groups $PO_4^{2-}$ are around 1 Hz and just above the thermal threshold.

2. Second condition is that Josephson energy determined by the membrane voltage defines Josephson energy which is above thermal energy. This gives $Q_{em}eV \geq 2.88T$ for far from vacuum extremals. For almost vacuum extremals the classical $Z^0$ field proportional to the classical em field contributes to the coupling and one must replace the charge $Q_{em}$ of charge carrier with effect em charge $Q_{eff}$ [K10]: this increases the scale of Josephson energies roughly by a factor 10. For far from vacuum extremals Josephson energies are near thermal energies whereas for almost vacuum extremals they are in visible and UV region, and one can identify bio-photons and EEG photons as decay products of dark Josephson photons.

3. Superconductivity prevails only below some critical temperature whereas vacuum extremal property is expected to be possible only above some critical temperature. This suggests that cell membrane functions properly only in a narrow temperature range. The range 36-37 C is suggested by the fact that the effects of ELF em fields on vertebrate brain are observed only in this range.

Josephson frequency $f_J$ is inversely proportional to $\hbar$ and would scale in the case of EEG would scale as

$$f_J = \frac{T}{T_{room}} \times f_{J,room} \ ,$$

where $f_{J,room} \simeq 5$ Hz holds true. alpha band and its harmonics and also the widths of theta and beta bands would scale like $B$. The positions of theta and beta bands would scale like temperature, and one would have the formula

$$f_{n,\pm} = \frac{B}{B_E} n f_c \pm \frac{T}{T_{room}} f_J$$

for the frequencies in the generalized beta and theta bands, when $k_d = 44$ holds true also in the high-$T$ environment.

It is illustrative to consider some examples.

1. *Mantle-core boundary*
   The temperature is $T = 4000$ K $\sim 13 T_{room}$ at the mantle-core boundary. This temperature allows simple ordinary molecules like carbon monoxide and water (due to the high pressure). Thermal energy is still eV and below Josephson energy and super-conductivity is possible only if cyclotron energies are high enough. For 5 Hz cyclotron frequency $r = 47$ gives energy of order eV. One could thus consider the possibility that both the super-conductivity and criticality could be possible in scaled up temperature range.

2. *Sunspots*
   The average temperature of the solar photosphere is about 5800 K whereas the minimum temperature is $T_{min} = 4000$ K and same as the temperature at mantle-core boundary. Inside sunspots the temperature varies in the range 3000-4800 K and sunspots, which are analogous to tornadoes, would be good candidates for the seats of solar life forms. Spectral analysis demonstrates the presence of water inside sunspots [E3]. There is also evidence for a solid calcium ferrite surface at photosphere [E5].

   The value of the sunspot magnetic field is between 1600-2500 Gauss and thus cyclotron frequency is about $3200 - 5000$ times higher than at the surface of Earth. Also in this case $k_d = 44$ level would correspond to thermally stable "EEG" photons with frequencies in the range of ordinary EEG.

### 6.4.2 What could the analog of EEG for IT look like?

In the following estimates for cyclotron frequencies are for the possibly existing dark companion $B_{end} = 2B_E/5$ of the Earth's magnetic field for which the effects of ELF fields on vertebrate brain provide a direct support.

If the sensory representations of IT life-forms are realized at the personal magnetic canvas and at magnetosphere in the same manner as ours, the cyclotron frequency of the representing ion at distance $r_1$ is must be same as the cyclotron frequency of the represented ion at distance $r_0$. Assuming that magnetic field strength scales like $1/r^3$, this gives cyclotron transitions at the distance of about

$$r_1(A) = (A/A_1)^{1/3} \times r_0 \ ,$$

giving

$$y(A, A_1) = (A/A_1)^{1/3} \times x \ .$$

Here $r_0 = xR$ is the radius associated with the life-form, and $r_1 = yR$ is the distance at which the sensory representation is realized. $R$ denotes the radius of Earth and $A$ the mass of the ion at $r_0$ associated with IT cyclotron transition and $A_1$ the mass of the ion at $r_1$ defining the cyclotron transitions associated with the sensory representation.

If the most important frequencies of generalized EEG correspond to cyclotron frequencies, if prebiotic live resides at the mantle-core and core-inner core boundaries, and if the magnetic field inside Earth behaves as dipole field in a reasonable approximation, one can deduce the EEG frequency range of aliens by scaling the human frequency range by the ratio

$$x^{-3} = (\frac{R}{r})^3 = \left[\frac{f_S(r)}{f_S(R)}\right]^3 \quad ,$$

where $r$ is the distance of the boundary region from the center of the Earth. The constraint that representation is realized in inner magnetosphere gives the bound $y \leq 6$ and the constraint that it is realized in ionosphere gives $y \simeq 1$.

*1. Biosphere*

In this case the basic equation is obtained by putting $x = 1$ in the general equation so that one has

$$y = (\frac{A}{A_1})^{1/3} \quad .$$

For protonic representations with $A_1 = 1$ possible in entire inner magnetosphere the constraint $y \leq 6$ allows all possible values of $A$.

*2. Mantle-core boundary*

For mantle-core boundary the ratio is roughly $x^{-3} = 7.1$ so that the EEG frequency range $1.5 - 90$ Hz scales up to $107 - 639$ Hz. Sensory representations can in this case be realized as ionic transitions in atmosphere. The basic equation is

$$y = (\frac{A}{A_1})^{1/3} x \quad ,$$

where $A$ is the mass number of the ion in mantle-core boundary and $A_1$ is the mass number of representative ion. For protonic representation one has

$$y = 1.92 A^{1/3} \quad .$$

The condition $y \leq 6$ guarantees that representation is realized in the inner magnetosphere and gives $A \leq 27$. This corresponds in ordinary EEG to frequencies $f \geq 11$ Hz. For $A_1 > 1$ also scaled up variants of alpha and theta frequencies are representable: note however that the densities of these ions are probably much smaller than in ionosphere.

One can consider also ionospheric ion representations satisfying $y \simeq 1$ for mantle-core boundary. Now the mass numbers of the ions involved are related by

$$\frac{A}{A_1} \simeq x^{-3} \simeq 7.1 \quad .$$

The biologically most interesting ions have $A > 7$ and are representable. One manner to realize this sensory representation is using cells or brains of various organisms and one might consider the possibility that we actually are life-forms which have developed as magnetospheric sensory representations of the life-forms at the mantle-core boundary.

*3. Core-inner core boundary*

For core-inner core boundary the ratio is roughly $x^{-3} = 263$ for $f_S(r) = 50$ Hz and $x^{-3} = 135$ for $f_S(r) = 40$ Hz. In this case only electronic sensory representations are possible and one has

$$y = (\frac{A m_p}{m_e})^{1/3} x \quad ,$$

1. For $x^{-3} = 263$ this gives

$$y \simeq 1.98 \times A^{1/3} \quad .$$

The range $[1, 6]$ for $y$ corresponds to the inner magnetosphere and the upper bound $A \leq 27$ and to scaled up variants of cyclotron frequencies above 11 Hz in ordinary EEG. Only beta and gamma bands would be represented.

2. For $x^{-3} = 135$

$$y \simeq 2.48 \times A^{1/3}$$

The upper bound for $A$ is $A \leq 14$ and to the scaled up variants of cyclotron frequencies above $\sim 20$ Hz in ordinary EEG.

*4. Inner core-most inner core boundary*

The boundary of the most inner core of radius 300 km could also be carrier of life-forms, perhaps plasmoid like life-forms. The simplest hypothesis is that the magnetic field associated with the plasmoids is the Earth's magnetic field in the core region of Earth, which would be constant and of order .2 Tesla below this distance if dipole approximation makes sense.

If important "EEG" frequencies correspond to cyclotron frequencies, part of the "EEG" would be scaled up by a factor $2^{169-157} = 2^{12} \simeq 4000$ so that EEG frequency range $.25 - 90$ Hz would be mapped to $1 - 360$ kHz. Ionic cyclotron frequencies would be in the MHz range with proton cyclotron frequency equal to 1.2 MHz. The cavity resonance frequency analogous to the lowest Schumann frequency for a structure with radius 300 km is 159 Hz.

If the sensory representations of IT life-forms possibly existing at at $r_0 = 300$ kilometers are realized as electronic cyclotron transitions one has

$$y \simeq .59 \times A^{1/3} \quad .$$

Ions with $A \geq 6$ would be represented above Earth's surface. All ionic representations would be realized in Earth's interior.

# 7 Comparison Of Mcfadden's Views With TGD

In his book Quantum Evolution [I67] Johnjoe McFadden discusses the deep problems of molecular biology from quantum point of view and develops very interesting ideas about evolution and consciousness. Because of deep insights about what is not understood in biology, this discussion should provide new insights for any quantum consciousness theorist attempting to build a bridge between theory and biological reality. In the sequel McFadden's vision is compared with TGD view and some new ideas inspired by it in TGD framework are proposed.

## 7.1 General Ideas

Before dwelling into concrete examples, it is good to compare McFadden's general starting points with those of TGD.

1. In accordance with most interpretations of quantum mechanics, McFadden assumes that the initial situation involved no de-coherence and that the biological evolution means basically the emergence of de-coherence, essentially the appearance of conscious observers performing quantum measurements.

   In TGD framework the situation is just the opposite: evolution means the emergence of effective macro–temporal quantum coherence meaning that the duration of sharp mental images (sub-selves) increased. During the primordial stage typical lifetime of self was of order $10^4$ Planck times and defined minimal de-coherence time. Dark matter hierarchy provides and hierarchy of Planck constants a concrete realization for a hierarchy of moments of consciousness with increasing geometric duration and quantum parallel dissipation which is second new element of TGD picture.

   The number theoretic generalization of Shannon entropy having negative values for rational and even algebraic entanglement is a further mathematical concept. Quantum computers are basic examples of systems possessing positive number theoretic negentropy, and this certainly conforms with the genuine information content of multi-verse states. It is not clear whether Negentropy Maximization is really consistent with the Second Law of thermodynamics and one must keep mind open for the possibility that Second Law is illusion created by the neglect of dark matter hierarchy meaning at the same time neglect of living life forms.

2. McFadden does not fix his views about quantum measurement theory but assumes that decoherence is an outcome of quantum measurements performed by environment or some subsystem of it. McFadden sees enzymatic action as a basic example of quantum measurement in which an amplification to a macroscopic phenomenon occurs.

   In TGD framework one can imagine two basic elements.

   (a) The emergence of symbolic representations as names of molecules made possible lock and key mechanism and "molecular sex". Once it is possible to name molecules, it becomes possible to regard bio-chemical pathways as analogs of computer programs proceeding rather deterministically. As already found, this idea has very concrete implications for understanding of bio-catalysis.

   (b) The most important bio-molecules could be seen as selves with especially long wake-up periods in a highly negentropic state of macro–temporal quantum coherence, and able to perform intentional actions applying the time mirror mechanism (see **Fig. ??** in the appendix of this book) (`http://tgdtheory.fi/appfigures/.jpg`), which is also The magnetic bodies of bio-structures are at the top of the intentional hierarchy.

3. McFadden sees quantum Zeno effect and its inverse as basic quantum control tools used by enzymes to increase reaction rates or induce mutations. Although the Zeno effect has also TGD counterpart, the intentional action of molecular magnetic bodies based on time mirror mechanism seems a more plausible option. Long ranged dark weak forces, in particular charge entanglement by $W$ MEs, exotic ionization, and the control of the strength of the screening of the classical $Z^0$ force provides an additional mechanisms of enzyme control explaining chiral selection. Sol-gel transition inducing polymerization and its reverse allows to control the stability of bio-polymers. The leakage of particles between space-time sheets is a further control mechanism and involved with the time mirror mechanism.

4. McFadden assumes that the superpositions of peptide-environment product states involving different peptides with different neutron and proton numbers are possible so that the measurement involves also measurement of proton and neutron numbers. This option looks implausible because it is very difficult to think that states with different fermion numbers, masses, and charges would quantum superpose.

   In fact, it has become clear quite recently that TGD could in well-defined sense allow also quantum superpositions of different DNA molecules. This kind of superpositions are routinely assumed for coherent states of Cooper pairs in super-conductivity although they break conservation of charge, fermion number, and energy. The point is that in zero energy ontology (ZEO) [K6] the total quantum numbers of physical states always vanish and the states decompose into positive energy part such that negative energy part located in its geometry future. Therefore it is possible to have quantum superpositions which in positive energy ontology, which is excellent approximation, would look like quantum superpositions of different DNA molecules. This possibility is not discussed in this chapter but it is needless to say that it could mean a revolution in the understanding of living matter. Even thermodynamics could be interpreted in a completely new manner since thermodynamical states which are "superpositions" of states with different values of conserved charged could have genuine quantal counterparts.

### 7.1.1 McFadden's view about biochemistry

McFadden represents a very general view about the essentials of bio-chemistry.

1. Protons associated with hydrogen bonds and electronic Cooper pairs serve as basic tools of quantum bio-control.

2. The localization of proton induces what McFadden interprets as a quantum measurement of proton's position.

In TGD framework the mechanism of catalytic action based on the temporary dropping of proton from the $H_N$-atom associated with catalyst or reactant, replaces this mechanism. Catalytic action could be seen as a short lasting period of "group sex" between catalyst and reacting

molecules. Liberation of standard metabolic energy quantum is automatically involved with the process.

In many-sheeted space-time particles topologically condense at all space-time sheets having projection to given region of space-time so that this option makes sense only near the boundaries of space-time sheet of a given system. Also p-adic phase transition increasing the size of the space-time sheet could take place and the liberated energy would correspond to the reduction of zero point kinetic energy. Particles could be transferred from a portion of magnetic flux tube portion to another one with different value of magnetic field and possibly also of Planck constant $h_{eff}$ so that cyclotron energy would be liberated. In the following only the "dropping" option is discussed.

### 7.1.2 Important problems of quantum biology

The following list provides examples of problems that McFadden wants to understand in terms of quantum physics.

1. The extreme effectiveness of enzyme action.

2. The mechanism of mutations, in particular that of adaptive mutations and multiple mutations.

3. Evolution.
   i) The loss of complexity in computational models of evolution contra the increase of complexity in real evolution.
   ii) The emergence of the first self replicators.
   iii) The evolution of extremely complex reaction pathways, such as the one leading to the buildup of the $ATP$ ase enzyme.

## 7.2 Enzyme Action

Enzymes as quantum mouse traps is the metaphor introduced by McFadden. Typically enzyme catches the reactant molecules to a fixed conformation and fires a proton to the substrate molecule inducing in this manner a re-organization of some chemical bonds. The enzyme gains the lost proton later from a water molecule.

Mouse trap metaphor conforms completely with the TGD described view about catalytic action and also with the idea about enzyme as a quantum critical system.

*1. Production of lactic acid from pyruvate*

McFadden represents the production of the lactic acid from pyruvate, which is one of the last steps of catabolism, as a typical example of enzyme action. The process involves LDH, lactate dehydrogenase, catalyzing the transformation of the pyruvate to lactic acid, and NADH providing a proton and an electron pair. LDH donates the proton involved with the transformation of C=0 to C-O-H. NADH in turn provides proton and electron pair so that C=O is replaced with H-C-OH. $NAD^+$ receives proton and a compensating electron pair from water and $LDH_-$ receives a proton from a water molecule.

*2. Catabolism of lactose*

Second example used my McFadden relates to the catabolism of lactose induced by the enzyme beta galactose. The rate of the process is trillion times higher than one might expect. McFadden proposes that the process involves a localization of proton in certain amino-acid of the beta galactose to a particular hydrogen bond. If the localization occurs to a correct hydrogen bond, the proton is injected to the lactose molecule and induces hydration. The suggestion is that a repeated quantum measurement of proton's position in beta galactose keeps the proton in the correct position so that the decay occurs with a much higher rate than it would occur otherwise.

It is not necessary to repeat how the catalysis could be understood in TGD framework. The decay of the lactose involves hydrolysis in which lactose molecule receives water $H_N$-O-H molecule from the environment and the loss of proton de-stabilizes the negatively charged molecule.

Hydrolysis could involve local gel-sol type transition transforming ordered water to ordinary water, which is able to provide the needed water molecule. The gel-sol transition could closely

correlate with the non-standard localization of the proton inside enzyme. The process could involve an intentional action of a magnetic body of some system involved and thus negative energy topological light rays and charge entanglement by $W$ MEs.

## 7.3 Quantum Evolution

McFadden considers evolution from a quantum point of view. After the criticism of the RNA world paradigm McFadden poses several questions. How complexity could have emerged during the evolution? What was the first self-replicator? How the complex metabolic pathways could have evolved? What might be the quantum mechanisms of adapted and multiple mutations?

### 7.3.1 How evolution can create complexity?

McFadden pays attention to the fact that in the computational models of evolution final states tend to be less complex than the initial ones. This can be seen as a consequence of dissipation which leads to asymptotic self-organization patterns which are very simple. This is just the opposite of what is observed in Nature (note however the fact that the rapid extinction of new species after Cambrian explosion might be interpreted in terms of a loss of complexity).

In TGD framework the ability of living systems to circumvent the loss of complexity is due the facts that TGD Universe is quantum critical and p-adic cognition implies p-adic evolution predicting the emergence of systems characterized by increasing values of the p-adic prime and the integer characterizing the levels of dark matter hierarchy serving as their "intelligence quotients".

At the molecular level TGD allows to resolve this puzzle elegantly. During the pre-biotic exotic RNA period the predecessor of the genetic code is realized as many-to-one replication of exotic RNAs meaning a loss of information. This occurred for both singlet and doublet exotic RNA and for their composite forming a double helix with the size of the singlet helix being scaled up by a factor two. This however led to a dead alley involving only the RNAs representing the maximal invariant set of the RNA→RNA mapping as an asymptotic state. Final state was indeed simpler than the initial state.

At some stage the product code transformed to a code coding for RNA triplets, and amino-acids which originally catalyzed the mapping of RNA to RNA, took the role of the coded molecules. RNAs were mapped to DNAs by reverse transcriptase and the high error rate of the reverse transcription implied a rapid mutational rate. The many-to-one character of RNA→RNA replication implying the dead alley thus transformed from a curse to a blessing since it represented implicitly the protein-DNA genetic code.

### 7.3.2 Criticism of RNA world

McFadden represents severe critics against RNA world paradigm which is the dominating vision about pre-biotic evolution [I66]. The basic objections are following.

1. In water environment bio-polymers become un-stable against de-polymerization by hydration. This makes the idea of primordial sea implausible. The presence of the ordered water could resolve this problem even in the standard physics based models. In many-sheeted space-time the hypothesis that pre-biotic evolution occurred intra-terrestrially in the womb of the magnetic Mother Gaia makes sense and could resolve basic objections against the notion primordial sea.

2. Enzymatic action requires chiral selection. In TGD framework this can be interpreted as a strong indication for the necessity of the classical long ranged weak forces in the enzymatic control (say charge entanglement by $W$ MEs).

3. McFadden lists several reasons for why RNA is implausible as a pre-biotic chemical. RNA consists of three components: RNA base, ribose, and phosphate. RNA bases and phosphate have been generated in the experiments trying to simulate pre-biotic evolution but the spontaneous emergence of ribose looks implausible. The problem is that a plethora of other sugars are produced.

Some property of ribose should distinguish it from the other sugars. In TGD framework one might argue that for the ribose self "wake-up" periods or even periods of macro-temporal quantum coherence meaning sharp and non-entropic mental images are longer than for the other sugars. Quite generally, important bio-molecules could be identified as maximally autonomous systems able to "stay awake" and realize intentions.

A more concrete explanation is based on stability.

i) Both RNA, DNA and amino-acids are negatively charged and thus inherently unstable. The assignment of "names" to generalized hydrogen bonds represented by quark and antiquark at the ends of the magnetic flux tube to the basic building bricks of these polymers could make them stable and lead automatically to highly selective catalytic actions.

ii) Suppose that the OH groups associated with the sugars have tendency to form a hydrogen bond with water molecules leading to ionization of the water molecule and liberation of proton dropping to a larger space-time sheet so that the polymer generates negative charge. If the number of O-H groups is too large the resulting negative charge can de-stabilize polymers formed by ribose, phosphate, and RNA nucleotides. Note that also the formation of double strand a liberates one proton per hydrogen bond which has a further de-stabilizing effect. This could explain why RNA with 4 O-H groups forms only short double strands whereas DNA having only 3 O-H groups forms very long double strands.

4. One can also wonder why just phosphate, ribose and RNA bases find each other and why the large number of other combinations are not realized. The naming based on flux tubes would restrict dramatically the possible combinations able to form spatially and temporally coherent systems bound together by flux tubes and automatically lead to a final state in which molecules having no braids with environment disappear from the system. Phosphate, ribose and RNA base could also find each other by tuning to common wave length by sending negative energy MEs entangling them with each other.

5. The presence of RNA bases, phosphate and ribose is not enough. McFadden finds it difficult to understand why only RNA molecules amongst many other reaction products of its three basic components are selected. In laboratory the activation of the RNA base allows to select RNA as a dominant reaction product. One possibility is that the liberation of activation energy helps to overcome the potential wall hindering the formation of RNA. This is could also due to the fact that the bound states of the activated RNA base with other two components are short-lived or decay to RNA in accordance with the idea RNA selves have especially long wake-up periods and is winner in the fight for survival. Magnetic body could be able to intentionally activate the RNA bases using universal metabolism present even without $ATP$ ase machinery.

6. In the laboratory isolation, purification, and channeling of the reactants to the reaction volume are crucial parts of the process producing RNA and ribozymes, and almost-self-replicators. In the conventional chemistry framework it is very difficult to imagine how these processes could have occurred during pre-biotic evolution.

   The notion of magnetic body might come in rescue. Magnetic flux quanta could make possible highly controlled reaction network. A possible concrete toy model goes as follows. Suppose that quantum-classical correspondence holds true in the sense that the shape of the magnetic flux tube containing charged particles reacts to the presence of the charged particles so that it can be regarded as a classical orbit of a charged particle in the average magnetic field inducing Lorentz force. This makes sense only if a given magnetic flux tube contains particles with a fixed charge-to-mass ratio, and means that magnetic body indeed isolates and purifies the reactants to the magnetic flux tubes and allows them to react at the nodes of the magnetic web.

### 7.3.3 Evolution of metabolism

McFadden describes basic aspects of catabolism in an enjoyable manner. Catabolism can be seen as a process in which electrons from the orbitals of complex bio-molecules (in particular glucose)

are gradually transferred to the orbitals of oxygen atoms. This process releases energy used as a metabolic energy in the form of $ATP$ molecules.

In the standard chemistry framework the mechanisms behind $ADP \to ATP$ transformation seem miracle like. It is not easy to understand how an evolution based on mere chance and necessity could have led to the recent form of this machinery: intermediate steps seem to be simply absent. For instance, according to McFadden the reaction pathways generating the $ATP$ ase enzyme catalyzing the generation of $ATP$ involves 13 steps and all these steps are necessary. The probability that this pathway could have been generated by a random change is infinitesimally small and comparable to that for a monkey playing with a typewriter to compose Shakespeare's sonnets by accident.

*1. Universal metabolic currencies*

In TGD framework the predicted universal metabolic currencies remove partially the veil of mysteries surrounding the evolution of metabolism.

The dropping of a proton from atomic space-time sheet to a larger one generates a universal metabolic energy quantum. Thus metabolism would have been present already before the chemical storage of the metabolic energy. At the pre-biotic period the generation of negative energy topological light rays with photon energy $\sim .5$ eV could have induced the dropping of protons and remote utilization of the liberated energy. Indeed, the model for intra-terrestrial life led to the hypothesis that the infrared radiation corresponding to a temperature of about 4000 K near the mantle-core boundary could have provided the energy quanta of about.4 eV driving protons back to the atomic space-time sheets. The evolution of photosynthesis led later to the chemical storage of the metabolic energy.

The mitochondrial battery is kept at the potential of.15 eV by the metabolic energy feed. This process involves oxidation process in which electrons from the orbitals of molecules like glucose end down to the orbitals of oxygen atoms. The electron pairs are provided by NADH molecules in mitochondrial metabolism occurring in the water filled space between mitochondrial membranes. The energy liberated in this manner drives protons from the interior of the mitochondria to the space between the membranes. $NAD^+$ ion then receives the compensating electronic Cooper pair from water later.

The molecular battery provides the energy to generate $ATP$ molecules serving as universal energy currencies. Three protons leaking back along the channel inside $ATP$ ase molecule, which is analogous to the wire connecting the plus and minus poles of a battery, gain a net energy of $3 \times .15 = .45$ eV. This energy they donate to a proton, which uses it to get back to the atomic space-time sheet of the $ATP$ molecule.

*2. Does metabolism generate cell level qualia?*

In a philosophical mood one could wonder the purpose of the endless $ATP$ Karma's cycle: why not just the primitive metabolism involving only.5 eV photons? A partial explanation is the possibility to store metabolic energy chemically so that system becomes less dependent on environment. A connection with the TGD based model of sensory receptor as a quantum capacitor suggests a deeper interpretation. The dielectric breakdown of the quantum capacitor gives rise to qualia which correspond to the increments of the total quantum numbers at either electrode when the dielectric breakdown occurs. ATPase could be seen as generating local di-electrical breakdown inducing primitive protonic qualia as a side product.

*3. Molecular intentionality*

The basic challenge of the bio-chemistry based approach to evolution is to understand how simple reaction steps coherently integrate to long multi-step reaction pathways. The assumption of molecular intentionality simplifies dramatically this task. Indeed, the best manner to understand and plan a complex electronic instrument is to know its purpose. The manual provides explanation of the purpose and magnetic body serves as the manual of the bio-logical body. For instance, it is much easier to understand how the reaction pathway leading to $ATP$ ase has developed if one knows that the function of this pathway is to liberate universal metabolic energy quanta from mitochondrial battery besides possibly producing protonic qualia.

The fact the number of steps is 13 suggests 13-adicity and it would be interesting to see whether various reaction pathways tend to have a prime number of steps. It deserves to be noticed that

$k = 169 = 13^2$ defines the p-adic prime associated with the magnetic flux tubes of the Earth's magnetic field and its possible dark companion $B_{end} = 2B_E/5$, and that the micro-tubular surface defines naturally cognitive code with $k = 13^2$ bits consisting of 13 13-bit sequences defined by tubuline conformations for a full $2\pi$ twist around micro-tubule.

Biological evolution could be seen as being induced by the evolution of cognition and of intentional actions. By the properties of the p-adic topology it proceeds from long time and length scales to shorter ones (p-adically short corresponds to something long in the real sense since rational space-time points are common to real and p-adic sectors of the imbedding space). This would suggest that the evolution of bio-logical functions is induced by the evolution of the intentional actions of the magnetic bodies, which were initially like rough sketches and gradually became more and more refined. Also motor skills develop in the same manner.

*4. The emergence of molecular pathways*

The emergence of names attached to molecules makes possible generation of computer program like dynamics in which programs call corresponds to association of molecules with names conjugate to some name of catalyst molecule to clusters so that catalytic action leading to a particular final state becomes possible.

The names of molecules could dictate the dynamics to a high degree. Situation could be like in the human society: knowing that person carries the label "physics teacher" allows to make amazingly precise long term predictions about the daily behavior of the person whereas the knowledge of all imaginable chemical and physical data about the person would not allow to predict anything interesting about the activities of the person in time scales longer than few seconds.

### 7.3.4 Quantum mechanism of mutations

McFadden suggests the reduction of the superposition of normal and enol configurations of T nucleotide to a tautomeric enol configuration as a quantum mechanism of mutation. The position measurement of the proton can locate it to the second nitrogenic hydrogen bond and thus transform T nucleotide to the isomeric but short-lived enol configuration having only two hydrogen bonds connecting it to the complementary base. In the enol state DNA replication assigns G instead of A with T.

Zeno effect could allow to effectively freeze T to this configuration and thus increase the rate of mutations. The same mechanism could work also at the level DNA→ mRNA transcription and protein translation and assign lys instead of glu to the enol configuration.

The mechanism poses an additional condition to the proposal that DNA nucleotides correspond to quarks and antiquarks. The question is what determines which quark or antiquark corresponds to a given nucleotide and the mechanism of mutation based on disappearance of hydrogen bond suggests that the number of hydrogen bonds (2 or 3) determines this so that one would have correlation with with the weak isospin of quark (u or d) and number of hydrogen bonds (3 or 2).

*1. Adaptive mutations of E. coli*

In adaptive mutations the bacterium E. coli unable to catabolize lactose to get metabolic energy develops a mutation allowing it to generate beta galactose inducing the decay of the lactose. This mutation occurs with a probability which is higher than predicted by randomness. McFadden poses the question how the information about the presence of the lactose is communicated from the environment to the DNA level.

If life would be mere quantum chemistry, the only possibility would be that the information transfer sequence DNA→mRNA→ proteins of Central Dogma is somehow reversed. What McFadden suggests is DNA-mRNA-betagalactoce-lactose entanglement such that DNA appears as a superposition of ordinary and enol configurations. Lactose would take the role of quantum measurer of the proton's position inside T nucleotide, and Zeno effect would increase the rate of the mutation.

In TGD Universe the bacterial magnetic body receives information about the presence of lactose and its intention to "eat" lactose is transformed to a desire represented by a negative energy ME entangling directly with DNA. The intention of the magnetic body of E. coli would be to push the DNA to enol configuration by kicking the proton to the abnormal position. Negative $W$ ME could induce long lasting entanglement with normal and enol configurations of T nucleotide so

that the enol configuration would appear with a higher probability than in the absence of quantum entanglement and mutated DNA results more often in the replication. The alternative option is that magnetic body induces the gel-sol transition inducing mutation in the manner already described.

Quite generally, feeding of dark protons to atomic space-time sheets and gel-sol transition would serve as switches used by the cellular magnetic body to realize its desires. This mechanism could be seen as a refined form of remote metabolism providing metabolic energy for the starving bacterium.

*2. Multiple mutations of TB bacteria*

TB (tubercle bacillus) bacteria are able to develop a simultaneous resistance against several drugs [I67]. This occurs for bacteria which have only brief growth periods followed by long dormant periods. McFadden interprets dormant periods in terms of entanglement with the environment. When this period ends even multiple mutations could result in the quantum measurement at DNA level.

In the TGD framework the magnetic body of TB population would receive information about the fates of various members of the population in the multi-drug environment and would have a strong desire to develop multi-drug resistance. The long dormant periods of bacteria allowing them to survive bring in mind the sleeping periods of higher life forms, and suggests the entanglement of the bacteria with the other members of the population, also those living in the geometric past and already deceased as victims of the drugs. This kind of entanglement would allow the magnetic body to manipulate the genomes of the still-living bacteria so that they have better changes to survive in the multi-drug environment. McFadden does not discuss whether the simple mechanism of mutations working in the case of E. coli might be enough in the case of TB bacteria.

Note that the notion of hyper-genome allows to understand bacterial colonies as systems analogous to multi-cellulars controlled by genes expressed collectively.

*3. Mutations and intronic DNA*

The TGD based view about pre-biotic evolution allows to imagine more effective mechanisms of mutations replacing the simple mechanism utilized by E. coli and working in case of eukaryotes.

In the TGD Universe reverse transcriptase plays a key role in the pre-biotic evolution as a generator of the genetic variation. The variation is due to the high error rate of the reverse transcription. For instance, the amazing ability of the HIV virus (retro-virus) to adapt is based on the reverse transcription of HIV RNA to DNA. It would be strange if this ability would have been lost during the sub-sequent evolution. Perhaps fragments of DNA are transformed to mRNA also during dormant, "inwards directed" periods. mRNA fragments are however not translated to proteins now but transformed back to DNA fragments by reverse transcriptase replacing the previous DNA fragment in DNA with a new one. This mechanism might work at least in case of eukaryotes having cell nucleus and mean that mRNA is not transferred outside the nucleus. The replacement of DNA fragment need not occur immediately. mRNA fragments would thus act like retro-viruses to produce the needed genetic variation. In this framework ordinary retro-viruses such as HIV might be seen as kind of fallen angels.

This kind of activity in which collective selves of populations modify the genomes of their members might be present in all eukaryotes during sleeping (or more generally, dormant) periods. The generation of mutations might be one of the fundamental purposes of sleep and explain why sleep is so important for healing.

This mechanism of mutations might be still too primitive for eukaryotes. In TGD framework the intronic portion of DNA expresses itself as temporal field patterns using p-adic cognitive codes, in particular memetic code. Introns play the role of the computer software whereas genes take the role of the hardware. In this picture introns would be naturally involved with the control of the adaptive mutations of higher organisms. In the modern home computers hardware is becoming more and more dynamical, and computer metaphor suggest that the passive DNA could contain segments representing kind of computer store containing variants of various genes taken in use if required. Transposons might represent these new pieces of the hardware.

This replacement need not involve the removal of the old gene fragment and could be only functional. Computer metaphor inspires the idea that the intronic portion of DNA represents a given gene as a dynamical list of addresses, kind of links or program calls, specifying which portions of DNA contribute to the gene, and that this list characterizes how the splicing of mRNA occurs.

Therefore the mutation could occur at the intronic software level as a mere updating of the list representing the gene.

The challenge is to understand how this addressing might be realized physically. For instance, addressing might involve simply common fragments of DNA in meme and corresponding portions of gene serving as addresses making possible a "tuning to a common wave length". Alternatively, magnetic flux tubes might serve as space-time correlates of the links. They could be generated intentionally as wormhole magnetic fields consisting of pairs of positive and negative energy magnetic flux tubes parallel to DNA strand. The generation of wormhole magnetic fields identified as the basic motor activity of the magnetic body could also explain the appearance and disappearance of EEG bands. By the p-adic fractality similar mechanism could be at work also in DNA length scale.

*4. Could zero energy ontology be relevant for living matter?*

Zero energy ontology [K33] emerged originally from the observation that Robertson-Walker cosmologies correspond in TGD framework to vacuum extremals for which all conserved classical charges vanish (the non-conserved gravitational mass density does is non-vanishing). The construction of S-matrix led to a precise formulation of zero energy ontology.

Zero energy ontology states that physical states have vanishing net quantum numbers and consist of positive energy states at boundaries of future directed light-cones in the geometric past ("not so big bang" ) and negative energy states at the boundaries of past directed light cones in the geometric future ("not so big crunch" ) assignable to arguments of N-point function.

Due to the fact that conformal weights are complex it is possible to distinguish between positive energy particles propagating to the geometric future and negative energy particle propagating to geometric past. Phase conjugate laser photons contra ordinary laser photons represent basic empirical example about this distinction.

In the construction of S-matrix identified as entanglement coefficients between these tow kinds of states (this notion makes sense for hyper-finite factors of type $II_1$ since trace of unit matrix is now equal to unit) these states represent incoming and outgoing states of particle reaction so that measurement of reaction rates is basically quantum measurement in which time-like entanglement is reduced instead of space-like entanglement [K6].

A rather strong argument in favor of zero energy ontology comes from superconductivity [K4]. The models super-conductivity utilize formally the notion of coherent state of Cooper pairs involving quantum superposition of arbitrary numbers of Cooper pairs. This is in conflict with various conservation laws in standard ontology but in zero ontology it is quite possible to consider quantum superposition of zero energy states with various values of quantum numbers for positive energy states.

This opens the gates for rather fascinating speculations. Time-like charge entanglement would allow to imagine a time-like variant of the capacitor model of sensory receptor. For instance, sensory qualia could result in the reduction of coherent state of Cooper pairs to a state with a well defined charge.

Also different DNA sequences with different masses and charges might appear in quantum superpositions for time like entanglement and this might be relevant for evolution of genetic code. In particular, the model of McFadden for mutations might generalize dramatically. As a matter fact, the proposed identification of S-matrix (or rather its generalization M-matrix which need not be unitary) as time-like entanglement coefficients assumes the presence of all pairs of initial and final states appearing in the S-matrix in the superposition so that this possibility could be seen as a prediction.

# 8 Great Vision About Biological Evolution And Evolution Of Brain

The following great vision about evolution and is not perhaps strictly about hierarchy of EEGs. The hierarchy of dark matter and EEGs however leads to this vision naturally. The first part of vision relates to biological evolution. Second part is about the evolution of brain. Here the key thread is evolution of two kinds of intelligences, the ordinary fast intelligence evolving via the emergence of fast computation type activities and emotional slow intelligence developing via the

emergence of higher levels of dark matter hierarchy. The latter intelligence is what distinguishes us from animals.

## 8.1 Basic Assumptions

The great vision about evolution and brain relies on two several new notions and ideas.

1. Life as something in the intersection of real and p-adic worlds making possible negentropic entanglement- both space-like and time-like. This makes possible to understand what conscious intelligence is and NMP reduces evolution to a generation of negentropic entanglement (see **Fig.** `http://tgdtheory.fi/appfigures/cat.jpg` or **Fig. ??** in the appendix of this book). DNA as topological quantum computer hypothesis [K12] finds also a justification.

2. The notion of many-sheeted space-time (see **Fig.** `http://tgdtheory.fi/appfigures/manysheeted.jpg` or **Fig.** 9 in the appendix of this book) suggesting a universal hierarchy of metabolic energy quanta, and the notion of magnetic body.

3. Communication and control based on Josephson radiation and cyclotron transitions crucial for understanding bio-photons and EEG and its fractal generalization as a key element of bio-communications.

4. Zero energy ontology and the closely related notion of causal diamond (CD) assigning a hierarchy of macroscopic time scales to elementary particles coming as octaves of the basic time scale and justifying p-adic length scale hypothesis. Zero energy energy ontology also justifies the vision about memory and intentional action and the idea that motor action can be seen as time reversal of sensory perception.

5. The hierarchy of Planck constants and the identification of the fundamental evolutionary step as an increase of Planck constant. Evolutionary steps mean migration to the pages of the Big Book labeled by larger values of Planck constant and living system can be regarded as a collection of pages of the Big Book such that a transfer of matter and energy between the pages is taking place all the time. The change of the Planck constant implies either reduction or increase of the quantum scales-this leads to a model for biocatalysis and a model of cognitive representations as scaled down or scaled up "stories" mimicking the real time evolution.

6. A resonant like interaction between hierarchy of Planck constants and p-adic length scale hierarchy favoring the values of Planck constant proportional to powers of two, and idea that weak and color interactions are especially important in the length scales which correspond to Mersenne primes and Gaussian Mersennes. The simplest option is that weak bosons have their standard masses but appear as massless below their Compton length which scales up like $\hbar$ and preferred p-adic length scales correspond to Mersenne primes. Also copies of weak bosons and gluons with ordinary value of Planck constant and reduced mass scale can (and will) be considered.

### 8.1.1 How to identify the preferred values of Planck constant?

The basic problem is to identify the preferred values of Planck constant and here one can only make theoretical experimentation and all what follows must be taken in this spirit. One can consider assumptions which become increasingly stronger.

1. If only singular coverings of CD and $CP_2$ are possible Planck constant is a product of integers. Algebraic simplicity of algebraic extensions of rationals favors ruler and compass integers (Appendix).

2. A resonant interaction between the dark length scales and p-adic length scales with ordinary value of Planck constant favors Planck constants coming as powers of two.

3. An even stronger assumption would be that p-adic length scales coming as Mersennes and Gaussian Mersennes are especially interesting.

(a) If weak bosons can appear with the ordinary value of Planck constant only in the p-adic length scale $k = 89$, one obtains the condition

$$k_d = k - 89 \quad , \quad k \in \{89, 107, 113, 127, 151, 157, 163, 167\} \tag{8.1}$$

for the values of of $r = 2^{k_d}$ allowing dark weak bosons in p-adic length scales assignable to Mersennes. These values of $k_d$ assign to electrons and quarks dark p-adic length scales $L(k_{eff}) = \sqrt{r}L(k)$, $r \equiv \hbar/\hbar_0 = 2^{k_d}$. The scales could correspond to size scales of basic units of living systems.

(b) If weak bosons and possibily also gluons with ordinary value of Planck constant are possible in all p-adic length scales $L(k)$, $k \in \{89, 107, 113, 127, 151, 157, 163, 167\}$, one obtains much richer structure. This hierarchy defines defines secondary dark matter hierarchies from the condition that the scaling the p-adic length scale $L(k_1)$ in this set by $\sqrt{r}$, $r \equiv \hbar/\hbar_0 = 2^{k_d}$, gives a p-adic length scale equal to another p-adic length scale $L(k_2)$ in this set. This requires $k_d + k_1 = k_2$ so that the values

$$k_d = k_2 - k_1 \tag{8.2}$$

are favored for the scaling of $\hbar$. In this case the hierarchy of dark scales assignable to quarks and leptons is much richer. The tables below demonstrate that electron appears as its dark variant for all Mersennes and also in atomic length scales $k = 137, 139$ so that this option puts electron in a completely unique position.

4. Also other scales are possible. For instance, $r = 2^{47}$ required by 5 Hz Josephson frequency gives dark weak scale which corresponds $k = 136$ as a p-adic scale. The stages of sleep can be understood in terms of scaling of $\hbar$ by factor 2 and 4 so that also the atomic length scale $k = 137$ and the scale $k = 138$ are involved.

Since the experimental input is rather meager, one is forced to do theoretical experimentation with various hypothesis. The quantitative experimental tests are rather primitive but basically quantal.

1. The time scales assignable to CDs of leptons and quarks and their scaled up counterparts for the preferred values of Planck constant should define biologically important time scales. One might even speak about evolutionary level of electron. These time scales could define fundamental biorhythms and also time scales of long term memory and planned action.

2. Josephson frequencies and cyclotron frequencies scaling like $1/\hbar$ (if magnetic field scales down like $1/\hbar$) charactering biologically important ions and elementary particles. In accordance with the quantum criticality of living matter it is assumed that cell membrane corresponds to almost vacuum extremal so that classical $Z^0$ force is an essential element of the model. Also these frequencies should define fundamental bio-rhythms and characterize the evolutionary level of cell. Experimentally of special importance are the cyclotron frequencies assignable to $Ca^{++}$ ions.

3. The amplitude windows for electric field scaling like $\hbar$ for a particular cyclotron frequency define a basic prediction.

### 8.1.2 Tables about predicted time and length scales

The following tables summarize various predictions for time scales and length scales. They correspond to the most general assumption that exotic bosons with the ordinary value of Planck constant are possible in all length scales associated with Mersennes and Gaussian Mersennes.

Note that **Table 5** includes only the dark length scales associated with $k = 89$ gauge bosons.

| $k_d$ | $p_1$ | $p_2$ | | $k_d$ | $p_1$ | $p_2$ |
|---|---|---|---|---|---|---|
| 4 | 163 | 167 | | 38 | **89** | 127 |
| 6 | 107 | 113 | | 38 | 113 | 151 |
| 6 | 151 | 157 | | 40 | 127 | 167 |
| 6 | 157 | 163 | | 44 | 107 | 151 |
| 10 | 157 | 167 | | 44 | 113 | 157 |
| 12 | 151 | 163 | | 50 | 107 | 157 |
| 14 | 113 | 127 | | 50 | 113 | 163 |
| 16 | 151 | 167 | | 54 | 113 | 167 |
| 18 | **89** | 107 | | 56 | 107 | 163 |
| 20 | 107 | 127 | | 60 | 107 | 167 |
| 24 | **89** | 113 | | 62 | **89** | 151 |
| 24 | 127 | 151 | | 68 | **89** | 157 |
| 30 | 127 | 157 | | 74 | **89** | 163 |
| 36 | 127 | 163 | | 78 | **89** | 167 |

**Table 5:** The integers $k_d$ characterizing the preferred values of $r = \hbar/\hbar_0 = 2^{k_d}$ identified from the condition that the dark variant of p-adic length scale $L(p_1)$ corresponding to some ordinary p-adic length scale defined by Mersenne prime $M_p$ or Gaussian Mersenne $M_{G,p}$, $p \in \{89, 107, 113, 127, 151, 157, 163, 167\}$ corresponds to similar p-adic length scale $L(p_2)$. If one assumes that weak bosons can appear with ordinary value of Planck constant only in the p-adic length scale $k = 89$, only the rows with $p_1 = 89$ of the table are possible: in these cases $p_1$ is in boldface and the row has double underline. The corresponding values of $k_d$ are in the set $\{18, 24, 38, 62, 68, 74, 78\}$.

### 8.1.3 Electron and $u$ quark are different

Before continuing an important observation is in order. Electron is exceptional when compared to quarks. It appears as a dark particle in all p-adic length scales defined by biologically important Gaussian Mersennes and also in atomic length scales $k = 137$ and $k = 139$. The reason is trivial: by the basic assumptions electron must appear at same length scales as weak bosons above $k = 127$ since it corresponds to Mersenne prime. Also for the less general option (exotic intermediate gauge bosons are possible only as the dark variants of the standard ones) it appears at cell membrane length scale $k = 151$, which is due to the fact that one has $113 - 89 = 151 - 127 = 24$. Also $u$ quark can appear with $k_{eff} = 137, 139, 163, 167$ and also this is an accident. The light invariants of intermediate gauge bosons appearing in long p-adic length scales would naturally correspond to almost vacuum extremals making possible the criticality as the basic aspect of life. One must of course be very cautious about the masses of exotic counterparts of $u$ and $d$ quark: one can also consider the possibility that masses are identical.

## 8.2 Dark Matter Hierarchy And Big Leaps In Evolution

Dark matter hierarchy leads to an amazingly concrete picture about evolutionary hierarchy allowing to identify the counterparts for concepts like mineral, plant, and animal kingdom that we learned during schooldays and ceased to take seriously as students of theoretical physics as we learned that other sciences are just taxonomy. Even more, a view about what distinguishes between prokaryotes, eukaryotes, animal cells, neurons, EEG, and even about what makes cultural evolution, becomes possible. This view is also very useful when one tries to understand the role of microtubules.

The appearance of CDs scaled up in size by $r = \hbar/\hbar_0$ and space-time sheets scaled up in size by $\sqrt{r}$ means the emergence of new levels of structure and it is natural to identify big leaps in evolution in terms of emergence of new larger matter carrying space-time sheet magnetic flux sheets and corresponding magnetic bodies. If magnetic flux quanta are scaled by $r$ magnetic flux quantization conditions remain unaffected if magnetic field strengths scale down by $1/r$ so that the energies of cyclotron photons are not affected. The thickness of flux tubes can remain unchanged if the currents running at the boundaries of the flux quantum cancel the magnetic flux. As already

| $Z, W$ | d | u | e | $k_d$ |
|---|---|---|---|---|
| 89 | 120 | 124 | 127 | **0** |
| 93 | 124 | 127 | 131 | 4 |
| 95 | 126 | 129 | 133 | 6 |
| 99 | 130 | 133 | 137 | 10 |
| 101 | 132 | 135 | 139 | 12 |
| 103 | 134 | 137 | 141 | 14 |
| 105 | 136 | 139 | 143 | 16 |
| 107 | 138 | 141 | 145 | **18** |
| 109 | 140 | 143 | 147 | 20 |
| 113 | 144 | 147 | 151 | **24** |
| 119 | 150 | 153 | 157 | 30 |
| 125 | 156 | 159 | 163 | 36 |
| 127 | 158 | 161 | 165 | **38** |
| 129 | 160 | 163 | 167 | 40 |
| 133 | 164 | 167 | 171 | 44 |
| 139 | 170 | 173 | 177 | 50 |
| 143 | 174 | 177 | 181 | 54 |
| 145 | 176 | 179 | 183 | 56 |
| 149 | 180 | 183 | 187 | 60 |
| 151 | 182 | 185 | 189 | **62** |
| 157 | 188 | 191 | 195 | **68** |
| 163 | 194 | 197 | 201 | **74** |
| 167 | 198 | 201 | 205 | **78** |

**Table 6:** The dark p-adic length scales $\sqrt{r}L(k) = L(k_{eff})$, $k_{eff} = k + k_d$, of intermediate gauge bosons $Z, W$, d and u quarks, and electron for the values $r = 2^{k_d}$ of Planck constant defined in **Table 5**. The uppermost row gives the integers characterizing the p-adic length scales of the particles for the standard value of Planck constant. $k_{eff}$ characterizes also the CD times scale through the formula $T(CD, k_{eff}) = 2^{k_{eff}-127} \times .1$ seconds. The rows which correspond to the less general option for which only $M_{89}$ corresponds to weak bosons with ordinary value of Planck constants have double underline and the corresponding values of $k_d$ are in boldface.

| $k_1$ | $k_M$ | | $k_1$ | $k_M$ | | $k_1$ | $k_M$ | | $k_1$ | $k_M$ |
|---|---|---|---|---|---|---|---|---|---|---|
| 113 | 89 | | 113 | 107 | | 163 | 127 | | 163 | 157 |
| 127 | 89 | | 119 | 107 | | 167 | 127 | | 169 | 157 |
| 151 | 89 | | 123 | 107 | | 133 | 127 | | 173 | 157 |
| 157 | 89 | | 113 | 107 | | 139 | 127 | | 163 | 157 |
| 163 | 89 | | 117 | 107 | | 143 | 127 | | 167 | 157 |
| 167 | 89 | | 111 | 107 | | 133 | 127 | | 161 | 157 |
| 95 | 89 | | 175 | 113 | | 137 | 127 | | 169 | 163 |
| 109 | 89 | | 181 | 113 | | 131 | 127 | | 183 | 163 |
| 133 | 89 | | 187 | 113 | | 225 | 151 | | 207 | 163 |
| 139 | 89 | | 191 | 113 | | 229 | 151 | | 213 | 163 |
| 145 | 89 | | 119 | 113 | | 157 | 151 | | 219 | 163 |
| 149 | 89 | | 133 | 113 | | 171 | 151 | | 223 | 163 |
| 103 | 89 | | 157 | 113 | | 195 | 151 | | 177 | 163 |
| 127 | 89 | | 163 | 113 | | 201 | 151 | | 201 | 163 |
| 133 | 89 | | 169 | 113 | | 207 | 151 | | 207 | 163 |
| 139 | 89 | | 173 | 113 | | 211 | 151 | | 213 | 163 |
| 143 | 89 | | 127 | 113 | | 165 | 151 | | 217 | 163 |
| 113 | 89 | | 151 | 113 | | 189 | 151 | | 187 | 163 |
| 119 | 89 | | 157 | 113 | | 195 | 151 | | 193 | 163 |
| 125 | 89 | | 163 | 113 | | 201 | 151 | | 199 | 163 |
| 129 | 89 | | 167 | 113 | | 205 | 151 | | 203 | 163 |
| 95 | 89 | | 137 | 113 | | 175 | 151 | | 169 | 163 |
| 101 | 89 | | 143 | 113 | | 181 | 151 | | 175 | 163 |
| 105 | 89 | | 149 | 113 | | 187 | 151 | | 179 | 163 |
| 95 | 89 | | 153 | 113 | | 191 | 151 | | 169 | 163 |
| 99 | 89 | | 119 | 113 | | 157 | 151 | | 173 | 163 |
| 93 | 89 | | 125 | 113 | | 163 | 151 | | 167 | 163 |
| 145 | 107 | | 129 | 113 | | 167 | 151 | | 187 | 167 |
| 169 | 107 | | 119 | 113 | | 157 | 151 | | 211 | 167 |
| 175 | 107 | | 123 | 113 | | 161 | 151 | | 217 | 167 |
| 181 | 107 | | 117 | 113 | | 155 | 151 | | 223 | 167 |
| 185 | 107 | | 195 | 127 | | 235 | 157 | | 227 | 167 |
| 113 | 107 | | 201 | 127 | | 163 | 157 | | 181 | 167 |
| 127 | 107 | | 205 | 127 | | 177 | 157 | | 205 | 167 |
| 151 | 107 | | 133 | 127 | | 201 | 157 | | 211 | 167 |
| 157 | 107 | | 147 | 127 | | 207 | 157 | | 217 | 167 |
| 163 | 107 | | 171 | 127 | | 213 | 157 | | 221 | 167 |
| 167 | 107 | | 177 | 127 | | 217 | 157 | | 191 | 167 |
| 121 | 107 | | 183 | 127 | | 171 | 157 | | 197 | 167 |
| 145 | 107 | | 187 | 127 | | 195 | 157 | | 203 | 167 |
| 151 | 107 | | 141 | 127 | | 201 | 157 | | 207 | 167 |
| 157 | 107 | | 165 | 127 | | 207 | 157 | | 173 | 167 |
| 161 | 107 | | 171 | 127 | | 211 | 157 | | 179 | 167 |
| 131 | 107 | | 177 | 127 | | 181 | 157 | | 183 | 167 |
| 137 | 107 | | 181 | 127 | | 187 | 157 | | 173 | 167 |
| 143 | 107 | | 151 | 127 | | 193 | 157 | | 177 | 167 |
| 147 | 107 | | 157 | 127 | | 197 | 157 | | 171 | 167 |

**Table 7:** Table gives all weak boson length scales -both non-dark and dark implied by the assumption that all Mersennes primes and their Gaussian counterparts and their dark counterparts defined $k_d = k_i - k_j$ them are possible.

| particle | $Z, W$ | d | u | e |
|---|---|---|---|---|
| k | 89 | 120 | 123 | 127 |
| f(CD)/Hz | $2.7488 \times 10^{12}$ | 1280 | 160 | 10 |

**Table 8:** The fundamental frequencies associated with the CDs of intermediate gauge bosons $Z, W$, d and u quarks, and electron. Note that for intermediate gauge bosons the frequency of CDs corresponds to energy $E = 1.13 \times 10^{-2}$ eV and wavelength $\lambda = 1.01 \times 10^{-4}$ m (size of a large neuron).

| $Z, W$ | d | u | e | $k_d$ |
|---|---|---|---|---|
| 3.64e-13 | 7.81e-04 | 6.25e-03 | 1.00e-01 | **0** |
| 5.821e-12 | 1.25e-02 | 1.00e-01 | 1.60e+00 | 4 |
| 2.31e-11 | 5.00e-02 | 4.00e-01 | 6.40e+00 | 6 |
| 3.73e-10 | 8.00e-01 | 6.40e+00 | 1.02e+02 | 10 |
| 1.49e-09 | 3.20e+00 | 2.56e+01 | 4.10e+02 | 12 |
| 5.97e-09 | 1.28e+01 | 1.02e+02 | 1.65e+03 | 14 |
| 2.38e-08 | 5.12e+01 | 4.10e+02 | 6.55e+03 | 16 |
| 9.54e-08 | 2.05e+02 | 1.64e+03 | 2.62e+04 | **18** |
| 3.81e-07 | 8.19e+02 | 6.55e+03 | 1.05e+05 | 20 |
| 6.10e-06 | 1.31e+04 | 1.05e+05 | 1.68e+06 | **24** |
| 3.91e-04 | 8.39e+05 | 6.71e+06 | 1.07e+08 | 30 |
| 2.50e-02 | 5.37e+07 | 4.30e+08 | 6.87e+09 | 36 |
| 1.00e-01 | 2.15e+08 | 1.72e+09 | 2.75e+10 | **38** |
| 4.00e-01 | 8.59e+08 | 6.87e+09 | 1.10e+11 | 40 |
| 6.40e+00 | 1.37e+10 | 1.10e+11 | 1.76e+12 | 44 |
| 4.10e+02 | 8.80e+11 | 7.04e+12 | 1.12e+14 | 50 |
| 6.55e+03 | 1.41e+13 | 1.13e+14 | 1.80e+15 | 54 |
| 2.62e+04 | 5.63e+13 | 4.50e+14 | 7.21e+15 | 56 |
| 4.19e+05 | 9.01e+14 | 7.21e+15 | 1.15e+17 | 60 |
| 1.68e+06 | 3.60e+15 | 2.88e+16 | 4.61e+17 | **62** |
| 1.07e+08 | 2.31e+17 | 1.84e+18 | 2.95e+19 | **64** |
| 6.87e+09 | 1.48e+19 | 1.18e+20 | 1.89e+21 | **74** |
| 1.10e+11 | 2.36e+20 | 1.89e+21 | 3.02e+22 | **78** |

**Table 9:** The $\hbar$-scaled fundamental time scales $T(CD, k_{eff}) = 2^{k_{eff}-127} \times .1$ seconds associated with the CDs of intermediate gauge bosons $Z, W$, d and u quarks, and electron for the values $\hbar/\hbar_0 = 2^{k_d}$ of Planck constant defined in **Table 5**. The scales are expressed in seconds. The uppermost row gives the time scales of CDs for the standard value of Planck constant. The rows which correspond to the less general option for which only $M_{89}$ corresponds to weak bosons with ordinary value of Planck constants have double underline and the corresponding values of $k_d$ are in boldface.

found, this mechanism must be at work inside living organisms wheras in far away region flux quanta are scaled up in size.

The attractive hypothesis is that the leaps in evolution correspond to the emergence of dark variants of weak and possibly also color interactions in dark p-adic length scales which correspond to ordinary p-adic length scales characterized by Mersenne primes. These leaps would be quantum leaps but in different sense as thought usually. The emergence of higher dark matter levels would basically mean the integration of existing structures to larger structures. A good metaphor are text lines at the pages of book formed by magnetic flux sheets whose width is scaled up by $r$ as the new level of dark matter hierarchy emerges. The big leaps can occur both at the level of organism and population and organisms with rather low individual dark matter level can form societies with high dark matter levels and high collective intelligence (honeybees and ants are good example in this respect).

Certainly also other scalings of Planck constant than those summarized in tables are possible but these scalings are of primary interest. This intuition is supported by the observation that electron is completely exceptional in this framework. Electron's dark p-adic length scales corresponds to p-adic length scales $L(k)$, $k = 167, 169$, assignable to atomic and molecular physics and to the Gaussian Mersennes $M_{G,k} = (1+i)^k - 1$, $k \in \{151, 157, 163, 167\}$, assignable to the length scale range between cell membrane thickness 10 nm and nucleus size 2.58 $\mu$m. The corresponding p-adic length scales or corresponding electronic Compton lengths, the number of which is 23, are excellent candidates for the scales of basic building brickes of living matter and vary from electron's p-adic length scale up to 1.25 m ($k = 167$ defining the largest Gaussian Mersenne in cell length scale range) and defining the size scale of human body. The corresponding p-adic time scales are also highly interesting and vary from.1 seconds for electron defining the fundamental biorhythm to $9.6 \times 10^{14}$ years which is by 4-5 orders longer than the age of the observed Universe. For $k = 167$ the time scale is $1.1 \times 10^{11}$ years and is by one order of magnitude longer than the age of the observed Universe estimated to be $1.37 \times 10^{10}$ years [E1].

This conceptual framework gives rather strong guidelines for the identification of the levels of evolutionary hierarchy in terms of dark matter hierarchy. The outcome is a more detailed vision about big evolutionary leaps. Note that in the sequel only the general option is considered: the justification for this is that for this option electron appears as a dark particle for all length scales defined by Gaussian Mersennes as well as in atomic length scales. The basic vision in nutshell is that evolution means the emergence of dark weak and gluonic physics in both dark and ordinary length scales and that the size scales of the basic biostructures correspond to Mersenne primes and their Gaussian variants.

### 8.2.1 A sketch about basic steps in evolution

The vision about evolution depends on what one assumes about the initial state.

1. If one assumes that weak bosons with ordinary value of Planck constant were present in the begining, evolution would mean a steady growth of $k_d$. The problem is that small values of $k_d = k_1 - k_2$ correspond to the Gaussian Mersennes defining cellular length scales. If these exotic weak physics were present from the beginning, large parity breaking in cellular length scales would have been present all the time.

2. An alternative and perhaps more realistic view is that the evolution means the emergence of exotic weak physics corresponding almost vacuum extremals in increasingly longer length scales. A possible mechanism could have been the induction of exotic $\hbar_0$ variant of weak physics at the nearest Mersenne length scale $k_{next}$ by the dark variant of weak physics at level $k$ so that one would have $k_d = k_{next} - k$. The simplest induction sequence would have been $89 \to 107 \to 113 \to 127 \to 151 \to 157 \to 163 \to 167$ corresponding to $k_d \in \{18, 6, 14, 24, 6, 6, 4\}$. A possible interpretation of exotic $\hbar_0$ physics is in terms of almost vacuum extremals and non-standard value of Weinberg angle: also weak bosons of this physics would be light. This sequence defines the minimal values for $k_d$ but also larger values of $k_d$ are possible and would correspond to steps between neighbours which are not nearest ones.

The following sketch about the basic steps of evolution relies on the latter option.

*1. Elementary particle level*

Magnetic bodies with size scale defined by the sizes of CDs assignable to quarks and leptons and possibly also weak bosons (already now the size of big neuron emerges) corresponds to the lowest level of hierarchy with the sizes of the basic material structures corresponding to the Compton lengths of elementary particles. The fundamental bio-rhythms corresponding to frequencies 10, 160, and 1280 Hz appear already at this level in zero energy ontology which suggests that elementary particles play a central and hitherto unknown role in the functioning of living matter.

*2.* $89 \to 107$ *step with* $k_d = 18$

The first step would have been the emergence of $k_{eff} = 107$ weak bosons inducing $\hbar_0$ weak physics in $k = 107$ length scale characterizing also ordinary hadrons. This in turn would have led to the emergence of exotic nucleons possibly corresponding to almost vacuum extremals. The reduction of the model for the vertebrate genetic code to dark hadron physics [K30] is one of the most unexpected predictions of quantum TGD and assumes the existence of exotic- possibly dark- nucleons whose states with a given charge correspond to DNA, RNA, mRNA, and tRNA. The $\hbar_0$ variants of these nucleons would interact via weak bosons with hadronic mass scale. The exotic variants of the ordinary $k = 113$ nuclei would correspond to the nuclear strings consisting of exotic nucleons [K7, K30] and define nuclear counterparts for DNA sequences. Their dark counterparts could define counterparts of DNA sequences in atomic physics length scales. Therefore a justification for the previous observation that genetic code could be realized at the level of hadron physics and that chemical realization would be higher level realization finds justification. The anomalous properties of water could be also partly due to the presence of dark nucleons and the proposal was that the presence of exotic nuclei is involved with water memory [K18]. The possible existence of the analog of DNA-RNA transcription between ordinary DNA and its nuclear counterpart would have dramatic implications. For instance, one can imagine a mechanism of homeopathy based on this kind of transription process which would also allow a modification of genome by using dark nuclei to communicate the DNA sequences through the cell membrane to the target nuclei.

*3.* $107 \to 113$ *step with* $k_d = 6$

The next step would have been the emergence of $k_{eff} = 113$ weak bosons inducing $\hbar_0$ weak physics in $k = 113$ length scale characterizing also ordinary hadrons. Exotic variants of the ordinary nuclei possibly corresponding to almost vacuum extremals could have emerged interacting weakly (or actually relatively strongly!) via the exchange of weak bosons with mass scale of order 100 MeV. Also dark variants of the exotic $k = 107$ nucleons could have have emerged and formed exotic nuclei of size scale $k = 119$.

*4.* $113 \to 127$ *step with* $k_d = 14$

At this step weak bosons in electron mass scale would have emerged. Whether these weak bosons could have induced large parity breakings in atomic and molecular length scales is not clear. Viruses, which do not yet possess cell membrane could correspond to this level of hierarchy.

*5.* $127 \to 151$ *step with* $k_d = 24$

This step would have been fundamental since weak bosons in cell membrane length scale would have appeared. Note that by $113 - 89 = 24$ this step also leads from $k = 89$ weak bosons to $k = 113$ weak bosons. The weak bosons assignal to $k = 151$ could correspond to the weak interactions associated with almost vacuum extremals and $sin^2(\theta_W) = .0295$ could correspond to the weak physics in question.

$k_d = 24$ step for $k = 113$ $\hbar_0$ weak bosons would have produced them in $k_{eff} = 137$ atomic length scale with $L(137) \simeq .78$ Angstrom This could have naturally led to large parity breaking effects and chiral selection.

Dark $k_{eff} = 151$ electrons appearing in the TGD inspired model of high $T_c$ super-conductivity would have been a by-product of this step. Whether dark electrons could have transformed to light $\hbar_0$ electrons (of mass.25 keV) with a common mass scale of order $10^2$ eV with exotic weak bosons is an interesting question. The model of high $T_c$ super-conductivity predicts the presence of structures analogous to cell membrane. This would suggest that cell membranes emerged and chiral selection emerged at this step so that one could not distinguish the emergence of molecular life as a predecessor for the emergence of cell membrane like structures. This would conform with

the fact that DNA molecules are stable only inside cell nucleus. Note that for $k_{eff} = 151$ electron's CD has time scale $2^{24} \times .1$ seconds -that is 19.419 days (day=24 hours).

The smallest nanobes [I18] appearing in rocks have size 20 nm and could have emerged at this step. The size of the viruses [I33] is between 10-300 nm covers the entire range of length scales assignable to Gaussian Mersennes, which suggests that smallest viruses could have emerged at this step. Also the smallest [I17] [I17], which by definition have size smaller than 300 nm could have appeared at this stage.

*6. The remaining steps*

The remaining steps $k = 151 \to 157 \to 163 \to 167$ could relate to the emergence of coiling structure DNA and other structures inside cell nucleus. $k = 167$ would correspond to $k_d = 167 - 89 = 68$ to be compared with the value $k_d = 47$ required by 5 Hz Josephson frequency for the neuronal membrane for -70 mV resting potential. Note that $k_d = 48$ (state 1-2 of deep sleep) corresponds to $k = 163$.

By their smallness also double and triple steps defined by $k_d = k_{i+n} - k_i$, $n > 1$, are expected to be probable. As a consequence, electrons can appear as dark electrons at all the Gaussian Mersenne levels. At these steps the dark electrons corresponding to primes $k_{eff} = 137, 139$ would appear. For $k = 137$ dark electron appears with CD time scale equal to 128 seconds- rather precisely two minutes. The model for EEG suggests that the exotic weak bosons appear in the scales $k_{eff} = 136, 137, 138$.

Further multisteps from the lower levels of hierarchy would give structures with size scales above the size of cell nucleus possibly assignable to organs and structural units of brain. The dark levels assignable to electron are expected to be of special interest. It is encouraging that the longest scale assignable to electron in this manner corresponds to $k = 205$ and length scale of 1.28 m defining body size. As a consequence dark electrons are predicted at levels $k = 137, 139, 141, 143, 145, 147$ coming as octaves.

Prokaryotic cells (bacteria, archea) without cell nucleus for which cell membrane is responsible for metabolic functions and genome is scattered around the cell could have emerged at this step. This would mean that the emergence of the cell membrane thickness as a fundamental scale is not enough: also the size scale of membrane must appear as p-adic length scale. The sizes of most prokaryotes vary between 1 $\mu$m and 10 $\mu$m: the lower bound would require $k = 163$. There also prokaryotes with sizes between.2 $\mu$m ($k = 157$ corresponds to.08 $\mu$m) and 750 $\mu$m. Cell nuclei, mitochondria, and other membrane bounded cell nuclei would have evolved from prokaryotes in this framework. The sizes of eukaryote cells are above 10 $\mu$m and the fact that multicellular organisms are in question strongly suggests that the higher multisteps giving rise to weak bosons and dark electrons in length scales above $L(167)$ are responsible for multi-cellular structures.

This scenario leaves a lot of questions unanswered. In particular, one should understand in more detail the weak physics at various length scales as well as various exotic nuclear physics defined by dark nucleons and dark variants of nuclei.

### 8.2.2 Division of the evolution to that of biological body and magnetic body

Electron's Mersenne prime $M_{127}$ is the highest Mersenne prime, which does not correspond to a completely super-astrophysical p-adic length scale. In the case of Gaussian Mersennes $M_{G,k}$ one has besides those defined by $k$ in $\{113, 151, 157, 163, 167, \}$ also the ones defined by $k$ in $\{239, 241, 283, 353, 367, 379, \ 457, 997\}$ [A1]. The appropriately extended model for evolution allows to distinguish between three kinds of values of $k_{eff}$.

1. The values of $k_{eff}$ for which electron can appear as dark particle and thus satisfying $k_{eff} \leq 205$ (Table 5). These levels would correspond to structures with size below 1.25 m defined roughly by human body size and it is natural to assign the evolution of super-nuclear structures to the levels $167 < k_{eff} \leq 205$.

2. The values of of $k_{eff}$ for which dark gauge bosons are possible in the model. This gives the condition $k_{eff} \leq 235$. These levels correspond to structures in the range 1.25 m-40 km. The identification as parts of the magnetic body can be considered.

3. The values of $k_{eff}$ obtained by adding to the system also the Gaussian Mersenne pair $k \in \{239, 241\}$ allowing also the dark electrons. The lower size scale for these structures is 640 km.

4. The higher levels corresponding to $k_{eff}$ in $\{283, 353, 367, ...\}$. The lower size scale for these structures is 3 AU (AU is the distance from Earth to Sun).

$k_{eff} > 205$ levels would correspond to the emergence of structures having typically size larger than that of the biological body and not directly visible as biological evolution. This evolution could be hidden neuronal evolution meaning the emergence of extremely low Josephson frequencies of the neurons modulating higher frequency patterns and being also responsible for the communication of long term memories.

### 8.2.3 Biological evolution

In principle the proposed model allowing multisteps between hierarchy levels defined by Mersenne primes and their Gaussian counterparts could explain the size scales of the basic structures below the size scale 1.25 m identified in terms of the $k_{eff} \leq 205$ levels of the hierarchy.

*1. The emergence of cells having organelles*

The appearance of the structures with $k_{eff} > 167$ (possibly idetifiable as magnetic body parts) should correlate with the emergence of simple eukaryotic cells and organisms, in particular plant cells for which size is larger than 10 $\mu$m, which could correspond to $k_{eff} = 171$ for electron and dark variants of weak gauge bosons. $k_{eff} = 177$ is the next dark electron level and corresponds to 80 $\mu$m scale. It seems natural to assume that these dark weak bosons do not transform to their $\hbar_0$ counterparts at these space-time sheets.

Cell nucleus would be the brain of the cell, mitochondria would be the energy plant, and centrioles generating microtubules would define the logistic system. Also other organelles such as Golgi apparatus, ribosomes, lysosomes, endoplasmic reticulum, and vacuoles would be present. These organelles would live in symbiosis by topologically condensing to $k_{eff} \geq 171$ magnetic body controlling their collective behavior. Centrosomes associated with animal cells would not be present yet but microtubule organizing centers would already be there.

The recent observations show that centrioles are not always in the characteristic T shaped conformation. Daughter centrioles resulting during the replication of mother centriole use first ours of their lifetime to roam around the cell before becoming mature to replicate. A possible interpretation is that they are also life forms and that magnetic body utilizes daughter centrioles to perform some control functions crucial for the future development of the cell. For instance, centrioles visit the place where axonal growth in neurons starts.

Cytoskeleton would act as a counterpart of a central nervous system besides being responsible for various logistic functions such as transfer of proteins along microtobuli. Centrioles give also rise to basal bodies and corresponding cilia/flagella used by simple cells to move or control movement of air or liquid past them. Centriole pair would be also used by the magnetic body to control cell division.

The logistic functions are the most obvious functions of microtubules. Magnetic body would control cell membrane via signals sent through the cell nucleus and communicated to the cell membrane along microtubuli. Basal bodies below the cell membrane and corresponding cilia/flagella would serve as motor organs making possible cell motion. Tubulin conformations representing bits would allow microtubule surface to represent the instructions of the magnetic body communicated via via cell nucleus to various proteins moving along the microtubular surface so that they could perform their functions.

TGD based view about long memory recall as communication with geometric past allows also the realization of cellular declarative memories in terms of the conformational patterns. Memory recall corresponds to a communication with geometric past using phase conjugate bosons with negative energies reflected back as positive energy bosons and thus representing an "image" of microtubular conformation just like ordinary reflected light represents ordinary physical object. There would be no need for a static memory storage which in TGD framework would mean taking again and again a new copy of the same file.

Receptor proteins would communicate cell level sensory input to the magnetic body via MEs parallel to magnetic flux tubes connecting them to the magnetic body. We ourselves would be in an abstract sense fractally scaled up counterparts of receptor proteins and associated with dark matter iono-lito Josephson junction connecting the parts of magnetosphere below litosphere and above magnetosphere. The communication would be based on Josephson radiation consisting of photons, weak bosons, and gluons defining the counterpart of EEG associated with the level of the dark matter hierarchy in question.

*3. The emergence of organs and animals*

The emergence of magnetic bodies with $k_{eff}$ in the range $(177, 181, 183, 187, 189, 195, 201, 205)$ allowing both dark electron and weak bosons could accompany the emergence of multicellular animals. Magnetic body at this level could give rise to super-genome making possible genetic coding of organs not yet possessed by plant cells separated by walls from each other. The super structures formed from centrosomes and corresponding microtubuli make possible complex patterns of motion requiring quantum coherence in the scale of organs as well as memories about them at the level of organs.

*4. The emergence of nervous system*

$k_{eff}$ in the range $(187, 189, 195, 201, 205)$ allowing dark electrons and weak bosons gives size scales $(.25, .5, 4, 32, 128)$ cm, which could correspond to the scales of basic units of central nervous system. What would be of special interest would be the possibility of charged entanglement based on classical $W$ fields in macroscopic length scales. The emergence of the new level means also the integration of axonal microtobuli to "text lines" at the magnetic flux sheets making possible logistic control at the multineuronal level. The conformational patterns of the microtubular surface would code nerve pulse patterns to bit patterns representing declarative long term memories. An interesting question is whether the reverse coding occurs during memory recall.

### 8.2.4 The evolution of magnetic body

For mammals with body size below 1.25 m the levels $k_{eff} > 205$ cannot correspond to biological body and the identification in terms of magnetic body is suggestive. The identification of EEG in terms of Josephson frequencies suggests the assignment of EEG with these levels.

*1. The emergence of EEG*

EEG in the standard sense of the word is possessed only by vertebrates and one should understand why this is the case. The value of Josephson frequency equal to 5 Hz requires only $k_d = 47$ so that something else must be involved. A possible explanation in the framework of the proposed model comes from the following observations.

1. Besides the maximal p-adic scale $k = 205$ for which electron and weak bosons appears as dark variants the model allows also levels at which only gauge bosons appear as dark particles. From **Table 9**one finds that levels $k \in \{207, 211, 213, 217, 219, 221, 223, 225, 229, 235\}$ are allowed. Could it be that these levels and possibly some highest levels containing both electrons and gauge bosons as dark particles are a prerequisite for EEG as we define it. Its variants at higher frequency scales would be present also for invertebrates. The lowest Josephson frequency coded by the largest value of $\hbar$ in the cell membrane system determines the Josephson frequency.

2. The membrane potentials -55 mV (criticality against firing) correspond to ionic Josephson energies somewhat above 2 eV energy ((2.20, 2.74, 3.07, 2.31) eV, see Table 1). For 2 eV the wavelength 620 nm is near to $L(163) = 640$ nm. Therefore the Josephson energies of ions can correspond to the $L_e(k = 163)$ if one assumes that a given p-adic mass scale corresponds to masses half octave above the p-adic mass scale so that the opposite would hold true at space-time level by Uncertainty Principle. Josephson frequencies $f_J \in \{5, 10, 20, 40, 80, 160\}$ Hz correspond to $k_d \in \{47, 46, 45, 44, 43, 42\}$ giving $k_{eff} \in \{210, 209, 208, 207, 206, 205\}$.

   (a) Cerebellar resonance frequency 160 Hz would correspond to $k = 205$ -the highest level for for which model allows dark electrons (also 200 Hz resonance frequency can be understood since several ions are involved and membrane potential can vary).

| $k_d$ | $f_1/Hz$ | $f_2/Hz$ | $f_3/Hz$ |
|---|---|---|---|
| 0 | 707 | 1000 | 1412 |
| 4 | 177 | 250 | 354 |
| 6 | 89 | 1250 | 177 |
| 10 | 22.1 | 31.3 | 44.2 |
| 12 | 11.1 | 15.6 | 22.1 |
| 14 | 5.5 | 7.8 | 11.1 |
| 16 | 2.8 | 3.9 | 5.5 |
| 18 | 1.4 | 2.0 | 2.8 |
| 20 | 0.7 | 1.0 | 1.4 |
| 24 | 0.2 | 0.2 | 0.3 |

**Table 10:** The Compton frequencies obtained by scaling $2^{k_d/2}$ from the basic triplet $k_{eff} = (239, 240, 241)$. The values of $k_d$ correspond to those predicted by the model based on Mersenne primes.

   (b) The 80 Hz resonance frequency of retina would correspond to $k_{eff} = 206$ -for this level dark electrons would not be present anymore.

   (c) 40 Hz thalamocortical frequency would correspond to $k_{eff} = 207$.

   (d) For EKG frequencies are EEG frequencies below 20 Hz 12.5 and heart beat corresponds to .6-1.2 second cycle (the average.8 s corresponds to $k_{eff} = 212$).

3. Even values of $k_{eff}$ are not predicted by the model based on Mersenne primes allowing only odd values of $k_{eff}$ so that the model does not seem to be the whole truth. The conclusion which however suggests itself strongly is that EEG and its variants identified as something in the range 1-100 Hz, are associated with the levels in at which only dark weak bosons are possible in the proposed model. Note that the size scales involved with EEG would be above the size scale of human body so that we would have some kind of continuation of the biological body to be distinguished from the magnetic body. The time scales assignable to the dark CDs would be huge: for instance, $k = 205$ would correspond to $T = 2^{42} \times .1$s making about 1395 years for electron.

*2. Does magnetic body correspond to the space-time sheets carrying dark weak bosons?*

The layers of the magnetic body relevant for EEG have have size of order Earth size. Natural time scale for the moment of sensory consciousness is measured as a fraction of second and the basic building blocks of our sensory experience corresponds to a fundamental period of.1 seconds. This scale appears already at $\hbar_0$ level for electron CD. The natural question concerns the relationship of the magnetic body to the $k > 205$ space-time sheets carrying only gauge bosons in the model and having size scale larger than that of biological body. Do they correspond to an extension of biological body or should they be regarded as parts of the magnetic body? The following observations suggest that they could correspond to layers of the magnetic body responsible for the fractal variant of EEG.

1. The primary p-adic time scales (Compton times) $T(239)$ and $T(241)$ correspond to frequencies, which are $2^{\pm 1/2}$ kHz. The geometric average $k = 240$ corresponds to kHz frequency. Is the appearance of kHz scale a mere accident or do the frequencies assignable to the quark CDs correspond to Compton times $\propto \sqrt{2^{k_{eff}/2}}$?

2. One can apply scalings by $2^{k_d}$ to the triplet $(239, 240, 241)$ to get a triplet $(239 + k_d, 240 + k_d, 241 + k_d)$. The results are summarized in **Table 10**. Clearly the frequencies in question cover also the EEG range. Note that these frequencies scale as $\sqrt{1/r}$ whereas Josephson frequencies scale as $1/r$.

Also ZEG and WEG would appear but in much shorter scales dictated by $k_{eff}$ and might accompany EEG. Somehow it seems that the effective masslessness of weak bosons below given scale is highly relevant for life. One can of course ask whether some larger Gaussian Mersenne could change the situation. There is a large gap in the distribution of Gaussian Mersennes after $k = 167$ and the next ones correspond to $M_{G,k}$, with $k$ in $(239, 241, 283, 353, 367, 379, 457, 997)$ [A1]. The twin pair $k = (239, 241)$ corresponds to a length scales $(1.6, 3.2) \times 10^2$ km and the minimum value for $k_d$ are (72, 74) ($167 \to (239, 241)$ transition).

*3. Long term memory and ultralow Josephson frequencies*

What determines the time scale associated with long term memory is a crucial question if one really wants to understand the basic aspects of consciousness.

1. Does the time scale correspond to the size scale of CD assignable to electron scaled by $r = \hbar/\hbar_0$? In this case relatively small values of $r$ would be enough and $r = 2^{47}$ would give time scale of $10^{13}$ s for for electron's CD, which is about $3 \times 10^5$ years. This does not make sense.

2. Does Josephson frequency define the relevant time scale? In this case the long term memory would require the analog of EEG in the time scale of memory span. $k_{eff} = 205$ would give 6 ms time scale for memory from the assignment of $k_{eff} = 163$ to the Josephson photons at V=-50 mV implying $k_d = 42$. Minute scale would require $k_{eff} = 217$. The highest level $k_{eff} = 235$ allowed by the model involving only Gaussian Mersennes with $k \leq 167$ would correspond to a time scale of 77.67 days (day is 24 hours). For Gaussian Mersennes defined by $k_{eff} = (239, 241)$ the time scales become about (41.4, 82.8) months (3.4 and 6.8 years). These scales should also define important biorhythms. The claimed 7 years rhythm of human life could relate to the latter rhythm: note that the precise value of the period depends on the membrane potential and thus varies. The presence of the scaled up variants of the by $k_d \leq 78$ allows longer time spans of long term memory and the scaling defined by $k_d = 167 - 163 = 4$ scales up the span of long term memories to (54.4, 108.8) years.

*4. Cultural evolution*

Higher levels in the hierarchy would correspond mostly to the evolution of hyper-genome coding for culture and social structures. Introns are good candidate for the nucleotides involved. The development of speech faculty is certainly a necessary prerequisite for this breakthrough. Already EEG seems to correspond to dark layers of biological body larger than biological body so that one can cask whether the weak bosons and dark electrons in the length scales $k = 239, 241, 283, 353, 367, ...$ could be relevant for the collective aspect of consciousness and cultural evolution. Maybe the size scales $(175, 330)$ km and their scaled up variants by $k_d \leq 78$ might have something to do with the spatial scale of some typical social structure (not city: the area of New York is only 790 km$^2$).

# 9 Oil Droplets In Water Solution As A Primitive Life Form?

The origin of life is one the most fascinating problems of biology. The classic was carried out almost 60 years ago. In the experiment sparks were shot through primordial atmosphere consisting of methane, ammonia, hydrogen and water and the outcome was many of the amino-acids essential for life. The findings raised the optimism that the key to the understanding of the origins of life. After Miller's death 2007 scientists re-examined sealed test tubes from the experiment using modern methods found that well over 20 amino-acids - more than the 20 occurring in life - were produced in the experiments.

The Urey-Miller experiments have yielded also another surprise: the black tar consisting mostly of hydrogen cyanide polymer produced in the experiments has turned out to be much more interesting than originally thought and suggests a direction where the candidates for precursors of living cells might be found. In the earlier experiments nitrobenzene droplets doped with oleic anhydride exhibited some signatures of life. The droplets were capable to metabolism using oleic anhydride

as "fuel" making it possible for the droplet to move. Droplets sensed each other's presence and reacted to it and also demonstrated rudimentary memory.

In the sequel a model for the oil droplets as primitive life form is developed using as a constraint the TGD inspired quantum model for living matter. The key ingredients are the notions of magnetic body, the assignment of dark matter identified a hierarchy of macroscopic quantum phases to a hierarchy of Planck constants, zero energy ontology, the model for DNA-cell membrane system as topological quantum computer, and Negentropy Maximization Principle combined with the notion of number theoretic entropy. This entropy can be negative for rational and even algebraic entanglement probabilities, which inspires the vision about life as something in the intersection of real and p-adic worlds.

The basic objection against the identification of oil droplets as a primitive life form is that droplets have no genetic code and do not replicate. The TGD inspired model for dark nucleons however predicts that the states of dark nucleon are in one-one correspondence with DNA, RNA, tRNA, and amino-acid molecules and that vertebrate genetic code is naturally realized. The question is whether the realization of the genetic code in terms of dark nucleon strings might provide the system with genetic code and whether the replication could take place at the level of dark nucleon strings rather than droplets. TGD inspired quantum model of biology leads to a model for oil droplets as a primitive life form. In particular, a proposal for how dark genes could couple to chemistry of oil droplets is developed.

## 9.1 Intelligent Oil Droplets

New Scientist (see `http://tinyurl.com/y8qyxymd`) tells about a new twist related to the Urey-Miller experiment (see `http://tinyurl.com/y83eks2s`). Martin Hanczyc (see `http://tinyurl.com/ybvwbvg3`) and his colleagues of University of Southern Denmark in Odense are doing research with a rather ambitious goal: the discovery of the recipe of life. The highly demanding challenge is to find candidates for the protocell that preceded the recent cell. What makes the task so difficult that it is not even clear what one should be searching for. For instance, what basic characteristics distinguishing living matter from inanimate systems protocell is expected to have before one can speak about primitive life form? And if one accepts the dogmas of standard biology, one encounters also the nasty hen-egg question which came first: metabolism or the genetic machinery.

Hanczyc and his colleagues have been experimenting with simple candidates for primitive life forms: oily nitrobenzene [I20] (see `http://tinyurl.com/678a2a`) droplets doped with oleic anhydride [I23] (see `http://tinyurl.com/y7ua8mwq`) immersed in alkaline (see `http://tinyurl.com/zelgz`) aqueous solution (alkalinity is by definition an ability to reduce acidicity). They have found that these systems have some attributes generally associated with life. The recent experiments replaced oleic anhydrite with the black tar consisting of complex branched and fractal looking hydrogen cyanide (HCN) polymer [I11] (see `http://tinyurl.com/nehrmu4`) produced by Urey-Miller experiments and found that also now the droplets exhibit lifelike behavior: they sense and respond their neighbors and move towards "food" sources.

The earlier experiments using nitrobenzene droplets doped with oleic anhydridge immersed in alkaline solution began immediately to move along straight lines. What happened that the oleic anhydride at the surface of the droplet reacted with the water splitting to two oleic acid molecules [I22] (see `http://tinyurl.com/yf34q92`) by hydration. This dropped the surface tension of the droplet and by a kind of spontaneous symmetry breaking the reaction rate had maximum at some point of the droplet and a "hot spot" was generated drawing oleic anhydride from the interior of the droplet and generating a convective flow. A pH gradient develops along the surface. The oleic acid in turn moved along the droplet surface from the hot spot to the diametrically opposite side of the droplet [I54] (see (`http://tinyurl.com/yc627j5k`). The net effect was a linear motion. pH gradient is claimed to be essential for the generation of motion but I must admit that I do not quite understand this point. A primitive metabolism liberating energy is obviously in question. By momentum conservation the total momentum for the convective flow and flow of oleic acid was compensated by a center of mass motion of the droplet.

One could claim that this process belongs to the same class of self-organization processes as the generation of convection patterns as one heats liquid from below. Other researchers have however discovered that the oil droplets can also travel along chemical gradients, something known as chemotaxis used by many bacteria to find food and void threats. One oil droplet managed even

to (see "solve" (see http://tinyurl.com/yb7muvg) a complex maze containing "food" at its other end [I53]. Whether this kind of behavior can be regarded as a mere chemistry is far from obvious to me. To me this a achievement look like a genuinely goal directed intentional behavior.

Hanczyc has also found that when the oil droplets approach each other they change course to avoid collision, or can circle each other-like partners in Viennese waltz! Oil droplets seem to have even memory. By videoing the paths of oil droplets Hanczyc found that the decision to stop or continue was not random but the behavior at any point of orbits was affected by the earlier behavior. This is by the way an elegant experimental manner to show that non-deterministic behavior is not just randomness. The experiments have been also carried using instead of oleic anhydride mineral oil consisting of a mixture of alkanes having as building block polymers from from $CH_4$ by dropping two hydrogen from each C as also lipids have (methane $CH_4$ is the simplest alkane). What distinguishes mineral oil molecules from the oleic anhydride molecules are the oxygen atoms in the middle of the reflection symmetric linear molecule. Also now the droplets move although the process takes place with a slower rate.

The basic objections against the identification of the oil droplets as a life form is that they do not replicate and there is no genetic code. One must be however very cautious with this kind of statements. Maybe the primary life forms are not the droplets and the behavior of droplets reflects the control actions of these life forms on droplets. Perhaps also genetic code could be realized at at totally different level. The recent findings of the group of HIV Nobelist Montagnier [I57] (see http://tinyurl.com/2co7s6j) indeed suggest a new realization of genetic code in water closely related to to water memory and TGD suggests a concrete realization of this code [K18].

## 9.2 Some Key Ideas Of TGD Inspired Quantum Biology

Before proposing a model for intelligent oil droplets as a primitive life form its good to list some of the basic ideas of TGD inspired quantum biology.,

1. The basic hypothesis is that the dark matter at the magnetic flux tubes of the magnetic body assignable to any physical system serves as an intentional agent controlling the behavior of the ordinary matter [K9]. Dark matter can correspond to just the ordinary particles- at least electrons and protons- in a phase with non-standard large value of Planck constant forming macroscopic quantum phases. Also biologically important ions could form this kind of phases. TGD inspired nuclear physics [L2] allows also the bosonic counterparts of fermionic with same nuclear charge so that every fermionic ion could be accompanied by exotic bosonic ion so that Bose-Einstein condensates could become possible.

2. The model for dark nucleons [L2, K18] as entangled triplets of three quarks leads to the identification of the counterparts DNA, RNA, tRNA, and amino-acids as three-quark states and one can identify also vertebrate genetic code. DNA sequences correspond to dark nucleon sequences - dark nuclei - in this correspondence. The proposal is that dark proton sequences in water form dark nucleons with so large a Planck constant that nucleon size corresponds to size of singe DNA codon. There is indeed evidence that in atto-second time scale (time scale for corresponding causal diamonds) water obeys effective chemical formula $H_{1.5}O$ as far as scattering of electrons and neutrons is considered [D5, D9, D3]. This would suggest that 1/4 of protons are in dark large Planck constant phase in the experimental situation. This proportion is expected to depend on temperature and pressure and should explain the rich spectrum of anomalies of water [D6] by regarding it as a two phase system [K11]. Perhaps these protons could form dark nucleon sequences realizing genetic code. These sequences could replicate and evolve and could define at least the analog of DNA or RNA. Maybe even DNA-mRNa-amino-acids translation processing could take place. If a translation machinery transforming exotic DNA to ordinary has developed during evolution, this fundamental realization of genetic machinery might make possible kind of Research & Development making possible to experiment with different genomes. Evolution would not be a random process anymore [K18].

3. The proposal is that the ordered water layers associated with polar molecules dissolved in water are attached to the magnetic body of the molecule induced in water environment and that this magnetic body mimicking ithe original molecule is an essential element of this primitive

life [K18]. The self-organization processes of these layers induced by external perturbations could be the predecessor of processes like protein folding and de-folding. The mechanism of water memory could be based on "dropping" of the magnetic bodies of molecules as a result of repeated shaking involved with homeopathic procedure inducing a sequence of catastrophes driving the evolution of these primitive life forms. One can also ask whether these magnetic bodies could define the analog of proteins providing one realization of dark matter genetic code.

4. If dark nucleons have been the predecessors of chemical life forms, one can circumvent the hen-egg question about whether the genetic code or metabolism came first. In zero energy ontology negative energy signals propagating in the direction of geometric past would in turn provide fundamental mechanism of intentional action, metabolism, and memory. If this is the case, evolution would have only led to a refinement of the fundamental mechanisms of life already existing: there would be no need to pull anything out of hat. The mechanisms for chemical storage and utilization of energy are needed and moving oil droplets would provide a primitive realization of these mechanisms.

5. The notion of negentropic entanglement (see **Fig.** `http://tgdtheory.fi/appfigures/cat.jpg` or **Fig. ??** in the appendix of this book) makes sense if one accepts the role of p-adic number fields and the vision about life as something residing in the intersection of real and p-adic worlds [K22]. Entanglement probabilities for negentropic entanglement must be rational or algebraic numbers in the algebraic extension of p-adic numbers involved and there is unique prime for which this entanglement entropy is maximally negative. Negentropic entanglement makes possible new kind of many particle states analogous to bound states but with negative binding energy. The reason is that negentropic entanglement is stable against state function reduction if Negentropy Maximization Principle determines its dynamics also in the case of negentropic entanglement. The proposal is that the mysterious high energy phosphate bond corresponds to negentropic entanglement and carries both metabolic energy and information [K3]. In this framework ATP-ADP cycle has also information theoretic interpretation as a transfer of conscious information.

The model for DNA as topological quantum computer [K12, K30] led among other things to an identification of magnetic flux tubes connecting bio-molecules as a basic building bricks of living matter.

1. Flux tubes are assumed to connect DNA nucleotides to lipids of the nuclear and cell membranes. Flux tubes could begin from =O in the double bonds R=O or from negatively charged oxygens. In the case of DNA R would correspond to the basic unit in phosphate deoxiribose backbone (see `http://tinyurl.com/69okq`) consisting of aromatic 5-cycle and $PO_4$ containing one =O and one $O^-$ [I10]. The lipid end would contain =O and -OH and the flux tube could end to either of these or possibly -OH ionized to $-O^-$ by a transformation of proton to dark proton.

2. The braiding of flux tubes makes topological quantum computation like processes possible [K12]. The contractions and expansions of flux tubes induced by phase transitions changing the value of Planck constant would be a basic control mechanism allowing to understand how two biomolecules (say DNA and its conjugate) can find each other in the thick soup of organic molecules. The reconnections of the magnetic flux tubes would be second basic control mechanism and ATP $\rightarrow$ADP process (see `http://tinyurl.com/clnu4`) [I2] involving splitting of phosphate group and liberating metabolic energy and its reverse would represent standardized reconnection process and its reversal.

3. The flux tube ends would contain quark and antiquark (u, d and their antiquarks are involved) coding for the four DNA letters A, T, C, G so that also dark quarks and their antiquarks would provide an elementary particle level realization for the codons. Note that topological quantum computation does not necessitate genetic code and therefore also the repeating DNA sequences regarded as junk could be used for topological quantum computations.

## 9.3 General Ideas About Oil Droplets As A Primitive Life Form

It is interesting to see what one obtains if one takes the dark nucleon realization of genetic code, the mechanism of water memory realized as magnetic bodies attached to the ordered water layers associated with polar molecules, the model for DNA as topological quantum computer, and the ideas about magnetic body with dark matter as fundamental bio-control as basic ingredients of the model of intelligent oil droplets.

1. The formation of hot spot on the oil droplet resembles spontaneous symmetry breaking. The interpretation as a generation of magnetic body of approximately dipolar magnetic field is attractive. The magnetic body would control the droplet. The change of the direction of the motion of the oil droplet would correspond to the change of the orientation of the magnetic body and would thus reduce to a motor action of the magnetic body.

2. The flux tubes of the magnetic body would be most naturally parallel to the direction of the nitrobenzene polymer strands. Oleic anhydride molecules and the hydrogen cyanid polymers would be transferred along the magnetic flux tubes of an approximately dipolar magnetic field entering to the hot spot from interior and the oleic acid molecules could move along the flux tubes continuing along the surface of the droplet to the diametrically opposite point. The migration of birds along magnetic field lines is a direct analogy for this.

3. The dark matter at the magnetic body would give the oil drop its "intelligence". The dark nuclear genome could be realized at the magnetic body and the magnetic bodies might define the replicating life form as in the TGD based model of water memory for which the magnetic bodies represent molecules as far as low frequency electromagnetic fields characterized by cyclotron frequencies are considered. One could see intelligent oil droplets as manifestation of control actions of a life form defined by dark matter at magnetic flux tubes and the first step in the process eventually leading to a complex control and coordination of the behavior of ordinary matter.

4. The ability of droplets to react to the presence of other droplets would be due to the communications between magnetic bodies based on low frequency photons at cyclotron frequencies but having energy above thermal energy if the value of Planck constant is large enough.

At least oleic anhydrite, hydrogen cyanide, and mineral oil can serve as a fuel of oil droplets and this raises the question what might be the common property shared by them. For illustrations of various molecules involved see **Figs.3**, **4**, **5**, **6**, **??**, **7** in the section containing figures. Certainly this property must relate to metabolism and the model for ordinary metabolism suggests that this property is shared also by the high energy phosphate bond.

1. Oleic anhydrite (see `http://tinyurl.com/y7ua8mwq`) is a lipid formed by as a fusion of two oleic acids consisting of a sequence of $CH_2$ units and the characteristic (C=O)-(O-H) group at its end. The burning of the molecule splits it to two oleic acids by hydration meaning utilizing one water molecule. The formation of oleic acid in turn involves dehydration so that the burning process is analogous to de-polymerization of DNA or amino-acid sequence by hydration.

2. Mineral oil (see `http://tinyurl.com/eoy5x`) is also a lipid and looks like oleic anhydride locally. In the ideal case however the crucial..(C=O)-O-(C=O)-.. portions are lacking. Oxygenation could however produce this kind of defects to the mineral oil molecules so that the mechanism of burning would remain the same.

3. Hydrogen cyanide (see `http://tinyurl.com/nv8qt8`) HCN involves valence bond of valence 3 between C and N. The polymers are constructed from H-C-N sequences with single valence bond between both C: s and N: s of two subsequent horizontal H-C-N units, which one can think of as being obtained from (H-C)-(H-C)... sequence and ..N-N-N... sequences with each N and C connected by horizontal valence bond. This polymer replaces oleic acid as a "fuel" reacting with water and liberating metabolic energy. These polymers - which would serve as primitive analogs of proteins- would be transferred along the magnetic flux tubes and burned at the hot spot by hydration. HCN has been proposed to have been a primitive precursor of

both amino acids and nuclei acids. With motivations coming from the general vision about quantum biology, it will be proposed that also hydrogen cyanide polymers contain in their C-backbone..(C=O)-O-(C=O)-.. portions as local defects due to oxygenation so that the burning would occur via hydration in all three cases.

## 9.4 What Are The Prerequisites For Metabolism And Topological Quantum Computation Like Processes?

The basic question is whether metabolism interpreted in TGD framework as negentropy transfer and thus requiring the analogs of high energy phosphate bond and ATP-ADP cycle is possible. The high energy phosphate bonds make also possible flux tube structures serving as a prerequisite for topological quantum computation like process. Both oleic anhydride, hydrogen cyanide and mineral oil can serve as a metabolic source and one should identify the common property of them making. This property should be the analog of high energy phosphate bond.

1. High energy phosphate bond carries metabolic energy. This bond is poorly understood and I have proposed that high energy phosphate bond carries negentropic entanglement which identified in TGD framework as the basic characteristic of life [K22]. In the middle of oleic anhydride there (C=O)-O-(C=O) structure and its splitting in hydration liberates energy. This suggests that this structure also now carries the negentropic entanglement and the metabolic energy. The splitting process of oleic anhydrite occurring at the hotspot would be analogous to ATP→ADP process involving splitting of $PO_4$ molecule from ATP.

2. Oleic acid is a lipid containing at its second end the characteristic (C=O)-OH group assumed to serve as a terminal for the magnetic flux tubes in the model of DNA-cell membrane system as quantum computer. In the presence energy feed one could imagine that the inverse process transforming oleic acid to oleic anhydride takes place and a primitive version of the metabolic cycle involving photosynthesis and cellular breathing can be imagined. Metabolic and quantum information processing would be very intimately related. By DNA as topological quantum computer analogy the magnetic flux tubes connecting oleic anhydride molecules would make be responsible for primitive topological quantum computation if present in the system.

3. Also when the tar from Urey-Miller experiment replaces oleic anhydrite small amount of oleic anhydride was used to build a film around oil droplet to lower surface tension. This suggests that the oleic anhydride has a deeper purpose and defines the analog of cell membrane and make possible for the magnetic flux tubes from the interior of the droplet to attach to the lipids? This could occur at least in the hot spot and at point opposite to it so that magnetic flux tubes would connect the diametrically opposite points of the droplet Oleic anhydride would therefore serve a dual purpose serving both as a metabolic resource and a building brick of the protocell membrane: metabolic energy would be accompanied by information. Also in real life lipids -about which fats are a special case- have this double role.

4. The process occurs also both for hydrogen cyanide and mineral oilandthis raises obvious objections since the energy and information carrying (C=O)-O-(C=O) structures making also possible the flux tube connects are not present in the ideal situation. One must however remember that the situation in real life is far from ideal and the most obvious idea is that the polymers as such are not enough: oxygen is the basic metabolic resource and oxygenation serving as the loading of metabolic batteries might be the crucial element.

   (a) The backbone of both oleic acid (see `http://tinyurl.com/yf34q92`), oleic anhydride, and of mineral oil polymers (see `http://tinyurl.com/eoy5x`) is $CH_2$ sequence common to all lipids. If some fraction of mineral oil polymers contain (C=O)-O -(C=O): s serving as carriers of metabolic energy and information the situation reduces to that for oleic anhydride apart from effects caused by the fact that the density of metabolic energy per volume is expected to be lower, which would explain why the motion is slower.

   (b) Also in the case of hydrogen cyanide (see `http://tinyurl.com/nv8qt8`) polymers one can imagine the presence of similar defect structures due to oxygenation. A portion

of...(H-C)-(H-C)-(H-C).... sequence would be replaced with....(H-C)-( C=O)-O-(C=O)-(H-C)... with three carbons lacking. The nitrogen sequence...N-N-N-N-N.. would split to...N-OH and OH-N... so that three nitrogens would be lacking. The total number of hydrogens would remain the same.

Under these assumptions the model explains all three cases using hydration as the basic mechanism of metabolism as well as the conditions required by DNA as topological quantum computer model. Note that the process consumes oxygen just as the ordinary breathing.

## 9.5 What About Genetic Code And Counterpart Of DNA?

Consider next the possible realization of the genetic code. The first thing to notice is that even in the case that genetic code is not realized the braiding would make possible topological quantum computation like processes and a realization of memory in terms of braiding patterns. Furthermore, chemical realization of the genetric code is not possible so that dark nucleons remain the only possibility in TGD framework. The challenge is to try imagine whether DNA like structures having flux tube connections with the counterparts of lipids in the cell membrane could exist. The following suggestion is a product of free imagination based on analogies and reflects my amateurish skills in biochemistry.

1. Aromatic rings (see `http://tinyurl.com/ycf3kv24`) [I3] are an essential element of both phosphate deoxiribose backbone of DNA and of DNA letters itself. Nitrobenzene molecule obeys chemical formula $(C_6H-5)$-$NO_2$ and contains benzene ring to which $NO_2$ nitro group is attached. The oily character is due to the benzene ring. Benzene rings could serve as a counterpart for the hydrocarbon 5-cycles appearing in phosphate deoxiribose backbone. Note however that in deoxiribose ring one carbon is replaced with O and two hydrogens with OH. Moreover, single benzene molecule would correspond to the counterpart of DNA triplet rather than single nucleoside. One could however argue that only a backbone is in question so that the differences might not matter.

2. One would naively expect that both nitrogen and phosphorus have same valence equal to three. In $PO_4$ phosporus has 5 valence bonds as a rule and the interpretation is that phosphorus tends to donate its valence electrons to get empty shell. This kind of states are known as oxidation states and are possible also for nitrogen: hydroxylamine $NO_2H$ is one example of this kind of state. In fact, from the from structural formula of nitrobenzene (see **Fig. 3** ) one finds that nitrogen gives one electron to second oxygen so that also this state can be regarded as an oxidation state. This inspires the idea that nitrogen takes the role of phosphorus at least partially.

3. If one does not allow oxidation states, the simplest manner to construct the analog of phosphate deoxiribose backbone is as structure ...X-X-X..., with X= R-O- $(R_1$-N)-O, where R denotes oleic anhydride and $R_1$ is for benzene residue. The bridges connecting benzene rings would be reflection symmetric. The breaking of reflection symmetry is however essential since it determines the reading direction of DNA.

4. If one accepts oxidation states, the simplest option is that in benzene-$NO_2$ complex $NO_2$ is replaced with (N=0)-O and the counterpart of phosphate deoxiribose backbone would have the structure ...X-X-X—, X=R- $(R_1$-N=0)-O with R denoting oleic anhydride and $R_1$ benzene. Oleic anhydride has valence bond to N so that N has 5 valence bonds as phosphorus in phosphate. Also the crucial =O is present. The units connecting subsequent benzene rings are not reflection symmetric anymore as indeed required. There is however no charged oxygen as in the case of ordinary DNA. Note that the analogs for AMP, ADP, ATP make sense since one can single replace P by N phosphate $PO_4$.

5. An interesting question is whether the nitrogen based metabolism could be realized as a primordial metabolism. Nitroglycerin (see `http://tinyurl.com/y9a23qen`) is analogous to tri-phosphate although the nitrates are not arrranged linearly as in ATP and is used as both heart medicine and as an active incredient of explosives. The latter use conforms with the idea about the presence of high energy nitrate bond in $NO_4$.

6. The two mirror image branches of oleic anhydride molecule consist of 15 carbon atoms and the structure is rather long as compared to the basic unit of phosphate deoxiribose backbone so that the distance between subsequent benzene units would be rather long- of order 10 Angstroms. On the other hand, 10 DNA codons correspond to 10 nm length in a good accuracy so that one codon would take 1 nm length also in this case. If double strand is formed, twisting is possible so that the scales could be the same. The size scale of the dark nucleon representing single DNA codon should correspond to the size scale of single oleic anhydride molecule and the required value of Planck constant would be of order $10^6$ as the ratio of this scale and nucleon size of order $10^{-15}$ meters.

7. The counterparts of DNA nucleotides forming a linear structure should join to the benzene rings. Dark nucleon sequences remain the only possibility if one wants a realization of genetic code. Each dark codon represented by dark nucleon would be connected by three flux tubes with quark and antiquark at their ends to single unit of the proposed structure. There would be three =O: s per single benzene ring. Since single benzene ring corresponds to single DNA codon three =O: s are indeed expected. Therefore =O: s could indeed correspond to terminals for flux tubes coming from single dark nucleon representing single DNA codon.

8. The division of oil droplet would be the analog of cell replication and would involve at the deeper level the replication of dark nucleon sequences. This requires the analog of DNA double strand and the analogs of DNA codons would be dark nucleons. Genetic codons could be realized in terms of flux tubes connecting dark nucleon sequences to the oleic acids or oleic anhydrides at the surface of the droplet. It remains to be seen whether the division can be achieve in real world.

To sum up, the proposed model is rather direct application of TGD based vision about life and the killer test is whether the mineral oil oil molecules and hydrogen cyanide molecules are not ideal but actually contain the (C=O)-O-(C= O) pieces carrying energy and information and serve as terminals for the magnetic flux tubes.

## 9.6 Another Approach To Protocell

Also the group led by Jack. W. Szostak (see `http://tinyurl.com/y8avsbzd`), who was the 2009 Nobel Prize winner in physiology - has carried out beautiful experiments in which they are able to create a candidate for protocell satisfying many of the basic requirements [I60].

One such condition is the ability of protocell to transfer various nutrient molecules through the protocell membrane. In modern cell pumps and channels consisting of proteins are believed to serve that purpose (for a different view see the remark below). Genetically coded proteins were however absent during the primordial era. Therefore the membrane is constructed of branching lipids believed to exists during prebiotic era allowing sugars which are basic building bricks of DNA to permeate to the protocell. Given the DNA template, the basic building bricks of DNA molecule assemble to a copy of DNA in this protocell.

What is still lacking is the generation of the template strand of DNA itself and also the replication of protocell. If dark DNA in the form of dark nucleon strings is really there, the template could result as the assembly of the basic bricks of DNA around it and above a proposal for the analog of this kind of process is suggested. The replication of the dark genes would have been also present from the beginning and would have preceded the replication of genes and protocell. Biological evolution could be seen as a migration from dark space-time sheets to ordinary ones and somewhat analogous to the migration of life from sea to land.

*Remark:* There are puzzling experimental findings about quantal currents through cell membrane even in absence of metabolic sources. In many-sheeted space-time [K27] one could interpret these currents as various kinds of Josephson currents running between cell interior and exterior along current carrying space-time shees. Pumps and channels would be more like a diagnostic tool allowing cell to measure the concentrations of various important biomolecules and ions.

At first sight the approaches of Szostak and Martin Hanczyc look very different. These approaches have however a lot of common at deeper level if one accepts TGD based view as DNA-cell membrane system or its more primitive version as a topological quantum computer like system relying on the braiding of magnetic flux tubes connecting the counterpart of DNA nucleotides to

the lipids of protocell membrane and on the prebiotic realization of genetic code at the level of dark nuclear physics.

One could also argue that the protocell of Hanczyk represents oil based life as opposed to life as we know it. In TGD framework this is a mis-interpretation. The protocells of Hanczyk live in an aqueous environment. Nitrobenzene oil is an aromatic compound as also sugars and contains nitrogen taking in the proposed scenario same role as phosphorus in ordinary life. Oleic anhydride is lipid and- would provide basic building brick for a particular variant of DNA like structure halfway between dark and completely chemical realization. Oleic anhydride would provide also the building bricks of protocell membrane and serve as a nutrient just like fat molecules- also lipids- serve in "real life".

# 10 Figures

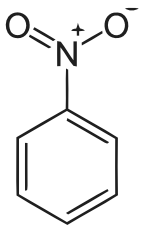

**Figure 3:** Nitrobenzene

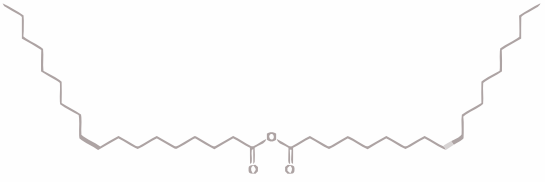

**Figure 4:** Oleic anhydride

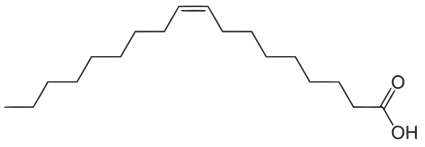


**Figure 5:** Oleic acid

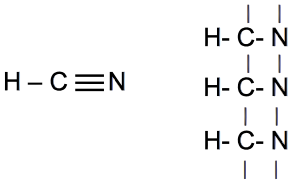


**Figure 6:** Hydrogen cyanide and hydrogen cyanide polymer.

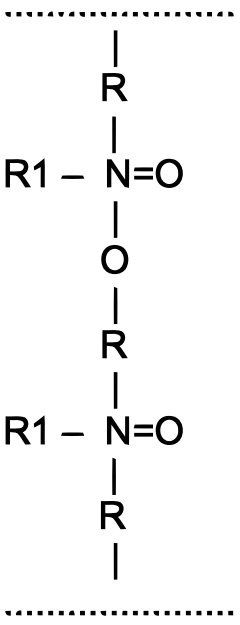


**Figure 7:** The analog of the deoxiribose phosphate backbone. R denotes oleic anhydride containing two =O: s and R1 benzene ring.

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