Evolution in Many-Sheeted Space-Time: Part II

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Contents

Abstract

This chapter is second part of a chapter devoted for the TGD view about prebiotic evolution but gradually extended so that it became natural to drop the attribute "prebiotic".

1. Quantum aspects of TGD inspired biology are discussed. Number theoretic vision based on the notion of adelic physics predicts a hierarchy of Planck constants giving rise to a hierarchy of phases of ordinary matter behaving like dark matter. The notion of magnetic body (MB) as a many-sheeted structure is introduced: the number theoretic origin of many-sheetedness was not clear when this chapter was written for the first timeand I proposed that the imbedding space itselfcould be many-sheeted.The notion of gravitational Planck constant introduced by Nottale is interpreted in the TGD framework as a source of quantum coherence at the gravitationalpart of MB even in astrophysical scales. Water memory and homeopathy are discussed as manifestations of MB of water and suggesting that water as such is a primitive prebiotic life form.
2. A great 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.
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. TGD based view about the evolution of genetic code is compared 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 This section is a little bit out of date.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.

1 Introduction

This chapter is the second part of a 2-part chapter devoted to the understanding of evolution in TGD Universe. The introduction to the first part describes the basic ideas and lists the basic questons attacked in these chapters. Here only the topics discussed in this chapter are listed.

1.1 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 [K22] 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. A quantum 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 [K4, K3]. 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 [I35, I36], [J2] 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 [L2]. 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 [K17].

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 [K15]: 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 [K17]. 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.

2. A great 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.

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.

   After writing this section quantum TGD based mathematical models of genetic code prediction correctly the numbers of codons coding for a given amino acid have evolved [L18, L4], and are discussed in [K5] and [L6].

4. The TGD based view about the evolution of genetic code is compared to the views of McFadden [I30] involving the proposal that different DNAs can quantum superpose. In standard ontology this proposal looks strange but in zero energy ontology (ZEO) it can be indeed considered. The TGD based vision about life is also compared with Jeremy England's views [I33]: England's paradoxical observation that entropy growth accompanies evolution finds explanation from the fact that p-adic counterparts of entropies can be negative and have interpretation as measures of cognitive information associated with entanglement.

To sum up, TGD does not yet provide a rather detailed view about prebiotic evolution. The magnetic body of water carrying dark matter and controlling ordinary biomolecules via their dark analogs 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` [L3].

2 Some aspects of TGD inspired quantum biology

TGD based explanation for the findings relies on the basic notions of TGD inspired quantum biology. The basic notions are magnetic body (MB) and hierarchy of Planck constants $h_{eff} = n \times h_0$ [K21, K27] emerging from the adelic physics as a prediction [L15, L16] but originally proposed on basis of anomalous effects of ELF em fields in living matter. The anatomy of MB has remained unclear hitherto but in this article a detailed model allowing to understand the formula $h_{gr} = h_{eff}$ for gravitational Planck constant and leading to a further formula for h_{gr} relating magnetism and gravitation.

A further central notion is TGD based model for water memory as the ability of the MB of water to control the thickness of its flux tubes to entrain with external frequencies and reproduce them. This is a central element in TGD based view about immune system and homeopathic effects [K6]. Cancer would reduce to a disease of the MB of the living system to high degree determined by the MB of water. Details of the bio-chemistry and even cell membrane dynamics would have surprisingly minor role in the model.

2.1 Is the cosmological constant really understood?

The interpretation of the coefficient of the volume term as cosmological constant has been a long-standing interpretational issue and caused many moments of despair during years. The intuitive picture has been that cosmological constant obeys p-adic length scale scale evolution meaning that Λ would behave like $1/L_p^2 = 1/p \simeq 1/2^k$ [K18].

This would solve the problems due to the huge value of Λ predicted in GRT approach: the smoothed out behavior of Λ would be $\Lambda \propto 1/a^2$, a light-cone proper time defining cosmic time, and the recent value of Λ - or rather, its value in length scale corresponding to the size scale of the observed Universe - would be extremely small. In the very early Universe - in very short length scales - Λ would be large.

It has however turned out that I have not really understood how this evolution could emerge! Twistor lift seems to allow only a very slow (logarithmic) p-adic length scale evolution of Λ [L28]. Is there any cure to this problem?

1. Could one consider the *total* action for preferred extremals - at least flux tubes - as proportional to effective cosmological constant Λ_{eff}? Since magnetic energy decreases with the are of string like $1/p \simeq 1/2^k$, where p defines the transversal length scale of the flux tube, one would have effective p-adic coupling constant evolution of Λ_{eff} approaching to Λ, which must be extremely small.

   The corresponding size scale would correspond to the density of the magnetic energy equal to that of dark energy. Flux tubes with quantized flux would have thickness determined by the length scale defined by the density of dark energy: $L \sim \rho_{vac}^{-1/4}$, $\rho_{dark} = \Lambda/8\pi G$. $\rho_{vac} \sim 10^{-47}$ GeV^4 (see `http://tinyurl.com/k4bwlzu`) would give $L \sim 1$ mm, which would could be interpreted as a biological length scale (maybe even neuronal length scale).

2. But can Λ be very small? In the simplest picture based on dimensionally reduced 6-D Kähler action this term is not small in comparison with the Kähler action! If the twistor spheres of M^4 and CP_2 give the same contribution to the induced Kähler form at twistor sphere of X^4, this term has maximal possible value!

   The original discussions in [K30, K18] treated the volume term and Kähler term in the dimensionally reduced action as independent terms and Λ was chosen freely. This is however not the case since the coefficients of both terms are proportional to $1/\alpha_K^2 S$, where S is the area of the twistor sphere which is same for the twistor spaces of M^4 and CP_2 if CP_2 size defines the only fundamental length scale. I did not even recognize this mistake.

The proposed fast p-adic evolution of the cosmological constant would have extremely beautiful consequences. Could the original intuitive picture be wrong, or could the desired p-adic length scale evolution for Λ be possible after all? Could dynamics somehow give it? To see what can happen one must look in more detail the induction of twistor structure.

1. The induction of the twistor structure by dimensional reduction involves the identification of the twistor spheres S^2 of the geometric twistor spaces $T(M^4) = M^4 \times S^2(M^4)$ and of T_{CP_2} having $S^2(CP_2)$ as fiber space. What this means that one can take the coordinates of say $S^2(M^4)$ as coordinates and imbedding map maps $S^2(M^4)$ to $S^2(CP_2)$. The twistor spheres $S^2(M^4)$ and $S^2(CP_2)$ have in the minimal scenario same radius $R(CP_2)$ (radius of the geodesic sphere of CP_2. The identification map is unique apart from $SO(3)$ rotation R of either twistor sphere. Could one consider the possibility that R is not trivial and that the induced Kähler forms could almos cancel each other?

2. The induced Kähler form is sum of the Kähler forms induced from $S^2(M^4)$ and $S^2(CP_2)$ and since Kähler forms are same apart from a rotation in the common S^2 coordinates, one has $J_{ind} = J + R(J)$, where R denotes the rotation. The sum is $J_{ind} = 2J$ if the relative rotation is trivial and $J_{ind} = 0$ if R corresponds to a rotation $\Theta \to \Theta + \pi$ changing the sign of $J = sin(\Theta)d\Theta \wedge d\Phi$.

3. Could p-adic length scale evolution for Λ correspond to a sequence of rotations - in the simplest case $\Theta \to \Theta + \Delta_k\Theta$ taking gradually J from $2J$ at very short length scales to $J = 0$ corresponding to $\Delta_\infty\Theta = \pi$ at very long length scales? A suitable spectrum for $\Delta_k(\Theta)$ could reproduce the proposal $\Lambda \propto 2^-k$ for Λ.

4. One can of course ask whether the resulting induced twistor structure is acceptable. Certainly it is not equivalent with the standard twistor structure. In particular, the condition $J^2 = -g$ is lost. In the case of induced Kähler form at X^4 this condition is also lost. For spinor structure the induction guarantees the existence and uniqueness of the spinor structure, and the same applies also to the induced twistor structure being together with the unique properties of twistor spaces of M^4 and CP_2 the key motivation for the notion.

5. Could field equations associated with the dimensional reduction allow p-adic length scale evolution in this sense?

   (a) The sum $J + R(J)$ defining the induced Kähler form in $S^2(X^4)$ is covariantly constant since both terms are covariantly constant by the rotational covariance of J.

   (b) The imbeddings of $S^2(X^4)$ as twistor sphere of space-time surface to both spheres are holomorphic since rotations are represented as holomorphic transformations. This in turn implies that the second fundamental form in complex coordinates is a tensor having only components of type $(1,1)$ and $(-1,-1)$ whereas metric and energy momentum tensor have only components of type $(1,-1)$ and $(-1,1)$. Therefore all contractions appearing in field equations vanish identically and $S^2(X^4)$ is minimal surface and Kähler current in $S^2(X^4)$ vanishes since it involves components of the trace of second fundamental form. Field equations are indeed satisfied.

   (c) The solution of field equations becomes a family of space-time surfaces parametrized by the values of the cosmological constant Λ as function of S^2 coordinates satisfying $\Lambda/8\pi G = \rho_{vac} = J \wedge (*J)(S^2)$. In long length scales the variation range of Λ would become arbitrary small.

6. If the minimal surface equations solve separately field equations for the volume term and Kähler action everywhere apart from a discrete set of singular points, the cosmological constant affects the space-time dynamics only at these points. The physical interpretation of these points is as seats of fundamental fermions at partonic 2-surface at the ends of light-like 3-surfaces defining their orbits (induced metric changes signature at these 3-surfaces). Fermion orbits would be boundaries of fermionic string world sheets.

   One would have family of solutions of field equations but particular value of Λ would make itself visible only at the level of elementary fermions by affecting the values of coupling constants. p-Adic coupling constant evolution would be induced by the p-adic coupling constant evolution for the relative rotations R for the two twistor spheres. Therefore twistor lift would not be mere manner to reproduce cosmological term but determine the dynamics at the level of coupling constant evolution.

7. What is nice that also $\Lambda = 0$ option is possible. This would correspond to the variant of TGD involving only Kähler action regarded as TGD before the emergence of twistor lift. Therefore the nice results about cosmology obtained at this limit would not be lost.

2.2 The notion of magnetic body

Magnetic flux tubes and field body/magnetic body (MB) are basic notions of TGD implied by the modification of Maxwellian electrodynamics [K14, K7, K12]. Actually a profound generalization of space-time concept is in question. Magnetic flux tubes are in well-defined sense building bricks of space-time - topological field quanta - and lead to the notion of field body/MB as a field identity assignable to any physical system: in Maxwell's theory and ordinary field theory the fields of different systems superpose and one cannot say about magnetic field in given region of space-time that it would belong to some particular system. In TGD only the effects on test particle for induced fields associated with different space-time sheets with overlapping M^4 projections sum.

The hierarchy of Planck constants $h_{eff} = n \times h_0$, where h_0 is the minimum value of Planck constant, is second key notion. h_0 need not correspond to ordinary Planck constant h and both the observations of Randell Mills [L10] and the model for color vision [L22] suggest that one has $h = 6h_0$. The hierarchy of Planck constants labels a hierarchy of phases of ordinary matter behaving as dark matter.

Magnetic flux tubes would connect molecules, cells and even larger units, which would serve as nodes in (tensor-) networks [**?**] [L9]. Flux tubes would serve as correlates for quantum entanglement and replace wormholes in ER-EPR correspondence proposed by Leonard Susskind and Juan Maldacena in 2014 (see `http://tinyurl.com/y7za98cn` and `http://tinyurl.com/ydckw5u7`). In biology and neuroscience these networks would be in a central role. For instance, in brain neuron nets would be associated with them and would serve as correlates for mental images [L12, L23]. The dynamics of mental images would correspond to that for the flux tube networks.

2.3 Hierarchy of Planck constants, space-time surfaces as covering spaces, and adelic physics

From the beginning it was clear that $h_{eff}/h = n$ corresponds to the number of sheets for a covering space of some kind. First the covering was assigned with the causal diamonds. Later I assigned it with space-time surfaces but the details of the covering remained unclear. The final identification emerged only in the beginning of 2017.

2.3.1 Number theoretical universality and hierarchy of extensions of rationals

Number theoretical universality (NTU) leads to the notion of adelic space-time surface (monadic manifold) involving a discretization in an extension of rationals defining particular level in the hierarchy of adeles defining evolutionary hierarchy. The formulation of this vision is proposed in [L11, L16, L15].

The key constraint is NTU for adelic space-time containing sheets in the real sector and various padic sectors, which are extensions of p-adic number fields induced by an extension of rationals which can contain also powers of a root of e inducing finite-D extension of p-adic numbers (e^p is ordinary p-adic number in Q_p).

One identifies the numbers in the extension of rationals as common for all number fields and demands that imbedding space has a discretization in an extension of rationals in the sense that the preferred coordinates of imbedding space implied by isometries belong to extension of rationals for the points of number theoretic discretization. This implies that the versions of isometries with group parameters in the extension of rationals act as discrete versions of symmetries. The correspondence between real and p-adic variants of the imbedding space is extremely discontinuous for given adelic imbedding space (there is hierarchy of them with levels characterized by extensions of rationals). Space-time surfaces typically contain rather small set of points in the extension ($x^n + yn^2 = z^n$ contains no rationals for $n > 2$!). Hence one expects a discretization with a finite cutoff length at space-time level for sufficiently low space-time dimension $D = 4$ could be enough.

After that one assigns in the real sector an open set to each point of discretization and these open sets define a manifold covering. In p-adic sector one can assign 8:th Cartesian power of ordinary

p-adic numbers to each point of number theoretic discretization. This gives both discretization and smooth local manifold structure. What is important is that Galois group of the extension acts on these discretizations and one obtains from a given discretization a covering space with the number of sheets equal to a factor of the order of Galois group.

2.3.2 Effective Planck constant as dimension of extension of rationals and number of sheets of space-time surface as covering space

$h_{eff}/h_0 = n$ was identified from the beginning as the number of sheets of poly-sheeted covering assignable to space-time surface. The number n of sheets would naturally a factor of the order of Galois group implying $h_{eff}/h = n$ bound to increase during number theoretic evolution so that the algebraic complexity increases. Note that WCW decomposes into sectors corresponding to the extensions of rationals and the dimension of the extension is bound to increase in the long run by localizations to various sectors in self measurements [K9]. Dark matter hierarchy represents number theoretical/adelic physics and therefore has now rather rigorous mathematical justification. It is however good to recall that $h_{eff}/h = n$ hypothesis emerged from an experimental anomaly: radiation at ELF frequencies had quantal effects of vertebrate brain impossible in standard quantum theory since the energies $E = hf$ of photons are ridiculously small as compared to thermal energy.

Indeed, since n is positive integer evolution is analogous to a diffusion in half-line and n unavoidably increases in the long run just as the particle diffuses farther away from origin (by looking what gradually happens near paper basket one understands what this means). The increase of n implies the increase of maximal negentropy and thus of negentropy. Negentropy Maximization Principle (NMP) follows from adelic physics alone and there is no need to postulate it separately. Things get better in the long run although we do not live in the best possible world as Leibniz who first proposed the notion of monad proposed!

2.3.3 Formula for the gravitational Planck constant and some background

The formula

$$\hbar_{gr} = \frac{GM_D m}{v_0} \tag{2.1}$$

for the gravitational Planck constant was originally introduced by Nottale [E2]. Here v_0 is a parameter with dimensions of velocity: I have considered argument allowing to deduce information about the value of $\beta_0 = v_0/c$ as the ratio of the M^4 size of the system and the size of its magnetic body [L19]. Values of order $\beta_0 \sim 10^{-3}$ are encountered.

Since m disappears from the predictions by Equivalence Principle it is not at all clear what kind limitations one has for m and one can even assume that m corresponds to particle mass without change in predictions. In Nottale's original formula m is mass of planet and M_D the mass of Sun but m could be even mass of elementary particle without change in predictions. The assumption has been $m/M_D << 1$. The replacement of M_D with total mass $M_D + m$ and m by reduced mass $M_D m/(M_D + m)$ does not affect the formula and the asymmetry between m and M_D would become more natural asymmetry between total mass and reduced mass.

For $Mm < v_0 m_{Pl}^2$ one must have $h_{gr} = h$, which suggests that quite generally one must have $m \geq \sqrt{v_0} M_{Pl}$ and $M \geq \sqrt{v_0} M_{Pl}$. The formula is non-relativistic but one can consider a relativistic generalization in which m and M are replaced by energies [K26] .

The formula is expected to hold true at the magnetic flux tubes mediating gravitational interaction. M_D has been interpreted as dark gravitational flux at the gravitational flux tubes with a fixed value of h_{eff} and should be a fraction of the total gravitational flux M. These flux tubes define $n_{gr} = h_{eff}/h_0$-sheeted covering of M^4.

Also a more general formula

$$h_{gr} = h_{eff} \quad , \quad h_{eff} = n_{gr} \times h_0 \quad , \quad h = 6h_0 \quad . \tag{2.2}$$

has been assumed. The support for the formula $h = 6h_0$ is discussed in [L10, L22]. The value of h_{gr} can be very large unlike the value of h_{eff} associated with say valence bonds.

One important implication of the formula is that the cyclotron energy spectrum does not depend on the mass of charged particle at all and is therefore universal. The assumption has been that the spectrum is in visible and UV range assignable to bio-photons [K15, K16]. One can however consider also the possibility that also the energies between the thermal energy at physiological temperature and visible photon energies are allowed.

2.3.4 What does one really mean with gravitational Planck constant?

There are important questions related to the QFT-GRT limit of TGD.

1. *What does one mean with space-time as covering space?*

The central idea is that space-time corresponds to n-fold covering for $h_{eff} = n \times h_0$. It is not however quite clear what this statement does mean.

1. How the many-sheeted space-time corresponds to the space-time of QFT and GRT? QFT-GRT limit of TGD is defined by identifying the gauge potentials as sums of induced gauge potentials over the space-time sheets. Magnetic field is sum over its values for different space-time sheets. For single sheet the field would be extremely small in the present case as will be found.

2. A central notion associated with the hierarchy of effective Planck constants $h_{eff}/h_0 = n$ giving as a special case $\hbar_{gr} = GMm/v_0$ assigned to the flux tubes mediating gravitational interactions. The most general view is that the space-time itself can be regarded as n-sheeted covering space. A more restricted view is that space-time surface can be regarded as n-sheeted covering of M^4. But why not n-sheeted covering of CP_2? And why not having $n = n_1 \times n_2$ such that one has n_1-sheeted covering of CP_2 and n_2-sheeted covering of M^4 as I indeed proposed for more than decade ago [K28] but gave up this notion later and consider only coverings of M^4? There is indeed nothing preventing the more general coverings.

3. $n = n_1 \times n_2$ covering can be illustrated for an electric engineer by considering a coil in very thin 3 dimensional slab having thickness L. The small vertical direction would serve and as analog of CP_2. The remaining 2 large dimensions would serve as analog for M^4. One could try to construct a coil with n loops in the vertical direction direction but for very large n one would encounter problems since loops would overlap because the thickness of the wire would be larger than available room L/n. There would be some maximum value of n, call it n_{max}.

   One could overcome this limit by using the decomposition $n = n_1 \times n_2$ existing if n is prime. In this case one could decompose the coil into n_1 parallel coils in plane having $n_2 \geq n_{max}$ loops in the vertical direction. This provided n_2 is small enough to avoid problems due to finite thickness of the coil. For n prime this does not work but one can of also select n_2 to be maximal and allow the last coil to have less than n_2 loops.

   An interesting possibility is that that preferred extremal property implies the decomposition $n_{gr} = n_1 \times n_2$ with nearly maximal value of n_2, which can vary in some limits. Of course, one of the n_2-coverings of M^4 could be in-complete in the case that n_{gr} is prime or not divisible by nearly maximal value of n_2. We do not live in ideal Universe, and one can even imagine that the copies of M^4 covering are not exact copies but that n_2 can vary.

4. In the case of $M^4 \times CP_2$ space-time sheet would replace single loop of the coil, and the procedure would be very similar. A highly interesting question is whether preferred extremal property favours the option in which one has as analog of n_1 coils n_1 full copies of n_2-fold coverings of M^4 at different positions in M^4 and thus defining an n_1 covering of CP_2 in M^4 direction. These positions of copies need not be close to each other but one could still have quantum coherence and this would be essential in TGD inspired quantum biology [L21].

   Number theoretic vision [L16, L15] suggests that the sheets could be related by discrete isometries of CP_2 possibly representing the action of Galois group of the extension of rationals defining the adele and since the group is finite sub-group of CP_2, the number of sheets would be finite.

The finite sub-groups of $SU(3)$ are analogous to the finite sub-groups of $SU(2)$ and if they action is genuinely 3-D they correspond to the symmetries of Platonic solids (tetrahedron,cube,octahedron, icosahedron, dodecahedron). Otherwise one obtains symmetries of polygons and the order of group can be arbitrary large. Similar phenomenon is expected now. In fact the values of n_2 could be quantized in terms of dimensions of discrete coset spaces associated with discrete sub-groups of $SU(3)$. This would give rise to a large variation of n_2 and could perhaps explain the large variation of G identified as $G = R^2(CP_2)/n_2$ suggested by the fountain effect of superfluidity [L24].

5. There are indeed two kinds of values of n: the small values $n = h_{em}/h_0 = n_{em}$ assigned with flux tubes mediating em interaction and appearing already in condensed matter physics [L14, L22, L10] and large values $n = h_{gr}/h_0 = n_{gr}$ associated with gravitational flux tubes. The small values of n would be naturally associated with coverings of CP_2. The large values $n_{gr} = n_1 \times n_2$ would correspond n_1-fold coverings of CP_2 consisting of complete n_2-fold coverings of M^4. Note that in this picture one can formally define constants $\hbar(M^4) = n_1\hbar_0$ and $\hbar(CP_2) = n_2\hbar_0$ as proposed in [K28] for more than decade ago.

2. Planck length as CP_2 radius and identification of gravitational constant G

There is also a puzzle related to the identification of gravitational Planck constant. In TGD framework the only theoretically reasonable identification of Planck length is as CP_2 length $R(CP_2)$, which is roughly $10^{3.5}$ times longer than Planck length [L24]. Otherwise one must introduce the usual Planck length as separate fundamental length. The proposal was that gravitational constant would be defined as $G = R^2(CP_2)/\hbar_{gr}$, $\hbar_{gr} \simeq 10^7\hbar$. The G indeed varies in un-expectedly wide limits and the fountain effect of superfluidity suggests that the variation can be surprisingly large.

There are however problems.

1. Arbitrary small values of $G = R^2(CP_2)/\hbar_{gr}$ are possible for the values of $\hbar_{gr}$ appearing in the applications: the values of order $n_{gr} \sim 10^{13}$ are encountered in the biological applications. The value range of G is however experimentally rather limited. Something clearly goes wrong with the proposed formula.

2. Schwartschild radius $r_S = 2GM = 2R^2(CP_2)M/\hbar_{gr}$ would decrease with $\hbar_{gr}$. One would expect just the opposite since fundamental quantal length scales should scale like $\hbar_{gr}$.

3. What about Nottale formula [E2] $\hbar_{gr} = GMm/v_0$? Should one require self-consistency and substitute $G = R^2(CP_2)/\hbar_{gr}$ to it to obtain $\hbar_{gr} = \sqrt{R^2(CP_2)Mm/v_0}$. This formula leads to physically un-acceptable predictions, and I have used in all applications $G = G_N$ corresponding to $n_{gr} \sim 10^7$ as the ratio of squares of CP_2 length and ordinary Planck length.

Could one interpret the almost constancy of G by assuming that it corresponds to $\hbar(CP_2) = n_2\hbar_0$, $n_2 \simeq 10^7$ and nearly maximal except possibly in some special situations? For $n_{gr} = n_1 \times n_2$ the covering corresponding to $\hbar_{gr}$ would be n_1-fold covering of CP_2 formed from n_1 n_2-fold coverings of M^4. For l $n_{gr} = n_1 \times n_2$ the covering would decompose to n_1 disjoint M^4 coverings and this would also guarantee that the definition of r_S remains the standard one since only the number of M^4 coverings increases.

If n_2 corresponds to the order of finite subgroup G of $SU(3)$ or number of elements in a coset space G/H of G (itself sub-group for normal sub-group H), one would have very limited number of values of n_2, and it might be possible to understand the fountain effect of superfluidity [L24] from the symmetries of CP_2, which would take a role similar to the symmetries associated with Platonic solids. In fact, the smaller value of G in fountain effect would suggest that n_2 in this case is larger than for G_N so that n_2 for G_N would not be maximal.

2.3.5 New constraint between h_{gr} and h_{eff}

Cyclotron frequencies and energies in magnetic field B and charged particle with charge Ze and mass m are proportional to the ZeB/m. The energy spectrum of bio-photons would be covered by a spectrum of magnetic field strengths B. A special field strength $B_{end} = 0.2$ Gauss has emerged

in biological applications from the beginning and the first guess is that it defines a lower bound for the spectrum of visible photon energies [L20, L17, L27]. One can fix the value of h_{gr} and therefore of GM_D/v_0 if one requires that dark photon frequency of say $f_l = 10$ Hz corresponds to the lower bound $f_h = 400$ THz for visible frequencies as $h_{gr} = f_h/f_l$: in this case would would have $n_{gr} = 4 \times 10^{13}$.

The variation of B means variation of cyclotron frequency and I have proposed that the audible frequencies correspond to a spectrum of B for the flux tubes involved with hearing [K10], and that even 12-note scale represent in terms of rational frequency ratios might have a preferred role [L4, L26].

The formula $h_{gr} = h_{eff}$ is not enough to fix the model completely. A formula fixing the relationship between B and GM_D/v_0 would be needed. This formula should be consistent with $h_{gr} = h_{eff}$. Dimensional analyst would start from the geometry of the situation.

Magnetic flux tubes are characterized by two parameters: length L_c and radius R_B.

1. Length scale naturally corresponds to the cyclotron wave length

$$L_c = \lambda_c = \frac{1}{f_c} = \frac{2\pi m}{ZeB} \quad . \tag{2.3}$$

   L_c is proportional to the mass m of the charged particle so that charge particles with different mass are with different mass flux tubes with different length and therefore different onion-like layers of MB. Charged dark particles are like books about different topics at different shelves so that living matter is extremely well-organized: something totally different from a chaotic soup of charged ions.

2. The radius of the flux tube is obtained from the flux quantization. For ordinary cylindrical flux tube with constant B the condition is $BS = k\hbar$ and for $S = \pi R^2$ the radius would be

$$R_B(h,k) = \sqrt{\frac{k\hbar}{\pi eB}} = \sqrt{\frac{k}{\pi}} L_B \quad , \quad L_B = \sqrt{\frac{\hbar}{eB}} \quad . \tag{2.4}$$

   .

   For $k = 1$ and for $B = B_{end} = .2$ Gauss one has $R_B(h,1) = 3.3$ μm to be compared with p-adic length scale $L(167) = 2.5$ μm assignable to Gaussian Mersenne $M_{G,167} = (1+i)^{167} - 1$. Magnetic length L_B is in this case $L_B = 5.8$ μm slightly larger than $L(169)$.

3. For $h_{eff} = n \times h_0$, $h = 6h_0$ the formula would generalize to

$$R_B(h_{eff},k) = \sqrt{\frac{k\hbar_{eff}}{\pi eB}} = \sqrt{\frac{n}{6}} R_c(h,k) = \sqrt{\frac{nk}{6}} R_B(h,1) \quad . \tag{2.5}$$

   Note that here n is rather small such as the value of n assignable to valence bonds.

4. The natural guess is that this formula applies at the small part of the MB restricted to the "biological body" of the living system defining that part of system, which corresponds to relatively small values of h_{eff}. The value of h_{eff} would indeed vary, being larger than h for instance for valence bonds [L14]. For dark flux tubes with small value of n the radius would be scaled up by $\sqrt{n}$ such as biological system for fixed value of B. Same happens if the value of flux is scaled by m.

   For the simplest flux tubes carrying monopole flux having string world sheet as M^4 projection geodesic sphere as CP_2 projection, the cross section is not circular disk but CP_2 geodesic sphere with radius R. I this case R is fixed. The M^4 projection of these objects is however unstable against thickening and for spherical cross section- think of two disks glued along boundaries but having different CP_2 projections, the area is $4\pi R^2$, where R corresponds to the radius of M^4 projection. Area is reduced by factor 4 from that for non-monopole flux tube and radius is reduced by factor 1/2.

One can guess the additional constraint on h_{gr} without more detailed analysis of what MB really is using dimensional analysis and I will postpone this analysis later.

1. The first natural guess is that one has

$$\frac{h_{gr}}{h_0} = n_{gr} = x\frac{L_c}{R_B(h_{eff},k)} = x(6\pi)^{3/2}\frac{1}{(nk)^{1/2}}\frac{L_B}{l_C(m)} \ ,$$
$$L_B = \sqrt{\frac{\hbar}{eB}} \ , \ l_C(m) = \frac{\hbar}{m} \ . \tag{2.6}$$

   x is some numerical constant. h_{gr}/h_0 is proportional to the ratio l_B/l_C of the magnetic length and Compton length $l_C = m/\hbar$ of the charged particle.

2. Alternative guess replaces the radius of the magnetic flux tube with the magnetic length L_B.

$$\frac{h_{gr}}{h_0} = n_{gr} = x\frac{L_c}{L_B} == x6^{3/2}\pi\frac{1}{n^{1/2}}\frac{L_B}{L_C(m)} \ , \tag{2.7}$$

   This formulas is related by factor $\sqrt{k}pi$ the first formula and has no dependence on h. It is difficult to say anything about exact value of the numerical constant x.

3. h_{gr} is proportional to m so that the formulas are consistent with $h_{gr} = h_{eff}$ formula. Combining these formulas one obtains

$$\frac{GM_D}{h_0 v_0} = \frac{r_S(M_D)}{2} = x2\pi\sqrt{\frac{n}{6Z}}\sqrt{\frac{\hbar}{eB}} \ . \tag{2.8}$$

   This formula does not depend on m and gives the value of GM_D/v_0 assignable to the flux tubes carrying magnetic field with strength B and particles with charge Z. One can say that the Schwartschild radius $r_S = 2GM_D$ characterixing M_D is proportional to magnetic length. The first option gives

$$r_S(M_D) = x \times 2 \times 6^{1/2}\pi^{3/2}\frac{1}{(nk)^{1/2}}v_0 l_B \ . \tag{2.9}$$

   For Earth Schwartschild radius is $r_{S,E} = 8.87$ mm and if $M_D < M_E$ holds true, one obtains for a given value of v_0 upper bound for the magnetic length and therefore lower bound for B. I have considered in [L19] a model for v_0 and combining this model for this formula, one obtains rather strong constraints on the parameters and also on the minimal value of B. The order of magnitude for v_0 is $v_0 \sim 10^{-3}$.

   M_D/v_0 would not depend on the mass of the charged particles at the flux tube (universality) but would depend on their charge Z unless the parameter x has a compensating $Z-$dependence. Therefore electrons and their Cooper pairs would have different value of GMD/v_0. One could perhaps interpret r_S/v_0 as analog of star radius applying to particular dark matter part of Earth. It would be considerably larger than Schwartchild radius.

4. Note that the condition $GM_D m/v_0 = n_{gr}\hbar$ can be written as

$$r_S(M_D) = 2n_{gr}l_C \ . \tag{2.10}$$

2.3.6 Estimate of G/G_N from the delocalization at magnetic flux tubes

The following argument is for a situation in which the mass m corresponds to the mass of ion. By Equivalence Principle m however disappears from the formulas involving gravitational interaction of Earth, and cyclotron frequencies remain invariant for cyclotron BE condensate. Therefore the formulas apply for the BE condensate ions with total mass equal to a multiple of Planck mass $m_P = \hbar_0/R$.

The de-localization length of dark matter wave functions in the gravitational field is much longer than for ordinary value of Planck constant: essentially the height to which particle can rise with given initial velocity V_0 in the gravitational field with gravitational constant G. This would conform with the idea that dark particles are delocalized at the flux tubes in the scale of cyclotron wave-length.

The condition that the height h for the orbit equals to cyclotron wavelength gives an estimate for G_N/G. One can estimate the height $h = R - R_E$ from energy conservation assuming that particle has initial vertical velocity V_0 at the surface of Earth and cyclotron wavelength λ_c:

$$\frac{V_0^2}{2} = \frac{G}{G_N}\left[\frac{GM}{R_E} - \frac{GM}{R}\right] \ ,$$

$$h = \lambda_c = \frac{1}{f_c} = \frac{2\pi m}{neB} \ .$$

One obtains an estimate for G/G_N as

$$\begin{aligned} \frac{G}{G_N} &= V_0^2 \frac{(R_E+h)R_E}{r_S h} \ , \quad R = R_E + h \ , \\ h &= \frac{\lambda_c}{n} = \frac{1}{nf_c} = \frac{2\pi m}{neB} \ . \end{aligned} \tag{2.11}$$

This gives

$$\frac{G}{G_N} = nV_0^2 \times \frac{R_E(R_E+\frac{\lambda_c}{n})}{r_S\lambda_c} = nV_0^2 \times \frac{R_E(R_E+\frac{2\pi eB}{neBm})}{r_S} \times \frac{eB}{2\pi m} \ . \tag{2.12}$$

The condition that value of G/G_N is constant quantizes the value of V_0. For small value of h one has $V_0^2 n \simeq constant$. For $R_E \sim \lambda_c$ and nV_0^2 is of order unity, the order of magnitude would be $G/G_N \sim R_E/r_S \sim 7 \times 10^8$.

2.4 What can one say about the detailed anatomy of the MB?

The details of the anatomy of the MB have remained rather fuzzy hitherto. The following is an attempt to formulate more explicitly and coherently the earlier ideas scattered in books and articles about TGD. There are several empirical facts and theoretical constraints that one can use.

1. There is the notion of dark DNA as dark nuclei consisting of sequences of dark protons. The notion of dark nucleus is central concept in TGD based model of "cold fusion" [L13]. Dark proton sequences are parallel with and in the vicinity of ordinary DNA strands and ordinary codons and dark proton triplets representing them [L8] are paired.

2. Pollack effect [L5] [L5] for water is assumed to generate dark DNA. Part of protons go to the flux tube and negative charge is generated in ordinary matter and ends to negative charge of phosphates associated with the ordinary DNA nucleotides. Ordinary DNA would pair with dark DNA serving as predecessor and controller of ordinary DNA. Also RNA, amino-acids, and tRNA would have dark predecessors and similar pairing would occur.

3. Experiments of Peter Gariaev et al - in particular the discovery of phantom DNA [I24] - and of Montagnier [I26] [L1] provide further valuable information.

Consider now what MB could look like.

1. MB has two parts. The small part has size of the physical system consisting of ordinary matter plus parts with relatively small h_{eff} assignable to structures such as valence bonds. The flux tubes of this part of MB connect parts of the system to a network and tensor network is an excellent mathematical model for what is involved. Flux tubes serve as topological correlates for entanglement and even prerequisites for it.

   In living matter one can imagine that the basic units of ordinary matter - say cells - are organized at parallel flux tubes. For $B_{end} = .2$ Gauss, which seems to define an especially important endogenous magnetic field, the radius r_B is of cell size. The value of proton cyclotron frequency is 300 Hz in this case and happens to correspond to the rotation frequency of the "shaft" of the ATPase as power generator.

   60 Hz frequency was found to lead to a transformation of cancer cells to ordinary ones and this suggests that cyclotron frequency for $B = B_{end}/5$ is involved. The flux tubes would contain 5 cells in their cross section and one can argue that dark proton quantum coherence at gravitational flux tubes with this thickness could give rise coherence in 5-cell length scale and lead to the cure of cancer.

2. The large part of MB - with size of the order Earth radius for $f_c = 60$ Hz corresponds to long flux tubes with large effective Planck constant $h_{gr}/h_0 = n$. Effective value of Planck constant is indeed in question since n_{gr} is the number sheets of the space-time surface as covering space and Planck constant has value h_0 (rather than $h = 6h_0$) at each sheet of the covering. At QFT limit sheets are effectively replaced with single one, and one must allow the "real" Planck constant to have non-standard values.

   What space-time surface as covering does mean has been already discussed, and it seems that the identification as $n = n_1 \times n_2$ covering, where n_1 is the number of sheets as covering of CP_2 realized in the recent case as disjoint flux tubes in M^4 and n_2 is the number of sheets as covering of M^4. Gravitational constant identified as $G = R^2/\hbar_2$ would allow to avoid unphysical predictions since n_2 could be limited to a rather narrow range by symmetry considerations.

   The cyclotron energies are scaled up by $h_{eff}/h_0 = n_{gr}$ and whatever the detailed anatomy of MB is this must be understood. Effectively one has n_{gr} photons with ordinary cyclotron energy and their energies sum up. This can be understood if the flux tubes define n_{gr}-fold coverings of M^4.

3. $h_{gr} = n_{gr}h_0$ correspond to quantum coherence in very long length scales whereas in the scale of organism the value of n is relatively small. The simplest idea is that n_{gr} disjoint flux tubes with small value of n and with given thickness determined by flux quantization coming from the living system combine to form single n_{gr}-sheeted flux tube with length given by $L_c = \lambda_c = 2\pi m/ZeB$ having no dependence on h_{eff}.

   This would be like a large number of cables combining a single cable. The threads of the cable would be now on top of each other in CP_2 direction! A rather exotic space savings! This would combine the sensory information coming from the separate flux tubes to a single super-cable and make the control of the system easy. Central nervous system would have spinal chord as an analogous unit both geometrically and functionally albeit in totally different scale. One of the first proposals was that MB provides an almost topographic representation of the biological body [K8].

   One can estimate the volume of the region with coherence forced by quantum gravitational coherence as $V_{gr} = n_{gr}V(unit)$, where $V(unit)$ is the volume of the basic unit presumably determined by flux tube radius. If $V(unit)$ equals to volume a^3 of cube with side a, V_{gr} corresponds to a cube with side $a_{gr} = n_{gr}^{1/3}a$.

   The assumption that the energies of EEG photons in alpha band with $f = 10$ Hz correspond to ordinary photons at the lower end of the bio-photon spectrum having frequency 400 THz gives n_{gr} as $n_{gr} = 4 \times 10^{13}$. For $n_{gr} = 4 \times 1013$ and $a = 5$ μ m giving lower bound for the volume of neuron one would have $a_{gr} = 0.2$ m, roughly the size scale of brain.

4. The natural interpretation of the super-cables is as gravitational flux tubes. The gravitational flux associated with the ordinary flux tubes would combine to the dark gravitational flux tubes involving n_1 parallel flux tubes in M^4, each of them consisting of n_2 flux tubes on top of each other in CP_2 direction. This combination could take place repeatedly. Could the parameter M_D in $h_{gr} = n_{gr}h_0$ correspond to the portion of the Earth's gravitational flux flowing along these flux tubes? The sum of the masses M_D should over values of field strengths and charged particle masses should give the total mass M_E of Earth if the guess is correct.

   One must of course be extremely cautious in interpretations. For instance, flux tubes carrying Kähler charge the flux tubes should be closed and give rise to a kind of Dirac monopole like structure with return flux. This would mean that gravitational flux returns back, possibly along different space-time sheets. But the flux lines are closed also for the ordinary magnetic fields. Can this really be consistent with the Newtonian view about gravitation in which gravitational flux flows to infinity? The answer is far from obvious: the many-sheeted space-time in which space-time sheets are glued along the boundaries would that part of the flux can return and part goes to larger space-time sheets and in principle there is no largest space-time sheet so that one would obtain effectively monopoles.

5. An entire fractal hierarchy of magnetic field strengths is predicted. A good guess is that field strengths are given by p-adic length scale hypothesis, that is have scales given by $B(k) \propto 1/L(k)^2$, where $L(k) \propto 2^{k/2}$ is the p-adic length scale assignable to $p \simeq 2^k$. This would mean hierarchy of flux tubes with radii $L(k)$ and at each level the combination to super-cables representing gravitational flux tubes would take place.

   One has $M_D \propto v_0/\sqrt{B} \propto v_0 2^{k/2}$. For a fixed value of v_0, the sum can converge only if the number of p-adic length scales involved is finite. The radius R_E of Earth certainly gives this kind of upper bound and corresponds to a rather modest value of k ($L(151)$ correspond to 10 nm) . Also v_0 can depend on p-adic length scale. The sizes of living organisms give a more stringent upper bound on k.

2.5 Water memory and homeopathy

There is a lot of support about the representation of water memory as extremely low frequencies (ELF) of radiation associated with water [I21, I22]. These ELF frequencies can be stored electronically and they produce the same effects as the bio-active chemical, whose presence induced these frequencies in water. At the age of IT the idea about the existence of representations of bio-active molecules as frequency patterns able to induce the biological effects of molecules without the presence of molecules should not raise grave objections. For instance, brain generates this kind of representations by entrainment to external frequencies and water might play a crucial role also here. Few years ago HIV Nobelist Montagnier did experiments giving support for water memory and the procedure involved a part very similar to that used in preparing homeopathic remedies [I26] [L1].

The description of water memory in TGD Universe would look like follows.

1. In TGD framework these frequencies would correspond to cyclotron frequencies assignable to MBs of molecules, and immune system is proposed to have emerged from the ability of water to mimic the MBs of invader molecules and learning to recognize them [K6] by resonant coupling at these frequencies.

   This would take place via entrainment made possible by the variation of the thickness of the flux tube inducing variation of the cyclotron frequency. In entrainment the cyclotron frequency of the flux tube would co-incide with the external frequency. MB having flux tubes with modified thickness would be able to produce cyclotron radiation at the these frequencies and couple to the invader molecule resonantly. The coupling would involve also topological part as reconnection of flux tubes with same thickness and carrying same charged particles to make resonance possible.

   One can visualize living systems as systems having magnetic tentacles consisting of U-shaped flux tubes forming thus locally pairs of flux tube tubes and searching for flux similar flux tubes

of other systems, in particular bio-active molecules. The recognition of invader molecules is a crucial part of immune systems and this mechanism would be an essential part of immune action besides cyclotron resonance.

2. In TGD universe water is very special substance in that it contains both ordinary water and its dark variant. What makes it dark is that dark magnetic flux tubes representing long hydrogen bonds are present for some portion of water [L25] (see `http://tinyurl.com/y8fvwbp9`): the length of bonds scales as n or perhaps even n^2. The presence of these flux tubes makes any liquid phase a network like structure, and one ends up with a model explaining an anomaly of thermodynamics of liquids at criticality known already in Maxwell's time. This leads to a model explaining the numerous anomalies of water in terms of the dark matter.

   For instance, the dark part of water with non-standard Planck constant transforms to ordinary water in freezing. As a consequence, a large amount of energy is liberated. This explains why water has anomalously large latent heat of fusion. One can also understand why the volume of water increases in freezing and decreases in heating in the interval 0-4 °C. The anomalies of water are largest at physiological temperature $T_{phys} \sim 37$ °C suggesting that the dark portion of water is largest at T_{phys}. Dark fraction of water would be essential for life.

3. Pollack effect [L5] (see `http://tinyurl.com/oyhstc2`) requiring feed of energy - as IR radiation for instance - generates so called exclusion zones (EZs), which are negatively charged regions. A fraction of protons from water must go somewhere and the TGD inspired proposal [L5] (see `http://tinyurl.com/gwasd8o`) is that the protons transform to dark protons at magnetic flux tubes. The dark variants of particles quite generally have higher energies than ordinary ones and energy feed provides the needed metabolic energy go make the protons dark. In the case of homeopathy and water memory mechanical agitation creates provides the metabolic energy and would generate EZs accompanied by dark proton sequencies at flux tubes [K6].

4. The MB of water would be also a key central part of MB of the living system acting as intentional agent receiving sensory input from biological body and controlling it. Biochemistry would be kind of shadow dynamics. The ions provided by the living system would reside at the flux tubes of MB provided by water and as found the lengths of flux tubes and also the value of $h_{eff} = h_{gr}$ at the would distinguish between different ions. The gravitational flux tubes formed by combination of n_{gr} ordinary flux tubes to n_{gr} flux tubes with the same M^4 projection defining a covering of M^4 would define the large part of MB serving as intentional agent and communications would occur at cyclotron frequencies.

   Cell membranes would produce what I call generalized Josephson radiation, which would couple resonantly to cyclotron Bose-Einstein condensates at the flux tubes. Nerve pulse patterns would induce frequency modulation allowing to code sensory input represented by them and send it to MB which in turn could send control signals through genome [K11, K3, K23, K32].

   MB would be the seat of primary form of genetic code. Dark protons sequences at flux tubes representing genetic code [L8] and the analogs of the other basic biomolecules are realized in water.

2.6 What the view about magnetic body could mean at the level of DNA and other basic bio-molecules?

A more precise vision about the anatomy of MB leads to a flux of ideas and questions. Flux tubes from identical basic units (cells, DNA, identical proteins, etc) combine to form single many-sheeted flux tube so that the incoming flux tubes have same M^4 projection being on top of each other in CP_2 direction. This super cable is like umbilical chord! The structures form a Bose-Einstein condensate in abstract topological sense.

This opens fascinating possibilities for understanding of dark DNA.

1. Cells have identical DNAs. Earlier I have assumed that magnetic flux sheets go through DNA in transversal direction and that dark DNA in some sense is sequence of dark proton

triplets associated with flux tubes. Furthermore, DNA transcription requires that there are transversal flux tubes emerging from codons or perhaps even from nucleotides as flux tubes inside codon flux tube.

How to combine these views together with new view about combination of the DNAs flux tube to larger superstructure, one DNA from each cell in structure?

2. For single DNA each codon would correspond to 3-proton units organized linearly into a sequence. Each 3-proton unit must have a flux tube transversal flux to DNA strand and located at 2-D sheet. This brings in mind the structure of spine as anatomical and neurobiological analogy. This suggests that dark DNA codons formed by 3-proton units should be associated with these horizontal flux tubes in 2-D locally planar surface going through DNA.

3. These structures from $n_{gr} = h_{gr}/h_0 = h_{eff}/h_0$ separate cells should combine to single n_{gr}-sheeted gravitational flux tube with sheets on top of each other with same M^4 projection. This would be dark DNA at the level of MB. It would seem that given codon of each DNA must contribute a dark proton triplet so that there would be n_{gr} dark proton triplets at given flux tube which is however very long. The size scale - that is the length of the flux tube - is that of Earth typically and fixed by the cyclotron wave length λ_c.

   This would give a concrete topological meaning to quantum quantum coherence at the level of MB of bio-system. Also a view about how lower level conscious entities integrate to larger ones: one can imagine entire fractal hierarchy of structures integrating to larger structures integrating... In particular, altered states of consciousness could correspond to this kind of temporary integrations to higher level structures. Same should apply to other basic biological structures: cells, proteins, RNA, tRA. Dark realization of the genetic code predicts the dark variants of these biomolecules.

   This picture conforms with adelic physics [L15, L16] in which n_{gr} corresponds to the dimension of extension of rationals: the larger the value of n_{gr}, the higher the algebraic complexity and level of conscious intelligence.

4. Where are the dark protons and various dark ions at dark flux tubes? Along entire long flux tubes with length of order cyclotron wavelength for given charged particle? Or inside the organism?

   The model of dark DNA allows only the latter option. They must reside at the short portions of the magnetic flux tubes inside organism. For instance, the dark protons of dark DNA are associated with flux tubes parallel and in immediate vicinity of ordinary DNA strand and codon and dark codon a paired like codon and its conjugate in ordinary DNA.

   What makes these particles dark is that they are controlled by the gravitational flux tube and form a non-local quantum coherent unit containing n_{gr} particles.

This raises a long series of questions and fantastic challenges for visual imagination.

1. How do DNA and its conjugate relate at this level: do DNA and conjugate correspond to single closed long flux tube forming part of the "umbical chord" far from biological body?

2. What replication of DNA could mean topologically at the level of this super-DNA? What about description of transcription and translation at these super-levels. Are the ordinary replication, etc.. induced from this super level as mere shadow processes: this would explain their mysterious coherence?

3. What sexual reproduction and associated recombination of chromosomes could mean at super level? What does the growth of organisms mean at super level? Addition of new sheets to super DNA and its variants so that n_{gr} defined as the number of basic units grows and organism becomes more and more quantum intelligent?

3 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.

3.1 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 [K23] 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.

3.1.1 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

   $$k_d = k - 89 \quad , \quad k \in \{89, 107, 113, 127, 151, 157, 163, 167\} \tag{3.1}$$

   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

   $$k_d = k_2 - k_1 \tag{3.2}$$

   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.

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 1: 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 $\{18, 24, 38, 62, 68, 74, 78\}$.

3.1.2 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 1** includes only the dark length scales associated with $k = 89$ gauge bosons.

3.1.3 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.

3.2 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.

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 2: 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 1**. 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 3: 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	2.7488×10^{12}	1280	160	10

Table 4: 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 5: 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 1**. 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.

The appearance of CDs scaled up in size by $r = \hbar/\hbar_0$ and space-time sheets scaled up in size by $\sqrt{r}$ means the emergence of new levels of structure and it is natural to identify big leaps in evolution in terms of emergence of new larger matter carrying space-time sheet magnetic flux sheets and corresponding magnetic bodies. If magnetic flux quanta are scaled by r magnetic flux quantization conditions remain unaffected if magnetic field strengths scale down by $1/r$ so that the energies of cyclotron photons are not affected. The thickness of flux tubes can remain unchanged if the currents running at the boundaries of the flux quantum cancel the magnetic flux. As already found, this mechanism must be at work inside living organisms wheras in far away region flux quanta are scaled up in size.

The attractive hypothesis is that the leaps in evolution correspond to the emergence of dark variants of weak and possibly also color interactions in dark p-adic length scales which correspond to ordinary p-adic length scales characterized by Mersenne primes. These leaps would be quantum leaps but in different sense as thought usually. The emergence of higher dark matter levels would basically mean the integration of existing structures to larger structures. A good metaphor are text lines at the pages of book formed by magnetic flux sheets whose width is scaled up by r as the new level of dark matter hierarchy emerges. The big leaps can occur both at the level of organism and population and organisms with rather low individual dark matter level can form societies with high dark matter levels and high collective intelligence (honeybees and ants are good example in this respect).

Certainly also other scalings of Planck constant than those summarized in tables are possible but these scalings are of primary interest. This intuition is supported by the observation that electron is completely exceptional in this framework. Electron's dark p-adic length scales corresponds to p-adic length scales $L(k)$, $k = 167, 169$, assignable to atomic and molecular physics and to the Gaussian Mersennes $M_{G,k} = (1+i)^k - 1$, $k \in \{151, 157, 163, 167\}$, assignable to the length scale range between cell membrane thickness 10 nm and nucleus size 2.58 μm. The corresponding p-adic length scales or corresponding electronic Compton lengths, the number of which is 23, are excellent candidates for the scales of basic building brickes of living matter and vary from electron's p-adic length scale up to 1.25 m ($k = 167$ defining the largest Gaussian Mersenne in cell length scale range) and defining the size scale of human body. The corresponding p-adic time scales are also highly interesting and vary from.1 seconds for electron defining the fundamental biorhythm to 9.6×10^{14} years which is by 4-5 orders longer than the age of the observed Universe. For $k = 167$ the time scale is 1.1×10^{11} years and is by one order of magnitude longer than the age of the observed Universe estimated to be 1.37×10^{10} years [E1].

This conceptual framework gives rather strong guidelines for the identification of the levels of evolutionary hierarchy in terms of dark matter hierarchy. The outcome is a more detailed vision about big evolutionary leaps. Note that in the sequel only the general option is considered: the justification for this is that for this option electron appears as a dark particle for all length scales defined by Gaussian Mersennes as well as in atomic length scales. The basic vision in nutshell is that evolution means the emergence of dark weak and gluonic physics in both dark and ordinary length scales and that the size scales of the basic biostructures correspond to Mersenne primes and their Gaussian variants.

3.2.1 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 [K32] 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 [K20, K32] 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 [K6]. 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 [I6] appearing in rocks have size 20 nm and could have emerged at this step. The size of the viruses [I16] 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 [I5] [I5], which by definition have size smaller than 300 nm could have appeared at this stage.

6. The remaining steps

The remaining steps $k = 151 \to 157 \to 163 \to 167$ could relate to the emergence of coiling structure DNA and other structures inside cell nucleus. $k = 167$ would correspond to $k_d = 167 - 89 = 68$ to be compared with the value $k_d = 47$ required by 5 Hz Josephson frequency for the neuronal membrane for -70 mV resting potential. Note that $k_d = 48$ (state 1-2 of deep sleep) corresponds to $k = 163$.

By their smallness also double and triple steps defined by $k_d = k_{i+n} - k_i$, $n > 1$, are expected to be probable. As a consequence, electrons can appear as dark electrons at all the Gaussian Mersenne levels. At these steps the dark electrons corresponding to primes $k_{eff} = 137, 139$ would appear. For $k = 137$ dark electron appears with CD time scale equal to 128 seconds- rather precisely two minutes. The model for EEG suggests that the exotic weak bosons appear in the scales $k_{eff} = 136, 137, 138$.

Further multisteps from the lower levels of hierarchy would give structures with size scales above the size of cell nucleus possibly assignable to organs and structural units of brain. The dark levels assignable to electron are expected to be of special interest. It is encouraging that the longest scale assignable to electron in this manner corresponds to $k = 205$ and length scale of 1.28 m defining body size. As a consequence dark electrons are predicted at levels $k = 137, 139, 141, 143, 145, 147$ coming as octaves.

Prokaryotic cells (bacteria, archea) without cell nucleus for which cell membrane is responsible for metabolic functions and genome is scattered around the cell could have emerged at this step. This would mean that the emergence of the cell membrane thickness as a fundamental scale is not enough: also the size scale of membrane must appear as p-adic length scale. The sizes of most prokaryotes vary between 1 μm and 10 μm: the lower bound would require $k = 163$. There also prokaryotes with sizes between.2 μm ($k = 157$ corresponds to.08 μm) and 750 μm. Cell nuclei, mitochondria, and other membrane bounded cell nuclei would have evolved from prokaryotes in this framework. The sizes of eukaryote cells are above 10 μm and the fact that multicellular organisms are in question strongly suggests that the higher multisteps giving rise to weak bosons and dark electrons in length scales above $L(167)$ are responsible for multi-cellular structures.

This scenario leaves a lot of questions unanswered. In particular, one should understand in more detail the weak physics at various length scales as well as various exotic nuclear physics defined by dark nucleons and dark variants of nuclei.

3.2.2 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.

3.2.3 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 μm, which could correspond to $k_{eff} = 171$ for electron and dark variants of weak gauge bosons. $k_{eff} = 177$ is the next dark electron level and corresponds to 80 μm scale. It seems natural to assume that these dark weak bosons do not transform to their $\hbar_0$ counterparts at these space-time sheets.

Cell nucleus would be the brain of the cell, mitochondria would be the energy plant, and centrioles generating microtubules would define the logistic system. Also other organelles such as Golgi apparatus, ribosomes, lysosomes, endoplasmic reticulum, and vacuoles would be present. These organelles would live in symbiosis by topologically condensing to $k_{eff} \geq 171$ magnetic body controlling their collective behavior. Centrosomes associated with animal cells would not be present yet but microtubule organizing centers would already be there.

The recent observations show that centrioles are not always in the characteristic T shaped conformation. Daughter centrioles resulting during the replication of mother centriole use first ours of their lifetime to roam around the cell before becoming mature to replicate. A possible interpretation is that they are also life forms and that magnetic body utilizes daughter centrioles to perform some control functions crucial for the future development of the cell. For instance, centrioles visit the place where axonal growth in neurons starts.

Cytoskeleton would act as a counterpart of a central nervous system besides being responsible for various logistic functions such as transfer of proteins along microtobuli. Centrioles give also rise to basal bodies and corresponding cilia/flagella used by simple cells to move or control movement of air or liquid past them. Centriole pair would be also used by the magnetic body to control cell division.

The logistic functions are the most obvious functions of microtubules. Magnetic body would control cell membrane via signals sent through the cell nucleus and communicated to the cell membrane along microtubuli. Basal bodies below the cell membrane and corresponding cilia/flagella would serve as motor organs making possible cell motion. Tubulin conformations representing bits would allow microtubule surface to represent the instructions of the magnetic body communicated via via cell nucleus to various proteins moving along the microtubular surface so that they could perform their functions.

TGD based view about long memory recall as communication with geometric past allows also the realization of cellular declarative memories in terms of the conformational patterns. Memory

recall corresponds to a communication with geometric past using phase conjugate bosons with negative energies reflected back as positive energy bosons and thus representing an "image" of microtubular conformation just like ordinary reflected light represents ordinary physical object. There would be no need for a static memory storage which in TGD framework would mean taking again and again a new copy of the same file.

Receptor proteins would communicate cell level sensory input to the magnetic body via MEs parallel to magnetic flux tubes connecting them to the magnetic body. We ourselves would be in an abstract sense fractally scaled up counterparts of receptor proteins and associated with dark matter iono-lito Josephson junction connecting the parts of magnetosphere below litosphere and above magnetosphere. The communication would be based on Josephson radiation consisting of photons, weak bosons, and gluons defining the counterpart of EEG associated with the level of the dark matter hierarchy in question.

3. The emergence of organs and animals

The emergence of magnetic bodies with k_{eff} in the range $(177, 181, 183, 187, 189, 195, 201, 205)$ allowing both dark electron and weak bosons could accompany the emergence of multicellular animals. Magnetic body at this level could give rise to super-genome making possible genetic coding of organs not yet possessed by plant cells separated by walls from each other. The super structures formed from centrosomes and corresponding microtubuli make possible complex patterns of motion requiring quantum coherence in the scale of organs as well as memories about them at the level of organs.

4. The emergence of nervous system

k_{eff} in the range $(187, 189, 195, 201, 205)$ allowing dark electrons and weak bosons gives size scales $(.25, .5, 4, 32, 128)$ cm, which could correspond to the scales of basic units of central nervous system. What would be of special interest would be the possibility of charged entanglement based on classical W fields in macroscopic length scales. The emergence of the new level means also the integration of axonal microtobuli to "text lines" at the magnetic flux sheets making possible logistic control at the multineuronal level. The conformational patterns of the microtubular surface would code nerve pulse patterns to bit patterns representing declarative long term memories. An interesting question is whether the reverse coding occurs during memory recall.

3.2.4 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 5**one finds that levels $k \in \{207, 211, 213, 217, 219, 221, 223, 225, 229, 235\}$ are allowed. Could it be that these levels and possibly some highest levels containing both electrons and gauge bosons as dark particles are a prerequisite for EEG as we define it. Its variants at higher frequency scales would be present also for invertebrates. The lowest Josephson frequency coded by the largest value of $\hbar$ in the cell membrane system determines the Josephson frequency.

2. The membrane potentials -55 mV (criticality against firing) correspond to ionic Josephson energies somewhat above 2 eV energy ((2.20, 2.74, 3.07, 2.31) eV, see Table 1). For 2 eV the wavelength 620 nm is near to $L(163) = 640$ nm. Therefore the Josephson energies of ions can correspond to the $L_e(k = 163)$ if one assumes that a given p-adic mass scale corresponds to masses half octave above the p-adic mass scale so that the opposite would hold true at

space-time level by Uncertainty Principle. Josephson frequencies $f_J \in \{5, 10, 20, 40, 80, 160\}$ Hz correspond to $k_d \in \{47, 46, 45, 44, 43, 42\}$ giving $k_{eff} \in \{210, 209, 208, 207, 206, 205\}$.

   (a) Cerebellar resonance frequency 160 Hz would correspond to $k = 205$ -the highest level for for which model allows dark electrons (also 200 Hz resonance frequency can be understood since several ions are involved and membrane potential can vary).

   (b) The 80 Hz resonance frequency of retina would correspond to $k_{eff} = 206$ -for this level dark electrons would not be present anymore.

   (c) 40 Hz thalamocortical frequency would correspond to $k_{eff} = 207$.

   (d) For EKG frequencies are EEG frequencies below 20 Hz 12.5 and heart beat corresponds to .6-1.2 second cycle (the average.8 s corresponds to $k_{eff} = 212$).

3. Even values of k_{eff} are not predicted by the model based on Mersenne primes allowing only odd values of k_{eff} so that the model does not seem to be the whole truth. The conclusion which however suggests itself strongly is that EEG and its variants identified as something in the range 1-100 Hz, are associated with the levels in at which only dark weak bosons are possible in the proposed model. Note that the size scales involved with EEG would be 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 6**. 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.

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 6: 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.

1. Does the time scale correspond to the size scale of CD assignable to electron scaled by $r = \hbar/\hbar_0$? In this case relatively small values of r would be enough and $r = 2^{47}$ would give time scale of 10^{13} s for for electron's CD, which is about 3×10^5 years. This does not make sense.

2. Does Josephson frequency define the relevant time scale? In this case the long term memory would require the analog of EEG in the time scale of memory span. $k_{eff} = 205$ would give 6 ms time scale for memory from the assignment of $k_{eff} = 163$ to the Josephson photons at V=-50 mV implying $k_d = 42$. Minute scale would require $k_{eff} = 217$. The highest level $k_{eff} = 235$ allowed by the model involving only Gaussian Mersennes with $k \leq 167$ would correspond to a time scale of 77.67 days (day is 24 hours). For Gaussian Mersennes defined by $k_{eff} = (239, 241)$ the time scales become about (41.4, 82.8) months (3.4 and 6.8 years). These scales should also define important biorhythms. The claimed 7 years rhythm of human life could relate to the latter rhythm: note that the precise value of the period depends on the membrane potential and thus varies. The presence of the scaled up variants of the by $k_d \leq 78$ allows longer time spans of long term memory and the scaling defined by $k_d = 167 - 163 = 4$ scales up the span of long term memories to (54.4, 108.8) years.

4. Cultural evolution

Higher levels in the hierarchy would correspond mostly to the evolution of hyper-genome coding for culture and social structures. Introns are good candidate for the nucleotides involved. The development of speech faculty is certainly a necessary prerequisite for this breakthrough. Already EEG seems to correspond to dark layers of biological body larger than biological body so that one can cask whether the weak bosons and dark electrons in the length scales $k = 239, 241, 283, 353, 367, ...$ could be relevant for the collective aspect of consciousness and cultural evolution. Maybe the size scales $(175, 330)$ km and their scaled up variants by $k_d \leq 78$ might have something to do with the spatial scale of some typical social structure (not city: the area of New York is only 790 km^2).

4 A model of Genetic Code as Fusion of Doublet and Singlet Models

I have proposed a model for the evolution of genetic code as a fusion of singlet and doublet codes to triplet code already earlier. 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 [I40] 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 [J1], 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.

4.1 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 [I20]. 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 [I20] 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 [I31] (for an article about RNA genes and RNA world see [I39]). 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 [I1].

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

The beautiful results (for a popular summary see [I34]) 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 $\mathrm{tRNA}_3 \equiv \mathrm{tRNA}$. 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 [I9]. 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.

4.2.1 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 [I28] such that B forms a loop and C is a palindrome [I8] . 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 [I9] 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.

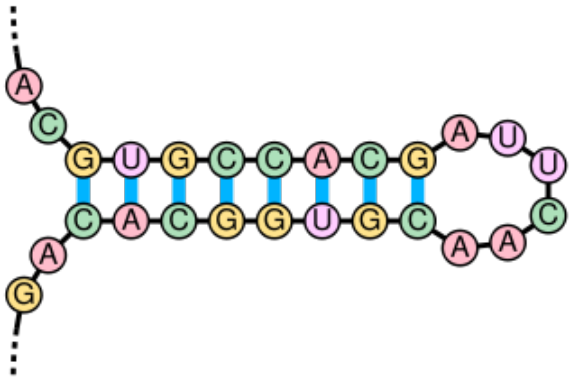

Figure 1: The structure of DNA hairpin (stem loop)

4.2.2 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.

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.

4.3 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.

4.3.1 The structure of the tRNA molecule

The shape of the tRNA molecule [I14] 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.

4.3.2 Wobble base pairing

The phenomenon of wobble base pairing [I17] 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) [I4]. The base-pairings for third nucleotide are $\{A-U, G-C, U-\{A, G\}, I-\{U, A, C\}\}$. The explanation

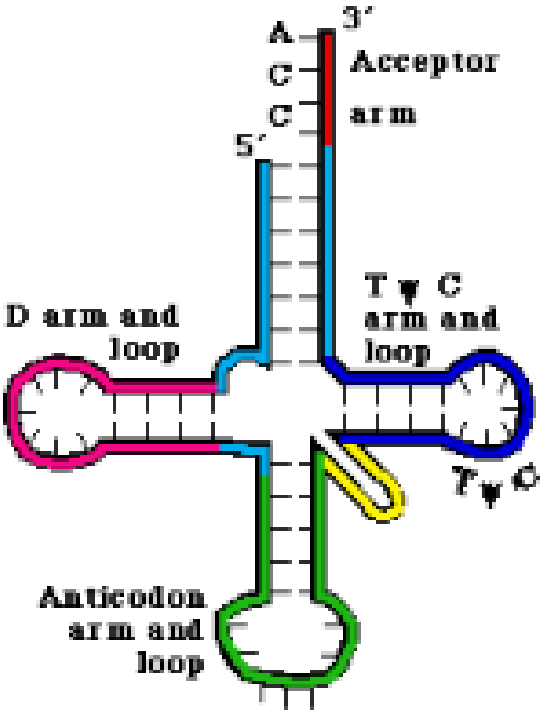

Figure 2: The structure of tRNA

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.

4.3.3 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 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 [I10] 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 [I15], 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 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 [I13] 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.

4.3.4 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 TψC arm. This is possible since all loops are physically near to each other. The structure of D and Tψ loops conforms with the assumption that the predecessor of the first *resp.* second loop has lost the coding *resp.* coded RNA. The structure of these loops forces also to conclude that all tRNA loops have been stem like structures before their deactivation just as the acceptor stem is. Deactivation of RNA_1 translation process must have

meant the completion of these stems to loops by addition of a conjugate of the conjugate of the coded RNA.

4.3.5 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 [I19]. The di-phosphate is cleaved out from dXTP and the liberated energy makes it possible to add the resulting dXMP to the growing DNA strand.

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

1. RNA_2 consists of exotic RNA doublets with nucleotides connected by $2', 5'$ monophosphate bonds. tRNA_2 brings $2', 5'$ doublet $\mathrm{XMP}_2 \circ \mathrm{YTP}_2$ to the growing strand and glues it to the $5'$ position of the ribose in the already existing polymer. The YTP suffers the cleavage $\mathrm{YTP}_2 \to \mathrm{YMP}_2$ as in the case of DNA polymerization and the amount of metabolic energy provided by the cleavage is the same. The formation of $\mathrm{XMP}_2 \circ \mathrm{YTP}_2$ proceeds by gluing of XTP_2 to YTP_2 by a similar process so that the net metabolic energy used per nucleotide is essentially the same as in the ordinary DNA polymerization.

2. RNA_1 consists of exotic RNA singlets connected by $2', 5'$ diphosphate bonds. tRNA_1 brings XTP_2 near the growing strand, the cleavage $\mathrm{XTP}_2 \to \mathrm{XDP}_2$ occurs, and XDP_2 is glued to the $5'$ position of the ribose of the previous RNA nucleotide. The amount of metabolic energy provided by the cleavage is roughly one half of that in the case of RNA_2 polymerization, and this might partially explain why diphosphate exotic RNA strands are rare whereas monophosphate exotic DNA strands can be found inside cells. On the other hand, it is $ATP \to ADP$ cleavage, which usually occurs in the ordinary metabolism instead of $ATP \to$ AMP cleavage: only during a very intense metabolism $ATP \to$ AMP cleavage occurs. Since ATP metabolism is a functional fossil from a very early period of evolution, one might expect that $ATP \to$ ADP cleavage has in fact occurred naturally, if not even more naturally, also in the polymerization of $2', 5'$ RNA during (exotic) RNA era.

3. In the case of double exotic RNA strand of ordinary and exotic RNA the predecessor of the recent tRNA formed by 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.

4.3.6 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 [I23] (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 [K25] 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 [D1] 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 [L10]. The first model is a variant of cold fusion model that might explain the energy production and the observed radiation at EUV energy range. Second model is a variant of hydrino atom assuming that ordinary hydrogen atom corresponds to $h_{eff}/h = n_H > 1$ and that catalyst containing hydrogen atoms with lower value of $n_h < n_H$ could induce a phase transition transforming hydrogen atoms to hydrinos with binding energy spectrum scaled up by scaling factor $(n_H/n_h)^2$ and radii scaled down by $(n_h/n_H)^2$. The findings of Mills favour the value $n_H = 6$.

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

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

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

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

$$\Delta E = E_{fn_f} - E_i = \frac{E_f}{n_f^2} - E_f(\frac{n_{Hf}}{n_{Hi}})^2 = E_i\left[(\frac{n_{Hi}}{n_{Hf}})^2 n_f^{-2} - 1\right] \quad . \tag{4.1}$$

   The condition $\Delta E > 0$ gives

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

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

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. 4.1 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 7 gives the liberated energies ΔE for transitions with $(n_i, n_f) = (1,2)$ in some cases.

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

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

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

4.4 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 [I40] 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 [K25].

4.4.1 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 RNA_2 and RNA_1, analogous to mRNA and proteins existed. RNA_2 can be identified as the ordinary $3', 5'$ RNA acting in the role of mRNA. A natural candidate for RNA_1 playing the role of proteins is $2', 5'$ RNA since it is generated in the experiments of Orgel and appears also in genomes. Of course, also other candidates can be considered and the structure of tRNA gives valuable information about the character of this RNA. The copying of RNA_2 to its

conjugate was the counterpart of RNA replication. The transcription of RNA_2 to RNA_1 was the counterpart of translation.

2. The structure of tRNA, call it $tRNA_3$, gives valuable information about the course of events leading to the translation of mRNA to amino-acids. The cross like structure of $tRNA_3$ and the decomposition of RNA triplet appearing in it to 2-codon and 1-codon suggests that it resulted as a fusion of two hairpin like molecules $tRNA_1$ and $tRNA_2$. $tRNA_2$ brought pairs of nucleotides forming the 2-codon part of RNA triplet to the growing RNA_2 sequence during replication and 2-code was simply RNA conjugation. $tRNA_1$ was involved with transcription of RNA_2 to RNA_1 bringing RNA_1 nucleotides one-by own to the growing sequence. In $tRNA_3$ the third nucleotide does not quite correspond to ordinary RNA but to to A, G, U or I(nositol) and is believed to differ geometrically from ordinary nucleotide, and one can assume that these nucleotides were the building blocks of RNA_1 possibly appearing in $2', 5'$ form. The phenomenon of the wobble pairing can be assumed to have been present already during RNA era so that correspondence 1-code was not not 1-to-1 nor deterministic but given by the correspondence $\{U \to A, C \to G, \{A, G\} \to U, \{U, A, C\} \to I\}$ deduced from the number 40 of tRNAs and assigning unique 1-codon to only G could be interpreted as a many-to-one and non-deterministic correspondence generating new RNA sequences from existing ones. If there was RNA_2 sequence coding for $tRNA_1$, this sequence appearing in hairpin structure could have coded the inverse of the translation. As a consequence, the occurrence of transcription and its reversal generated a rapid evolution by creating new kinds of RNA_2 sequences.

3. From the fact that amino-acids are attached to the ACC stem of $tRNA_2$, one can guess that the role of amino-acids during RNA era was to catalyze the replication. If single amino-acid would have catalyzed the attachment of given RNA doublet to the growing sequence, there would be at most 16 amino-acids and genetic coded would not depend at all on the third nucleotide. This is indeed the case for roughly half of the code table (both matter antimatter symmetry and isospin symmetry with respect to third codon). For those mRNA codons for which A, G and T, C correspond to different amino-acids (breaking of matter antimatter asymmetry but isospin symmetry) two amino-acids catalyzed the attachment. Same amino-acid could also catalyzed two different attachments (ser, arg, leu for standard genetic code).

4. The crucial step was the fusion of the 1-code and 2-code to 3-code took place via fusion of $tRNA_1$ and $tRNA_2$ to $tRNA_3$ along their ends containing RNA_1 nucleotide and RNA_2 doublet which thus combined to RNA triplet. Presumably $tRNA_3$ in its original form was translated from a linear mRNA molecule and transformed spontaneously to the cross like shape because of the presence of palindrome structures in both. The original functions of tRNAs were not possible anymore since the triplet was not at the end of the molecule. The catalyzing amino-acid however was at the ACC end of and the function of $tRNA_3$ became to assist the translation of mRNA to amino-acid sequence. For those 3-codons for which single amino-acid catalyzed the fusion of 2-codon, a full matter antimatter and isospin symmetry resulted. For those 3-codons for which two amino-acids catalyzed the fusion, a breaking of matter antimatter symmetry took place in the sense that for given mRNA codon only the $tRNA_3$ corresponding to single amino-acid was stable. Isospin symmetry was broken only weakly or not at all (human mitochondrial code). Thus codons with A, G as third nucleotide almost always coded the first amino-acid and those with T, C as the third nucleotide the second one. Stopping codons resulted when all $tRNA_3$ corresponding to mRNA triplet were unstable. That same RNA can code for both amino-acid and act as a stop codon in certain situations, can be understood if the stability of corresponding $tRNA_3$ depends on the chemical environment.

4.4.2 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 [I27] 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.

4.4.3 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 [J1] 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.

4.4.4 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.

4.5 Is RNA Era Continuing Inside Cell Nuclei?

The last issue of [I18] 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 [I3]. The Encyclopedia of DNA Elements (ENCODE) project has quantified RNA transcription patterns and found that while the "standard" RNA copy of a gene gets translated into a protein as expected, for each copy of a gene cells also make RNA copies of many other sections of DNA. In particular, intron portions ("junk DNA", the portion of which increases as one climbs up in evolutionary hierarchy) are transcribed to RNA in large amounts. What is also interesting that the RNA fragments correspond to pieces from several genes which raises the question whether there is some fundamental unit smaller than gene.

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

This picture conforms with TGD view about pre-biotic evolution. Plasmoids [I32], 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 $\hbar$ [K24]. 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 [I11] 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 [I7] are fundamental repeating units in eukaryotic chromatin [I2] 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 [I7] 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.

4.6 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 [I37], who is one of the pioneers in the field besides Y. Morita [I38] and E. O. Kajander [I25], 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.

4.6.1 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 [I37]. 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 [E3], and there is evidence that carbonaceous chondrite meteorite Allende [I37] 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 [I37], 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 [I25]. 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 [I37], the nanno-bacterial DNA exists and consists of very short strands.

4.6.2 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.

4.6.3 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 [K2]).

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

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

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

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

5 Comparison Of Mcfadden's Views With TGD

In his book Quantum Evolution [I30] Johnjoe McFadden discusses the deep problems of molecular biology from quantum point of view and develops very interesting ideas about evolution and consciousness. Because of deep insights about what is not understood in biology, this discussion should provide new insights for any quantum consciousness theorist attempting to build a bridge between theory and biological reality. In the sequel McFadden's vision is compared with TGD view and some new ideas inspired by it in TGD framework are proposed.

5.1 General Ideas

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

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

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

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

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

In TGD framework one can imagine two basic elements.

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

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

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

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

   In fact, it has become clear quite recently that TGD could in well-defined sense allow also quantum superpositions of different DNA molecules. This kind of superpositions are routinely assumed for coherent states of Cooper pairs in super-conductivity although they break conservation of charge, fermion number, and energy. The point is that in zero energy ontology (ZEO) [K19] 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.

5.1.1 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.

5.1.2 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.

5.2 Enzyme Action

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

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

1. Production of lactic acid from pyruvate

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

2. Catabolism of lactose

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

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

Hydrolysis could involve local gel-sol type transition transforming ordered water to ordinary water, which is able to provide the needed water molecule. The gel-sol transition could closely correlate with the non-standard localization of the proton inside enzyme. The process could involve an intentional action of a magnetic body of some system involved and thus negative energy topological light rays and charge entanglement by W MEs.

5.3 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?

5.3.1 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.

5.3.2 Criticism of RNA world

McFadden represents severe critics against RNA world paradigm which is the dominating vision about pre-biotic evolution [I29]. 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.

5.3.3 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 2π twist around micro-tubule.

Biological evolution could be seen as being induced by the evolution of cognition and of intentional actions. By the properties of the p-adic topology it proceeds from long time and length

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

4. The emergence of molecular pathways

The emergence of names attached to molecules makes possible generation of computer 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.

5.3.4 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 [I30]. 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 [K13] 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 [K19].

A rather strong argument in favor of zero energy ontology comes from superconductivity [K1]. 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.

6 Jeremy England's Vision About Life And Evolution

I had an intensive discussion with my son-in-law Mikko about the work of Jeremy England [I33] (`http://tinyurl.com/o64rd7o`). The article of the link is probably the most aggressive hyping I have ever seen but this should not lead to think that a mere hype is in question. There is also another, not so heavily hyped popular article at `http://tinyurl.com/m8s2jqt`. The material at the homepageof england lab (`http://tinyurl.com/ycdrdazq`) gives a good view about the work of England for those who cannot tolerate hyping.

England's work is indeed very interesting also from TGD point of view although it is based on standard physics.

In the sequel I will summarize this approach and compare it with TGD vision. The generalization of the thermodynamical approach to TGD framework leads to surprising new insights about the thermodynamical conditions making life and consciousness possible. The new elements relate to zero energy ontology (ZEO), hierarchy of Planck constants labelling levels in a hierarchy dark matters assignable with quantum criticality, the role of macroscopic quantum coherence associated

with gravitation, and strong form of holography. The TGD counterparts of Hawking temperature and Hagedorn temperature seem to be crucial for life and correspond to physiological temperature scales. Near Hawking temperature the special features of ZEO become manifest meaning that time reversals of "selves" (mental images) are generated with a considerable rate in heat bath and long term memory and planned action become possible.

6.1 Basic Ideas Of England's Theory

I try first to summarize England's vision.

1. Non-equilibrium thermodynamics (NET) is the starting point. NET has been for decades the theoretical framework underlying the attempts to understand living matter using the principles of self-organization theory. Living matter is never an isolated system: dissipation would take it to a totally dead state in this case - nothing would move. Water in the pond when there is no wind, is a good example.

   Self-organization requires an external energy feed - gravitational potential energy liberated in water flow in river or electric power feed to the hot plate below a teapot. This energy feed drives the system to a non-stationary state far from a thermal equilibrium state. Dissipation polishes out all details and leads to an asymptotic spatio-temporal self-organization patterns. The flow in a river and convection in the heated teapot. With high enough energy feed chaos emerges: water fall or boiling of tea pot.

2. The basic hypothesis of England is that evolution means increase in the ability to dissipate. This looks intuitively rather obvious. The evolving system tends to get to a resonance with the energy feed by oscillating with the same frequency so that energy feed becomes maximal and therefore also dissipation. The basic rule is simple: choose the easy option, ride on the wave rather than fighting against it! For instance, the emergence of photosynthesis means that the systems we call plants become very effective in absorbing the energy of sunlight. In this framework essentially all systems are alive to some degree.

   Dissipation means generation of entropy. Evolution of life and conscious intelligence would mean maximal effectivenes in the art of producing disorder. Now I am perhaps exaggerating. One should speak about "system's maximal ability to transfer entropy out of it": life is not possible without paper baskets. One could argue that the development of civilization durig last decades demonstrates convincingly that evolution indeed generates systems generating disorder with a maximal rate.

   One could argue that the definition is too negative. Living matter is conscious and there is genuine conscious information present. The fact is that evolution involves a continual increase of conscious information: the exponential explosion of science is the best proof for this. England's vision says nothing about it. Something is missing.

   It is however quite possible to imagine that the principle of maximal entropy generation is true and that the increase of the ability to produce entropy is implied by some deeper principle allowing to speak about living matter as something tending to increase conscious information resources. To formulate this idea one needs a theory of consciousness, thermodynamics is not enough.

3. England has a further idea. The evolution life is not climbing to Mount Everest but coming down from it. Life emerges spontaneously. This is definitely in conflict with the standard wisdom, in particular with the thermodynamical belief on thermal death of the Universe as all gradients disappear. Darwinian evolution would be a special case of a more general phenomenon, which could be called dissipation driven adaptation (DDA). I made a head-on-collision with this principle in totally different framework by starting from quantum criticality of TGD: if took time to fully realize that indeed: evolution could be seen as a sequence of phase transitions breaking in which certain infinite-dimensional symmetry was spontaneously broken to become just the same symmetry but in longer scale!

   Standard thermodynamics predicts the heat death of the Universe as all gradients gradually disappear. This prediction is problematic for England's argument suggesting that differentiation occurs instead of homogenization. Here the standard view about space-time might be

quite too simplistic to overcome the objection. In TGD many-sheeted space-time comes in rescue.

Here is an example about England's argumentation. It seems intuitively clear that replication increases entropy (it is not however clear whether just the splitting into pieces is even more effective manner to increase entropy!). This would suggest that DDA forces the emergence of replication. Very effective dissipators able to replicate, would increase the total effectiveness in dissipation and be the winners. The proposal to be tested is that bacterial mutations , which are best replicators are also best dissipators.

6.2 What Is Missing From England's Theory?

What is missing from England's theory? The answer is same as the answer to the question what is missing from standard physics.

1. What is conscious observer - self?

   Observer, which remains outsider to the physical world in the recent day physics - both classical and quantum. Hence one does not have a theory of consciousness and cannot speak about conscious information. Thermodynamics gives only the notion of entropy as a measure for the ignorance.

   Therefore there is a long list of questions that England's theory does not address. What are the physical correlates of attention, sensory perception, cognition, emotions relating closely to information, etc.? Is there some variational principle behing concious existence, and does it imply evolution? Could second law and DDA be seen as consequences of this variational principle?

   England does not say much about quantum theory since he talks only about thermodynamics but his hypothesis is consistent with quantum theory. The restriction to thermodynamics allows only statistical description and notions like macroscopic quantum coherence are left outside.

2. What is life?

   Again one has a long list of questions.

   What it is to be alive? What distinguishes between living and inanimate systems. What it is to die? How general phenomenon evolution is: does it apply to all matter? Also notions like self-preservation and death are present only implicitly in an example about a population of wine glasses whose members might gradually evolve to survive in an environment populated by opera sopranos.

   One can make also other kinds of questions. What really happens in replication? What is behind genetic code? Etc...

   England is a spiritual person and has made clear that the gulf between science and spirituality is something which bothers him . England even has the courage to use the word "God". Therefore it sounds somewhat paradoxical that England avoids using the concepts related to consciousness and life. This is however the only option if one does not want to lose academic respectability.

6.3 How Does England's Theory Relate To TGD?

It is interesting to see whether England's vision is consistent with TGD inspired theory of consciousness, which can be also seen as a generalization of quantum measurement theory achieved by bringing the observer part of the quantum physical world. In TGD framework several new principles are introduced and they relate to the new physics implied by the new view about space-time.

1. The new physics involves a generalization of quantum theory by introducing a hierarchy of Planck constants $h_{eff} = n \times h$ with various quantal length and time scales are proportional to h_{eff}. h_{eff} hierarchy predicts a hierarchy of quantum coherent systems with increasing size scale and time span of memory and planned action. h_{eff} defining a kind of intelligence quotient labels the levels of a hierarchy of conscious entities.

h_{eff} hierachy labels actually a fractal hierarchy of quantum criticalities: a convenient analogy is a ball at a top of ball at the top..... The quantum phase transitions inreasing h_{eff} occur spontaneously: this is the TGD counterpart for the spontaneous evolution in England's theory. Dark matter is what makes system alive and intelligent and thermodynamical approach can describe only what we see at the level of visible matter.

2. Second key notion is zero energy ontology (ZEO). Physical states are replaced by events, one might say. Event is a pair of states: initial state and final state. In ZEO these states correspond to states with opposite total conserved quantum numbers: positive and negative energy states. This guarantees that ZEO based quantum theory is consistent with the fundamental conservation laws and laws of physics as we understand them although it allows non-determinism and free will. Positive and negative energy states are localized at opposite boundaries of a causal diamond (CD). Penrose diagram - diamond symbol - is a good visualization and enough for getting the idea.

   State function CDreduction (SFR) is what happens in quantum measurement. The first SFR leads to a state which is one in a set of states determined once measurement is characterized. One can only predict the probabilities of various outcomes. Repeated quantum measurements leave the state as such. This is Zeno effect - watched kettle does not boil.

   In ZEO something new emerges. The SFR can be performed at *either* boundary of CD. SFR can occur several times at the same boundary so that the state at it does not change. The state at the opposite boundary however changes - one can speak of the analog of unitary time evolution - and the second boundary also moves farther away. CD therefore increases and the temporal distance between its tips does so also.

   The interpretation is as follows. The sequence of reductions at fixed bounary corresponds to a conscious entity, self. Self experiences the sequence of state function reductions as a flow of time. Sensory experience and thoughts, emotions, etc.. induced by it come from the moving boundary of CD. The constant unchanging part of self which meditators try to experience corresponds to the static boundary - the kettle that does not boil.

   Self dies in the *first* reduction to the opposite boundary of CD. Self however re-incarnates. The boundaries of self change their roles and the geometric time identified as distance between the tips of CD increases now in opposite direction. Time-reversed self is generated.

3. Negentropy Maximization Principle (NMP) stating roughly that the information content of consciousness is maximal. Weak form of NMP states that self has free will and can choose also non-maximal negentropy gain. The basic principle of ethics would be "Increase negentropy". p-Adic mathematics is needed to construct a measure for conscious information and the notion of negentropic entanglement (NE) emerges naturally as algebraic entanglement.

   The negentropy to which NMP refers is *not* the negative of thermodynamical entropy describing lack of information of outsider about state of system. This negentropy characterizes the conscious information assignable to negentropic entanglement (NE) characterized by algebraic entanglement coefficients with measure identified as a number theoretic variant of Shannon entropy. Hence NMP is consistent with the second law implied by the mere non-determinism of SFR.

   NMP demands that self during sequence of reductions at the same boundary generates maximum negentropy gain at the changing CD boundary. If self fails, it dies and re-incarnates (in a reduction to the opposite CD boundary more negentropy is generated). Selves do not want to die and usually they do not believe on re-incarnation, and therefore do their best to avoid what they see as a mere death. This is the origin of self-preservation. Self must collect negentropy somehow: gathering negentropic sub-selves (mental images) is a manner to achieve this. Plants achieve this by photosynthesis, which means generation of negentropy and storage of it to various biomolecules. Animals are not so saintly and simply eat plants and even other animals. We are negentropy thieves all.

   Re-incarnation also means increase of h_{eff} and getting to higher level in hierarchy and occurs unavoidably. As in England's theory, evolution occurs spontaneously: it is not climbing to Mount Everest but just dropping down.

4. England says "Some things we consider inanimate actually may already be 'alive'." This conforms with TGD view. Even elementary particles could have self: it is however not clear whether their SFR sequences contain more that one reduction to a fixed boundary - necessary for having a sense about the flow of time. Elementary particles would even cognize: in adelic physics every system has both real and p-adic space-time surfaces as its correlates. It can even happen that system has only p-adic space-time correlates but not the real one: this kind of systems would be only imaginations of real system! This is one of the most fascinating implications of strong form of holography which follows from strong form of General Coordinate Invariance forced by the new view about space-time.

   Clearly the notion of evolution generalizes from biological context to entire physics in TGD. One can speak about p-adic evolution and evolution as increase of h_{eff}. The most abstract formulation is number theoretical: evolution corresponds to the increase of the complexity of extension of rationals to which the parameters characterizing space-time surfaces belong to.

5. Does DDA emerge in TGD framework? NMP demands a lot of SFRs - also at the level of visible matter. The non-determimism of SFR alone means a loss of knowledge about the state of system and an increase of thermodynamical entropy so that living systems would generate entropy very effectively also in TGD Universe at the level of visible matter. If one believes that second law and NET imply DDA as England argues, then also TGD implies it at the level of visible matter. For dark matter the situation is different, since the outcome of SFR is not not random anymore. Seen from TGD perspective England's vision misses what is essential for life - the generation of phases of matter identifiable as the mysterious dark matter.

6. England talks about God. In a theory of consciousness predicting infinite self hierarchy, it is easy to assign the attribute "divine" to the levels of consciousness above given level of hierarchy. Personally I have nothing against calling the Entire Universe "God".

   One could give NMP the role of God. For strong form of NMP SFR would be almost deterministic except for ordinary matter for which entanglement is not algebraic and is therefore entropic: the universe would the best possible one in dark sectors and the worst one in the visible matter sector - Heaven and Hell! Weak form of NMP makes possible even more effective generation of negentropy than its strong form but allows self to make also stupid things and even SFRs with a vanishing negentropy gain: the outcome is state with no entanglement (system is in very literal sense alone in this state). The world in dark matter sectors is not anymore the best possible one but can become better and does so in statistical sense.

7. Replication is a crucial aspect of being alive. England argues that DDA allows to understand its emergence but does not tell about its mechanism. In TGD framework replication can be understood as an analog of particle decay - say photon emission by electron. This requires however a new notion: magnetic body. In Maxwell's theory one cannot assign any field identity to a physical system but TGD view about space-time forces to assign to a given system its field/magnetic body. The replication occurs primarily at the level of magnetic body carrying dark matter as large h_{eff} phases. Magnetic body replicates and ordinary visible matter self-organizates around the resulting copies of it. The dynamics of dark matter would induce also DNA replication, transcription and mRNA translation, and there are some indications that it is indeed "dark DNA" (dark proton sequences having DNA, RNA, amino-acids, and tRNA as biochemical counterparts), which determines what happens in transcription.

6.4 Could One Apply The Thermodynamical Approach Of England In TGD Framework?

It turns out possible to gain amazing additional insights about TGD inspired view of life and consciousness by generalizing England's approach [I33]. Several puzzling co-incidences find an explanation in the thermodynamical framework and the vision about solar system as a living quantum coherent entity gains additional support.

1. The situation considered in England's approach is a system - say biomolecule - in heat bath so that energy is not conserved due the transfer of energy between reactants and heat bath.

2. The basic equation is equilibrium condition for the reaction $i \to f$ and its time reversal $f^* \to i^*$. The initial and final state can be almost anything allowing thermodynamical treatment: states of biomolecule or even gene and its mutation. The ratio of the rates for the reaction and its time reversal is given by the ratio of the Boltzmann weights in thermal equilibrium:

$$\begin{aligned} \frac{R(i \to f)}{R(f^* \to i^*)} &= R \ , \\ R &= e^{-\frac{E_i - E_f}{T}} \ . \end{aligned} \tag{6.1}$$

   E_i and E_f denote the energies of initial and final state. This formula is claimed to hold true even in non-equilibrium thermodynamics. It is important that the ratio of the rates does not depend at all on various coupling constant parameters. The equilibrium condition must be modified if initial and final states are fermions but it is assumed that states can be described as bosons. Note that in heat bath even fermion number need not be conserved.

3. If the energy eigenstates are degenerate, the ratio R of Boltzman factors must be modified to include the ratio of state degeneracies

$$R \to \frac{D(E_i)}{D(E_f)} \times e^{-\frac{E_i - E_f}{T}} \ . \tag{6.2}$$

   This generalization is essential in the sequel.

   One can imagine two possible reasons for the presence of exponentially large factors compensating Boltzmann weights $D(E_i)$. The first reason is that for $h_{eff} = n \times h$ the presence of n-fold degeneracy due to the n-fold covering of space-time surface reducing to 1-fold covering at its ends at the ends of CD is essential. Second possible reason is that the basic object are magnetic flux tubes modellable as strings with exponentially increasing density of states. These mechanisms could quite well be one and same.

Consider now the basic idea inspired by this formula in TGD framework.

1. Since magnetic flux tubes are key entities in TGD inspired quantum biology, stringy dynamics suggests itself strongly. The situation thus differs dramatically from the standard biochemical situation because of the presence of dark matter at magnetic flux tubes to which one can assign fermion carrying strings connecting partonic 2-surfaces defining correlates for particles in very general sense.

2. The key aspect of stringy dynamics is Hagedorn temperature [**?**, **?**] (`http://tinyurl.com/yamnafy6`). Slightly below Hagedorn temperature the density of states factor, which increases exponentially, compensates for the Boltzmann factor. Hagedorn temperature is given by

$$T_{Hag} = \frac{\sqrt{6}}{2\pi} \frac{1}{\alpha'} \ , \tag{6.3}$$

   where α' is string tension. In superstring models the value of string tension is huge but in TGD framework the situation is different. As a matter fact, the temperature can be rather small and even in the range of physiological temperatures.

3. What makes T_{Hag} so special is that in the equilibrium condition reaction and its reversal can have nearly the same rates. This could have profound consequences for life and even more - make it possible.

In ZEO based quantum measurement theory and theory of consciousness time reversal indeed plays key role: self dies in state function reduction to the opposite boundary of CD and experiences re-incarnation as a time-reversed self. This process is essential element of memory, intentional action, and also remote metabolism, which all rely on negative energy signals travelling to geometric past assignable to time reversed sub-selves (mental images). The above formula suggests that intelligent life emerges near T_{Hag}, where the time reversed selves are generated with high rate so that system remembers and pre-cognizes geometric future as it sleeps so that memory planned action are possible.

4. String tension cannot be determined by Planck length as in string models if it is to be important in biology. This is indeed the case in TGD based quantum gravity. The gravitational interaction between partonic 2-surfaces is mediated by fermionic strings connecting them. If string tension were determined by Planck length, only gravitational bound states of size of order Planck length would be possible. The solution of the problem is that the string tension for gravitational flux tubes behaves like $1/h_{eff}^2$.

   In TGD framework string tension can be identified as an effective parameter in the expression of Kähler action as stringy action for preferred extremal strongly suggested by strong form of holography (SH) allowing the description of the situation in terms of fermionic strings and partonic 2-surfaces or in terms of interiors of space-time surfaces and Kähler action. $1/h_{eff}^2$ dependence can be derived from strong form of holography [K21] assuming electric-magnetic duality for Kähler form, and using the fact that the monopoles associated with the ends have same magnetic and electric charges.

5. The discussion of the analog of Hawking radiation in TGD framework [K21], [L7] led to an amazing prediction: the TGD counterpart of Hawking temperature turns out to be in the case of proton very near to the physiological temperature if the big mass is solar mass. This suggests that the entire solar system should be regarded as quantum coherent living system. This is also suggested by the general vision about EEG [K3]. Could Hawking temperature be near to the Hagedorn temperature but below it?

One can make this vision more detailed.

1. In ZEO the notion of heat bath requires that one considers reactants as subsystems. The basic mathematical entity is the density matrix obtained by tracing over entanglement with environment. The assumption that dark matter is in thermal equilibrium with ordinary matter can be made but is not absolutely crucial. The reactions transforming visible photons to dark photons should take care of the equilibrium. One could even assume that the description applies even in case of the negentropic entanglement since thermodynamical entropy is different from entanglement entropy negative for negentropic entanglement.

2. In TGD inspired quantum biology one identifies the gravitational Planck constant introduced by Nottale with $h_{eff} = n \times h$ [K21, K29, K26]. The idea is simple: as the strength of gravitational interaction becomes so strong that perturbation series fails to converge, a phase transition increasing the Planck constant takes place. $\hbar_{gr} = GMm/v_0 = \hbar_{eff} = n \times \hbar$ implies that $v_0/c < 1$ becomes the parameter defining the perturbative expansion. h_{gr} is assigned with the flux tubes mediating gravitational interaction and one can say that gravitons propagate along them.

   Note that this assumption makes sense for any interaction - say in the case of Coulomb interaction in heavy atoms: this assumption is indeed made in the model of leptohadrons [K31] predicting particles colored excitations of leptons lighter the weak bosons: this leads to a contradiction with the decay widths of weak bosons unless the colored leptons are dark. They would be generated in the heavy ion collisions when the situation is critical for overcoming the Coulomb wall.

   The cyclotron energy spectrum of dark particles at magnetic flux tubes is proportional to h_{gr}/m does not depend on particle mass being thus universal. In living matter cyclotron energies are assumed to be in the energy range of bio-photons and thus includes visible and UV energies and this gives a constraint on h_{gr} if one makes reasonable assumption about

strengths of the magnetic fields at the flux tubes [K15]. Bio-photons are assumed to be produced in the transformation of dark photons to ordinary photons. Also (gravitational) Compton length is independent on particle mass being equal to $L_{gr} = GM/v_0$: this is crucial for macrosopic quantum coherence at gravitational flux tubes.

3. The basic idea is that Hawking radiation in TGD sense is associated with all magnetic flux tubes mediating gravitational interaction between large mass M, say Sun, and small mass m of say elementary particle. How large m can be, must be left open. This leads to a generalization of Hawking temperature [L7] assumed to make sense for all astrophysical objects at the flux tubes connecting them to external masses:

$$T_{GR} = \hbar \frac{GM}{r_S^2 2\pi} = \frac{\hbar}{8\pi GM} \quad . \tag{6.4}$$

For Sun with Schwartschild radius $r_S = 2GM = 3$ km one has $T_{GR} = 3.2 \times 10^{-11}$ eV.

Planck constant is replaced with $\hbar_{gr} = GMm/v_0 = \hbar_{eff} = n \times \hbar$ in the defining formula for Hawking temperature. Since Hawking temperature is proportional to the surface gravity of blackhole, one must replace surface gravity with that at the surface of the astrophysical object with mass M so that radius $r_S = 2GM$ of the blackhole is replaced with the actual radius R of the astrophysical object in question. This gives

$$T_{Haw} = \frac{m}{8\pi v_0} (\frac{R_S}{R})^2 \quad . \tag{6.5}$$

The amazing outcome is that for proton the estimate for the resulting temperature for M the solar mass, is 300 K (27 C), somewhat below the room temperature crucial for life!

Could Hagedorn temperature correspond to the highest temperature in which life is possible - something like 313 K (40 C)? Could it be that the critical range of temperatures for life is defined by the interval $[T_{Haw}, T_{Hag}]$? This would require that T_{Haw} is somewhat smaller T_{Hag}. Note that Hawking temperature contains the velocity parameter v_0 as a control parameter so that Hawking temperature could be controllable. Of course, also $T_{Haw} = T_{Hag}$ can be considered. In this case the temperature of environment would be different from that of dark matter at flux tubes.

4. The condition $T_{Haw} \leq T_{Hag}$ allows to pose an upper bound on the value of the effective string tension

$$\frac{1}{\sqrt{\alpha'}} \geq \frac{m}{4\sqrt{6}v_0} \frac{R_S}{R} \quad . \tag{6.6}$$

REFERENCES

Mathematics

[A1] Gaussian Mersenne. Available at: `http://primes.utm.edu/glossary/xpage/GaussianMersenne.html`.

Condensed Matter Physics

[D1] Mills R et al. Spectroscopic and NMR identification of novel hybrid ions in fractional quantum energy states formed by an exothermic reaction of atomic hydrogen with certain catalysts, 2003. Available at: `http://www.blacklightpower.com/techpapers.html`.

Cosmology and Astro-Physics

[E1] Age of the universe. Available at: http://en.wikipedia.org/wiki/Age_of_the_universe.

[E2] Nottale L Da Rocha D. Gravitational Structure Formation in Scale Relativity, 2003. Available at: http://arxiv.org/abs/astro-ph/0310036.

[E3] McKay DS et al. Search for past life on Mars: possible relic biogenic activity in Martian meteorite ALH84001. *Science*, 273:924–926, 1996.

Biology

[I1] Centrosome. Available at: http://en.wikipedia.org/wiki/Centrosome.

[I2] Chromatin. Available at: http://en.wikipedia.org/wiki/Chromatin.

[I3] Identification and analysis of functional elements in one of the human genome by the ENCODE pilot project. Available at: http://www.nature.com/nature/journal/v447/n7146/edsumm/e070614-01.html.

[I4] Inosine. Available at: http://en.wikipedia.org/wiki/Inosine.

[I5] Nanobacterium. Available at: http://en.wikipedia.org/wiki/Nanobacterium.

[I6] Nanobe. Available at: http://en.wikipedia.org/wiki/Nanobe.

[I7] Nucleosome. Available at: http://en.wikipedia.org/wiki/Nucleosome.

[I8] Palindrome. Available at: http://en.wikipedia.org/wiki/Palindrome.

[I9] Programming biomolecular self-assembly pathways. *Nature*, 2007:318–322.

[I10] RNA sequences. Available at: http://www.staff.uni-bayreuth.de/~btc914/search/index.html.

[I11] Supercoil. Available at: http://en.wikipedia.org/wiki/Supercoil.

[I12] The Fourth Phase of Water: Dr. Gerald Pollack at TEDxGuelphU.

[I13] Transfer RNA. Available at: http://www.tulane.edu/~biochem/nolan/lectures/rna/trnaz.htm.

[I14] tRNA. Available at: http://en.wikipedia.org/wiki/tRNA.

[I15] tRNA. Available at: http://en.wikipedia.org/wiki/tRNA.

[I16] Virus. Available at: http://en.wikipedia.org/wiki/Virus.

[I17] Wobble base pair. Available at: http://en.wikipedia.org/wiki/Wobble_base_pair.

[I18] Coghlan A. Junk DNA makes compulsive reading. *New Scientist*, 2608, 2007. . Available at: http://www.newscientist.com/contents/issue/2608.html.

[I19] Lehninger AL. *Short course in biochemistry*. Worth Publishers, Inc., 1973.

[I20] King C. Biocosmology, 2003. Available at: http://www.dhushara.com/book/biocos/biocos.pdf.

[I21] Benveniste J et al. Human basophil degranulation triggered by very dilute antiserum against IgE. *Nature*, 333:816–818, 1988.

[I22] Benveniste J et al. Transatlantic transfer of digitized antigen signal by telephone link. *J Allergy and Clinical Immunology*, 99:175, 1989. Available at: http://www.digibio-.com/.

[I23] Dar N et al. Molecular trade-offs in rna ligases affected the modular emergence of complex ribozymes at the origin of life. *Royal Society. Open Science*, 2017. Available at: `http://tinyurl.com/y9ps2efz`.

[I24] Gariaev PP et al. Holographic Associative Memory of Biological Systems. *Proceedings SPIE - The International Soc for Opt Eng . Optical Memory and Neural Networks*, pages 280–291, 1991.

[I25] Kajander EO et al. Comparison of Staphylococci and Novel Bacteria-Like Particles from Blood. *Zbl Bakt Suppl*, 26, 1994.

[I26] Montagnier L et al. DNA waves and water, 2010. Available at: `http://arxiv.org/abs/1012.5166`.

[I27] Nakata M et al. End-to-End Stacking and Liquid Crystal Condensation of 6- to 20-Base Pair DNA Duplexes. *Science*, 2007. Available at: `http://www.sciencemag.org/cgi/content/abstract/318/5854/1276`.

[I28] Turberfield J A Green SJ, Lubrich D. DNA Hairpins: Fuel for Autonomous DNA Devices. *Biophys J*, 2006. Available at: `http://findarticles.com/p/articles/mi_qa3938/is_200610/ai_n16779588/pg_1`.

[I29] Horgan J. The World According to RNA. *Sci Am*, 1996.

[I30] McFadden J. *Quantum Evolution*. W. W. Norton & Company., 2000.

[I31] Travis J. Newfound RNA suggests a hidden complexity inside cells. *Science News*, 161(2):24, 2002.Available at: `http://www.sciencenews.org/articles/20020112/bob9.asp`.

[I32] Sanduloviciu M Lozneanu E. Minimal-cell system created in laboratory by self-organization. *Chaos , Solitons & Fractals*, 18(2):335, 2003. See also *Plasma blobs hint at new form of life*. New Scientist vol. 179, No. 2413 p. 20 September 2003, page 16.

[I33] England J Perunov N, Marsland R. Statistical Physics of Adaptation, 2014. Available at: `http://arxiv.org/pdf/1412.1875v1.pdf`.

[I34] Adler R. DNA 'fabricator' constructs walking DNA. *New Scientist* . Available at: `http://technology.newscientist.com/channel/tech/dn13192-dna-fabricator-constructs-walking-dna.html`, 2008.

[I35] Sheldrake R. *A New Science of Life: The Hypothesis of Formative Causation*. Inner Traditions Intl Ltd., 1995.

[I36] Sheldrake R. *The Presence of Past: Morphic Resonance and the Habits of Nature* . Icon Books Ltd, 2011.

[I37] Folk RL. Nanno-bacteria; surely not figments but what heaven are they? *Natural Sci* . Available at: `http://naturalSCIENCE.com`, 1, 1997.

[I38] Morita RY. Bioavailability of energy and starvation survival in nature. *Can J Micro-biol*, 34, 1988.

[I39] Eddy SR. Non-coding RNA genes and the modern RNA world. *Nature Reviews Genetics*, pages 919–929, 2001.

[I40] Gilbert W. The RNA World. *Nature*, 319, 1986.

Neuroscience and Consciousness

[J1] Words of truth. Available at: `http://www.reversespeech.com/words.shtml`.

[J2] ("editor") Bryant J. Sheldrake on Presentiment & Psychokinesis, 1999. Available at: `http://tinyurl.com/owrfolq`.

Books related to TGD

[K1] Pitkänen M. Bio-Systems as Super-Conductors: part I. In *Quantum Hardware of Living Matter*. Available at: http://tgdtheory.fi/pdfpool/superc1.pdf, 2006.

[K2] Pitkänen M. Crop Circles and Life at Parallel Space-Time Sheets. In *Magnetospheric Consciousness*. Available at: http://tgdtheory.fi/pdfpool/crop1.pdf, 2006.

[K3] Pitkänen M. Dark Matter Hierarchy and Hierarchy of EEGs. In *TGD and EEG*. Available at: http://tgdtheory.fi/pdfpool/eegdark.pdf, 2006.

[K4] Pitkänen M. General Theory of Qualia. In *Bio-Systems as Conscious Holograms*. Available at: http://tgdtheory.fi/pdfpool/qualia.pdf, 2006.

[K5] Pitkänen M. *Genes and Memes: Part II*. Online book. Available at: http://www.tgdtheory.fi/tgdhtml/genememe2.html., 2006.

[K6] Pitkänen M. Homeopathy in Many-Sheeted Space-Time. In *Bio-Systems as Conscious Holograms*. Available at: http://tgdtheory.fi/pdfpool/homeoc.pdf, 2006.

[K7] Pitkänen M. Magnetic Sensory Canvas Hypothesis. In *TGD and EEG*. Available at: http://tgdtheory.fi/pdfpool/mec.pdf, 2006.

[K8] Pitkänen M. *Magnetospheric Consciousness*. Online book. Available at: http://www.tgdtheory.fi/tgdhtml/magnconsc.html., 2006.

[K9] Pitkänen M. Negentropy Maximization Principle. In *TGD Inspired Theory of Consciousness*. Available at: http://tgdtheory.fi/pdfpool/nmpc.pdf, 2006.

[K10] Pitkänen M. Quantum Model for Hearing. In *TGD and EEG*. Available at: http://tgdtheory.fi/pdfpool/hearing.pdf, 2006.

[K11] Pitkänen M. Quantum Model for Nerve Pulse. In *TGD and EEG*. Available at: http://tgdtheory.fi/pdfpool/pulse.pdf, 2006.

[K12] Pitkänen M. *TGD and EEG*. Online book. Available at: http://www.tgdtheory.fi/tgdhtml/tgdeeg.html, 2006.

[K13] Pitkänen M. Construction of Quantum Theory: More about Matrices. In *Towards M-Matrix: part I*. Available at: http://tgdtheory.fi/pdfpool/UandM.pdf, 2012.

[K14] Pitkänen M. Quantum Mind, Magnetic Body, and Biological Body. In *TGD based view about living matter and remote mental interactions*. Available at: http://tgdtheory.fi/pdfpool/lianPB.pdf, 2012.

[K15] Pitkänen M. Are dark photons behind biophotons? In *TGD based view about living matter and remote mental interactions*. Available at: http://tgdtheory.fi/pdfpool/biophotonslian.pdf, 2013.

[K16] Pitkänen M. Comments on the recent experiments by the group of Michael Persinger. In *TGD based view about living matter and remote mental interactions*. Available at: http://tgdtheory.fi/pdfpool/persconsc.pdf, 2013.

[K17] Pitkänen M. Comparison of TGD inspired theory of consciousness with some other theories of consciousness. In *TGD based view about living matter and remote mental interactions*. Available at: http://tgdtheory.fi/pdfpool/consccomparison.pdf, 2013.

[K18] Pitkänen M. About twistor lift of TGD? In *Towards M-Matrix: Part II*. Available at: http://tgdtheory.fi/pdfpool/hgrtwistor.pdf, 2019.

[K19] Pitkänen M. Construction of Quantum Theory: M-matrix. In *Towards M-Matrix: Part I*. Available at: http://tgdtheory.fi/pdfpool/towards.pdf, 2019.

[K20] Pitkänen M. Cosmic Strings. In *Physics in Many-Sheeted Space-Time: Part II*. Available at: http://tgdtheory.fi/pdfpool/cstrings.pdf, 2019.

[K21] Pitkänen M. Criticality and dark matter. In *Hyper-finite Factors and Dark Matter Hierarchy*. Available at: http://tgdtheory.fi/pdfpool/qcritdark.pdf, 2019.

[K22] Pitkänen M. Dark Nuclear Physics and Condensed Matter. In *Hyper-finite Factors and Dark Matter Hierarchy: Part II*. Available at: http://tgdtheory.fi/pdfpool/exonuclear.pdf, 2019.

[K23] Pitkänen M. DNA as Topological Quantum Computer. In *Genes and Memes: Part I*. Available at: http://tgdtheory.fi/pdfpool/dnatqc.pdf, 2019.

[K24] Pitkänen M. Does TGD Predict the Spectrum of Planck Constants? In *Hyper-finite Factors and Dark Matter Hierarchy: Part I*. Available at: http://tgdtheory.fi/pdfpool/Planck.pdf, 2019.

[K25] Pitkänen M. Evolution in Many-Sheeted Space-Time. In *Genes and Memes: Part I*. Available at: http://tgdtheory.fi/pdfpool/prebio.pdf, 2019.

[K26] Pitkänen M. Quantum Astrophysics. In *Physics in Many-Sheeted Space-Time: Part II*. Available at: http://tgdtheory.fi/pdfpool/qastro.pdf, 2019.

[K27] Pitkänen M. Quantum gravity, dark matter, and prebiotic evolution. In *Genes and Memes: Part I*. Available at: http://tgdtheory.fi/pdfpool/hgrprebio.pdf, 2019.

[K28] Pitkänen M. Quantum Hall effect and Hierarchy of Planck Constants. In *Hyper-finite Factors and Dark Matter Hierarchy: Part II*. Available at: http://tgdtheory.fi/pdfpool/anyontgd.pdf, 2019.

[K29] Pitkänen M. TGD and Astrophysics. In *Physics in Many-Sheeted Space-Time: Part II*. Available at: http://tgdtheory.fi/pdfpool/astro.pdf, 2019.

[K30] Pitkänen M. The classical part of the twistor story. In *Towards M-Matrix: Part II*. Available at: http://tgdtheory.fi/pdfpool/twistorstory.pdf, 2019.

[K31] Pitkänen M. The Recent Status of Lepto-hadron Hypothesis. In *Hyper-finite Factors and Dark Matter Hierarchy: Part II*. Available at: http://tgdtheory.fi/pdfpool/leptc.pdf, 2019.

[K32] Pitkänen M. Three new physics realizations of the genetic code and the role of dark matter in bio-systems. In *Genes and Memes: Part II*. Available at: http://tgdtheory.fi/pdfpool/dnatqccodes.pdf, 2019.

Articles about TGD

[L1] Pitkänen M. DNA Waves and Water. Available at: http://tgdtheory.fi/public_html/articles/mont.pdf., 2011.

[L2] Pitkänen M. Sheldrakes Morphic Fields and TGD View about Quantum Biology. Available at: http://tgdtheory.fi/public_html/articles/sheldrake.pdf., 2011.

[L3] Pitkänen M. CMAP representations about TGD, and TGD inspired theory of consciousness and quantum biology. Available at: http://www.tgdtheory.fi/tgdglossary.pdf., 2014.

[L4] Pitkänen M. Geometric theory of harmony. Available at: http://tgdtheory.fi/public_html/articles/harmonytheory.pdf., 2014.

[L5] Pitkänen M. Pollack's Findings about Fourth phase of Water : TGD View. Available at: http://tgdtheory.fi/public_html/articles/PollackYoutube.pdf., 2014.

[L6] Pitkänen M. Jeremy England's vision about life and evolution: comparison with TGD approach . Available at: http://tgdtheory.fi/public_html/articles/englandtgd.pdf., 2015.

[L7] Pitkänen M. TGD view about blackholes and Hawking radiation. Available at: http://tgdtheory.fi/public_html/articles/hawkingnew.pdf., 2015.

[L8] Pitkänen M. About Physical Representations of Genetic Code in Terms of Dark Nuclear Strings. Available at: http://tgdtheory.fi/public_html/articles/genecodemodels.pdf., 2016.

[L9] Pitkänen M. Holography and Quantum Error Correcting Codes: TGD View. Available at: http://tgdtheory.fi/public_html/articles/tensornet.pdf., 2016.

[L10] Pitkänen M. Hydrinos again. Available at: http://tgdtheory.fi/public_html/articles/Millsagain.pdf., 2016.

[L11] Pitkänen M. p-Adicizable discrete variants of classical Lie groups and coset spaces in TGD framework. Available at: http://tgdtheory.fi/public_html/articles/padicgeom.pdf., 2016.

[L12] Pitkänen M. Artificial Intelligence, Natural Intelligence, and TGD. Available at: http://tgdtheory.fi/public_html/articles/AITGD.pdf., 2017.

[L13] Pitkänen M. Cold fusion, low energy nuclear reactions, or dark nuclear synthesis? Available at: http://tgdtheory.fi/public_html/articles/krivit.pdf., 2017.

[L14] Pitkänen M. Does valence bond theory relate to the hierarchy of Planck constants? Available at: http://tgdtheory.fi/public_html/articles/valenceheff.pdf., 2017.

[L15] Pitkänen M. Philosophy of Adelic Physics. In *Trends and Mathematical Methods in Interdisciplinary Mathematical Sciences*, pages 241–319. Springer.Available at: https://link.springer.com/chapter/10.1007/978-3-319-55612-3_11, 2017.

[L16] Pitkänen M. Philosophy of Adelic Physics. Available at: http://tgdtheory.fi/public_html/articles/adelephysics.pdf., 2017.

[L17] Pitkänen M. About dark variants of DNA, RNA, and amino-acids. Available at: http://tgdtheory.fi/public_html/articles/darkvariants.pdf., 2018.

[L18] Pitkänen M. About the Correspondence of Dark Nuclear Genetic Code and Ordinary Genetic Code. Available at: http://tgdtheory.fi/public_html/articles/codedarkcode.pdf., 2018.

[L19] Pitkänen M. About the physical interpretation of the velocity parameter in the formula for the gravitational Planck constant . Available at: http://tgdtheory.fi/public_html/articles/vzero.pdf., 2018.

[L20] Pitkänen M. Clustering of RNA polymerase molecules and Comorosan effect. Available at: http://tgdtheory.fi/public_html/articles/clusterRNA.pdf., 2018.

[L21] Pitkänen M. Could cancer be a disease of magnetic body? Available at: http://tgdtheory.fi/public_html/articles/nanotesla.pdf., 2018.

[L22] Pitkänen M. Dark valence electrons and color vision. Available at: http://tgdtheory.fi/public_html/articles/colorvision.pdf., 2018.

[L23] Pitkänen M. Emotions as sensory percepts about the state of magnetic body? Available at: http://tgdtheory.fi/public_html/articles/emotions.pdf., 2018.

[L24] Pitkänen M. Is the hierarchy of Planck constants behind the reported variation of Newton's constant? Available at: http://tgdtheory.fi/public_html/articles/variableG.pdf., 2018.

[L25] Pitkänen M. Maxwells lever rule and expansion of water in freezing: two poorly understood phenomena. Available at: http://tgdtheory.fi/public_html/articles/leverule.pdf., 2018.

[L26] Pitkänen M. New results in the model of bio-harmony. Available at: http://tgdtheory.fi/public_html/articles/harmonynew.pdf., 2018.

[L27] Pitkänen M. Sensory perception and motor action as time reversals of each other: a royal road to the understanding of other minds? Available at: http://tgdtheory.fi/public_html/articles/timemirror.pdf., 2018.

[L28] Pitkänen M. TGD view about coupling constant evolution. Available at: http://tgdtheory.fi/public_html/articles/ccevolution.pdf., 2018.