Exploration

On the Correspondence of Dark Nuclear Genetic Code & Ordinary Genetic Code

Matti Pitkänen [1]

Abstract

The basic problem in the understanding of the prebiotic evolution is how DNA, RNA, amino-acids and tRNA and perhaps even cell membrane and microtubules . The individual nucleotides and amino-acids emerge without the help of enzymes or ribozymes but the mystery is how their polymers emerged. If the dark variants of these molecules served as templates for their generation one avoids this hen-and-egg problem. The problem how just the biomolecules were picked up from a huge variety of candidates allowed by chemistry could be solved by the resonance condition making possible metabolic energy transfer between biomolecules and dark nuclei. Simple scaling argument shows that the assumption that ordinary genetic code corresponds to $h_{eff}/h = n = 2^{18}$ and therefore to the p-adic length scale $L(141) \simeq .3$ nm corresponding to the distance between DNA and RNA bases predicts that the scale of dark nuclear excitation energies is .5 eV, the nominal value of metabolic energy quantum. This extends and modifies the vision about how prebiotic evolution led via RNA era to the recent biology. Unidentified infrared bands (UIBs) from interstellar space identified in terms of transition energies of dark nuclear physics support this vision and one can compre it to PAH world hypothesis. p-Adic length scale hypothesis and thermodynamical considerations lead to ask whether cell membrane and microtubules could correspond to 2-D analogs of RNA strands associated with dark RNA codons forming lattice like structures. Thermal constraints allow cell membrane of thickness about 5 nm as a realization of $k = 149$ level with $n = 2^{22}$ in terms of lipids as analogs of RNA codons. Metabolic energy quantum is predicted to be .04 eV, which corresponds to membrane potential. The thickness of neuronal membrane in the range 8-10 nm and could correspond to $k = 151$ and $n = 2^{23}$ in accordance with the idea that it corresponds to higher level in the cellular evolution reflecting that of dark nuclear physics. The energy quantum of ordinary Josephson radiation is below the thermal energy for photons but the notion of generalized Josephson junction saves the situation. For massive particles associated with flux tubes the thermal energy $T/2$ is below the potential energy defined by action potential and that of metabolic energy quantum. Also microtubules could correspond to $k = 151$ realization for which metabolic energy quantum is .02 eV slightly below thermal energy at room temperature: this could relate to the inherent instability of microtubules. Also a proposal for how microtubules could realize genetic code with the 2 conformations of tubulin dimers and 32 charges associated with ATP and ADP accompanying the dimer thus realizing the analogs of 64 analogs of RNA codons is made.

Keywords: DNA, RNA, genetic code, dark, ordinary, prebiotic evolution.

1 Introduction

The idea about the realization of genetic code in terms of dark proton sequences giving rise to dark nuclei is one of the key ideas of TGD inspired quantum biology [24]. This vision was inspired by the totally unexpected observation that the states of three dark protons (or quarks) can be classified to 4 classes in which the number of states are same as those of DNA, RNA, tRNA, and amino-acids. Even more, it is possible to identify genetic code as a natural correspondence between the dark counterparts of DNA/RNA codons and dark amino-acids and the numbers of DNAs/RNAs coding given amino-acid are same as in the vertebrate code [24]. What is new is that the dark codons do not reduce to ordered products of letters.

[1]Correspondence: Matti Pitkänen `http://tgdtheory.com/`. Address: Rinnekatu 2-4 A8, 03620, Karkkila, Finland. Email: matpitka6@gamail.com.

During years I have considered several alternatives for the representations of genetic code. For instance, one can consider the possibility that the letters of the genetic code correspond to the four spin-isospin states of nucleon or quark or for spin states of electron pair. Ordering of the letters as states is required and this is problematic from the point of view of tensor product unless the ordering reflects spatial ordering for the positions of particles representing the letters. One representation in terms of 3-chords formed by 3-photon states formed from dark photons emerges from the model of music harmony [22]. By octave equivalence the ordering of the notes is not needed.

1.1 Insights

The above observations inspire several speculative insights.

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

2. Since nuclear physics precedes chemistry, one can argue that prebiotic life is based on these dark biomolecules serving as a template for ordinary biomolecules. To some degree biochemistry would be shadow dynamics and dark dynamics would be extremely simple as compared to the biochemistry induced by it. In particular, DNA replication, transcription, and translation would be induced by their dark variants. One can even extend this vision: perhaps also ordinary nuclear physics and its scaled up counterpart explaining "cold fusion" are parts of evolutionary hierarchy of nuclear physics in various scales.

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

1.2 Conditions on the model

The model must satisfy stringent conditions.

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

   Pyrimidines U, T, and C with single aromatic ring are are reported by NASA to be generated under outer space conditions (see `http://tinyurl.com/y7sh9zk4`). Carell et al [3] (see `http://tinyurl.com/z65kpyo`) have identified a mechanism leading to the generation of purines A and G, which besides pyrimidines A,T (U) are the basic building bricks of DNA and RNA. The crucial step is to make the solution involved slightly acidic by adding protons. TGD inspired model for the mechanism involves dark protons [25] [8].

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

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

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

3. Metabolic energy transfer between molecules and their dark variants must be possible by resonance condition. The dark nuclear energy scale associated with biomolecule could correspond to the metabolic energy scale of .5 eV. This condition fixes the model to a high extent but also other dark nuclear scales with their own metabolic energy quanta are possible

1.3 Vision

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

Simple scaling argument shows that the assumption that ordinary genetic code corresponds to $h_{eff}/h = n = 2^{18}$ and therefore to the p-adic length scale $L(141) \simeq .3$ nm corresponding to the distance between DNA and RNA bases predicts that the scale of dark nuclear excitation energies is .5 eV, the nominal value of metabolic energy quantum. This extends and modifies the vision about how prebiotic evolution led via RNA era to the recent biology. Unidentified infrared bands (UIBs) from interstellar space identified in terms of transition energies of dark nuclear physics support this vision and one can compre it to PAH world hypothesis.

p-Adic length scale hypothesis and thermodynamical considerations lead to ask whether cell membrane and microtubules could correspond to 2-D analogs of RNA strands associated with dark RNA codons forming lattice like structures. Thermal constraints allow cell membrane of thickness about 5 nm as a realization of $k = 149$ level with $n = 2^{22}$ in terms of lipids as analogs of RNA codons. Metabolic energy quantum is predicted to be .04 eV rather near to action potential .05 eV. The thickness of neuronal membrane in the range 8-10 nm and could correspond to $k = 151$ and $n = 2^{23}$ in accordance with the idea that it corresponds to higher level in the cellular evolution reflecting that of dark nuclear physics. The energy quantum of ordinary Josephson radiation is below the thermal energy for photons but the notion of generalized Josephson junction saves the situation. For massive particles associated with flux tubes the thermal energy $T/2$ is below the potential energy defined by action potential and that of metabolic energy quantum.

Also microtubules could correspond to $k = 151$ realization for which metabolic energy quantum is .02 eV slightly below thermal energy at room temperature: this could relate to the inherent instability of microtubules. Also a proposal for how microtubules could realize genetic code with the 2 conformations of tubulin dimers and 32 charges associated with ATP and ADP accompanying the dimer thus realizing the analogs of 64 analogs of RNA codons is made.

2 A model for dark nuclei as dark DNA

To make progress one must construct a concrete model for the dark nuclei. The basic idea [23] is that cylindrical variants of EZs discovered by Pollack [2] give rise to the dark counterparts of DNA, RNA, and

amino-acids as dark proton sequences. tRNAs would be analogs of tritium and ^{3}He.

2.1 Option I

Consider first the option, which I christen as Option I.

1. The TGD based model leads to the proposal for a formation of this kind of dark nuclear strings such that the distance between protons is rather precisely electron Compton length $L_e \simeq .4 \times 10^{-12}$ meters explains "cold fusion" in terms of dark nucleosynthesis which should have preceded ordinary nucleosynthesis by heating the material to the temperature required by it [27] [19].

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

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

   A scaling of n by 2^7 would give $L(141) = .3$ nm scale to be compared with .34 nm so that the p-adic length scale $L_e(k)$ would correspond to p-adic length scale $L(k)$ with $k = 141$. The value $h_{eff}/h = n = 2^{18}$ predicts nearly correct distance between nucleotides. The excitation energy scale about 1 MeV would scale down to .5 eV, which corresponds to the nominal value of the metabolic energy quantum and the bond energy of hydrogen bond.

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

3. The negative charge of DNA and RNA assignable to one oxygen of phosphate combining with ribose and DNA/RNA base could come from the tubular EZ formed in the formation of DNA. The negative charge of phosphates and the positive charge of dark protons could guarantee the stability of pairs of dark proton sequences and ordinary RNA and DNA.

   (a) DNA strand has radius of $R = 1$ nm. $L_e(141) = .3$ nm is considerably shorter than R. The Debye length R_D of DNA gives rough idea about the scale above which the negative charge of DNA nucleotides associated with the phosphates screened. R_D should be longer than R: otherwise it is possible to speak about charge of DNA only atomic length scales. One should have $R_D > R$: otherwise it does not make sense to assign negative DNA charge except in atomic length scales. $L_e(141) < R$ requires that the dark codons are pancake like structures.

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

   (b) Pancake structure suggests that the dark codons are separate horizontal units of dark quarks having length about $3L_e(141) = .9$ nm, which is still slightly shorter than R. A possible solution of the problem is that dark codons correspond to flux tube loops at the magnetic

body of DNA codon carrying three quarks. In this case the transversal size scale of dark codon could be much longer. This kind of flux loops are assigned also with the ordinary nuclei.

Remark: Scaled up hadron physics would be associated with flux tubes of the magnetic body of the codon at which one would have nucleons as 3-quark color singlets. I have already earlier proposed that scaled variants of hadron physics [9] appear in TGD inspired biology. One motivation comes from honeybee dance [1]!

4. What could force the decomposition to 3 dark proton units in 1-1 correspondence with the codons? Pancake model suggest that dark nucleus consisting in a well-defined sense of dark nuclei represented as nuclear strings, which are 3-proton analogs of tritium and ^{3}He and protons themselves contain dark quarks at horizontal flux loops. Many-sheeted space-time allows to consider this possibility and I have considered this already in the original nuclear string model for ordinary nuclei: in this case ^4He with very large binding energy could define one this kind of sub-units. Dark codons as genuine dynamical units would make natural the correspondence with ordinary codons.

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

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

   Dark weak interactions correspond to large value of n [27] so that in DNA length scale their proceed as fast as electromagnetic interactions (weak bosons would behave like massless particles below scaled up weak scale). This could make possible β decays changing the charges of the bonds between dark protons or dark neutrons [27] and lead to a stability by β emission.

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

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

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

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

3. The most natural possibility is that entanglement contains superposition of codon sequences in which each sequence codes for the same amino-acid. The chemical codons appearing in the superposition have different masses and chemical properties but in zero energy ontology (ZEO) this is possible. Situation would be like for a superconductor in which coherent state means superposition of states with different numbers of Cooper pairs and thus different fermion number in standard ontology but in ZEO this problem disappears.

2.2 Option II

Option I is not exact scaling up of nuclear physics since entangled 3-proton states are basic units: this is not the case in ordinary nuclear physics. Also neutrons are absent.

Could one have direct correspondence of nucleon states with the letters A, T, C, G so that the letters of the codon would not entangle? Their ordering would be however important.

For Option II this is possible: nucleon has two spin states and two isotopic spin states in one-one correspondence with A, T, C, G in suitable order. This kind of correspondence between spin-isospin states of quarks and A, T, C, G was actually the original proposal discussed in [7]. This would give rise to a realization of genetic code at the level of letters.

1. Could dark nuclei be formed as a pile of unentangled dark nucleons with size scale of order $L(141)$ and with vertical distance equal to that between RNA bases. For DNA and RNA would have dark proton sequences. For amino-acids, which are not always charged one would have also neutrons. This does not conform with the idea that Pollack effect is involved.

2. Now roughly one half of the dark letters are neutral so that RNA and DNA would have negative charge, which is one half of its charge in the scale $L_e(141)$. The TGD view about nuclear strings could come in rescue here [12]. The bonds between nuclei correspond to flux tubes with charge 0, +1, or -1. Ordinary nuclear physics do not predict them but TGD does. If the dark neutrons are connected to the next nucleon by a flux tube with charge +1, charge neutrality is achieved without losing the identity of nucleon as neutron.

3. The mechanism generating EZs favors dark proton sequences and the negative charge associated with phosphates could stabilize these sequences: this favors Option I.

4. There is also now a difference to ordinary nuclear physics in that in ordinary nuclear physics the order of letters formed by the spin states of p and n is not believed to matter. Now it matters and would be essential for the genetic code: if the order does not matter, one has only four codons! One can however ask whether the ordering of ordinary nuclear strings is actually matters but our measurement technology is not able to distinguish between the different orderings of nucleons. For instance, the energies of different nucleon orderings could be very nearly the same.

5. The correspondence of the letters of genetic code with dark nucleon states is natural for unentangled code. If the dark nucleons of the codon are allowed to entangle as the idea about evolution as generation of entanglement suggests, one obtains more complex structures than for dark protons.

   For codons formed from dark protons only 8 codons are possible. Also it seems that if dark code with unentangled letters existed, its evolution to a code with entangled letters is not plausible since it would suggest that the generation of entanglement induced also the entangled of the letters A,T,C,G of the ordinary code. This view is in conflict with the physical intuition. It would seem that ordinary DNA codons must be just product states of their letters and entangle as a whole to dark codons.

Some concluding remarks are in order.

1. Option II predicts only genetic codons but not the difference between DNA, RNA, amino-acids and tRNA like Option I. Neither does it predict genetic code as the mapping of codons to amino-acids. Thus Option II does not look promising. The idea about the evolution of genetic code is however too attractive to be given up.

   Perhaps ordinary nuclear physics and $n = 2^{11}$ dark counterpart correspond to steps in the evolution for which the codons had 1 and 2 letters, perhaps entangled for 2-letter code. The 4 letters could have been spin states of nucleons for ordinary nuclear physics. At this level one cannot speak about DNA, RNA, tRNA, and amino-acids. One can also imagine entanglement of the letters of 2-letter codon: maybe this could emerge at $n = 2^{11}$ level. At this level one could have simple analogs of the basic biomolecules. Codons would be dark proton analogs of deuterium.

2. The fact that DNA has forms a coil of thickness about $L_e(151) = 10$ nm suggests that also higher p-adic length scales and maybe even higher level dark nuclear physics are involved. Also the thickness of neuronal membrane has upper bound $L_e(151)$ to be contrasted with the thickness of ordinary cell membrane given by $L_e(149) = L_e(151)/2$.

3. Genetic code could have emerged from a simpler code [10]. If only dark protons are allowed, the unentangled product states would have only two letters giving rise to 8 codons if 3 dark protons serve as a unit. I have proposed that 2-letter and 1-letter codes preceded the 3-letter code and fused to 3-letter code. 2-letter code would have had 4 unentangled codons and 1-letter code 2 unentangled codons.

3 TGD view about the emergence of chemical life

Consider first the basic assumptions.

1. Dark DNA, RNA,... emerged before chemistry and serve as templates for ordinary DNA, RNA,... The replication, transcription, and translation for ordinary DNA, RNA,... are induced by the corresponding processes for their dark counterparts.

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

3. The amount of entanglement measured by entanglement negentropy (having a well-defined meaning in adelic physics [29]) is expected to increase gradually during evolution. Hence one expects generation of more and more entangled sequences of dark nucleons. At the bottom - perhaps ordinary nuclear physics - one would have the product states of dark nucleons. Perhaps dark nuclear physics with $n = 2^{11}$ came next. After that came $n = 2^{18}$ dark nuclear physics. But which came first: dark variants amino-acids, tRNA, RNA, or DNA and their chemical counterparts? And could one see even genes as entangled codon sequences coding for the same protein?

3.1 The quantum vision about the prebiotic evolution

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

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

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

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

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

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

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

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

   The emergence of DNA requires also the emergence of cell membrane. Could the emergence of cell membrane relate to the emergence of dark nuclei in the p-adic length scale $L(k)$, $k = 151$ and could the double layered structure of cell membrane serve as an analog for that of DNA double strand? Could lipid layers correspond to 2-D analogs of DNA strand with lipids taking the role of codons?

5. Could the full genetic code emerged in step-wise manner as proposed earlier [7, 16]? Genetic code can be seen in a good approximation as a fusion of 16-letter code and 4-letter code. This might be understood if the entanglement of dark codons emerges first as entanglement of only two first letters.

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

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

2. Metabolic energy quantum in the range .4-.5 eV could correspond to the energy scale of dark k=141 nuclear physics if 1 MeV is taken as the estimate for a typical nuclear binding energy. Hydrogen bonds also corresponds to this energy scale but this might be just what is needed to give rise to coherent metabolic activity.

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

There are some questions to ponder.

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

One ends up to a prediction of vertebrate genetic code also from a model of music harmony [22]. In fact, the model explains also its slight variation and the 2 additional amino-acids. Could this help to understand why the triplet code is so unique.

2. Could one imagine that also quarks and antiquarks were involved? Could dark nucleon pair with dark quark with same spin and isospin and color confinement forces dark proton triplets? Dark quarks indeed define a representation for A,T,C, G. In the model of topological computation [7, 16]. I have actually speculated with the possibility that dark quarks and antiquarks are paired with ordinary DNA codons.

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

3.2 Unidentified Infrared Bands as a test for the proposal

Unidentified Infrared Bands (UIBs) are an ill-understood phenomenon associated with radiation coming from interstellar space. There are also other analogous phenomena having no explanation in terms of molecular transitions [5] and one can ask whether they could be seen as signatures of dark nuclear physics.

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

2. Poly-aromatic hydrocarbons (PAHs) (see `http://tinyurl.com/atx4t9a`) are known to generate UIBs [5]. Therefore the UIBs from interstellar space could originate from PAHs.

3.2.1 TGD based models for UIBs

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

1. For years ago I discussed a model for UIBs based on p-adic length scale hypothesis [5]. The idea was that protons "drop" from atomic space-time sheet with $k = 137$ to a larger space-time sheet to $k_1 > 137$ space-time sheet and the difference of zero point kinetic energies is liberated as radiation [5]. The proposal was that the zero point kinetic energies give rise to a hierarchy of metabolic energy quanta.

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

2. Also dark nuclear transitions could explain UIBs. For $k = 141$ as the p-adic length scale of DNA letters would give nuclear energy scale $E = .5$ eV equal to the metabolic energy quantum by scaling 1 MeV for the ordinary nuclei. This is too high an energy but there are of course also smaller energies possible for the nuclear excitations possibly explaining the UIBs.

   The challenge is to explain not only the presence of these separate bands but also the band structure. Local wave functions for dark protons are localized in scale of .34 nm (DNA). Estimate for the energy scale associated with local excitations is obtained from particle in box model. The scale of these excitations is roughly $(L(137)/L(141))^2 = 2^{-4}$. These excitations could be generated thermally.

3. What about hydrogen bonds? The strength of hydrogen bond - essentially the bond energy - is in the range .4-.5 eV -, which as such does not correspond to the average UIB energy, which come

approximately as three lowest powers of two. The range of bond energies is .1 eV is smaller than the smallest UIB energy .11 eV.

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

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

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

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

2. In TGD inspired quantum biology axonal membrane can be seen as a generalized Josephson junction [13, 14, 15] decomposing nanoscopically to Josephson junctions defined by cell membrane proteins. The protein as junction would correspond to a magnetic flux tube along which various charged particles with $h_{eff} = n \times h$ flow possibly as supra currents. As a special case cell membrane acts like an ordinary Josephson junction. In this case the increment of the electrostatic energy of the Cooper pair over membrane given by $E_J = 2eV$ defines the energy of the smallest quantum of Josephson radiation.

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

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

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

Metabolic energy transfer between magnetic body and biological body (defined in very general sense for any system) is possible if the spectra of transition energies share common transition energies. Therefore

the spectrum of transition energies assignable to hydrogen bonds could have many transition energies common with that assignable to dark nuclear transitions and second and third explanation could be consistent with each other.

3.2.2 Model for hydrogen bond

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

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

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

   For proton in magnetic field of $B_{end} = .2$ Gauss the cyclotron frequency is 300 Hz and corresponds to $E_c(B_{end}) = 1.2 \times 10^{-12}$ eV. The identification of $E_c(B) = .5$ eVs would give $E_c(B) = n(B/B_{end}) \times E_c(B_{end}) = E_c(B) = .5$ eV. An estimate for B for the flux tube of hydrogen bond comes from flux quantization: $eBS = 1$ holds true for unit quantum of flux and for flux tube radius of one Angstrom this would give $B/B_{end} \sim 5 \times 10^8$. This gives the estimate $n \sim 10^8 \sim 2^{27}$. The rather large value conforms with the general vision for the values of n for dark protons whereas dark electrons of valence bonds would have much smaller values. The emergence of dark protons could be seen as the transition from chemistry already involving n as characterizer of valence bonds [28] to bio-chemistry.

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

   The membrane potential correspond to energy of .05 eV but metabolic energy quantum is 10 times larger. This looks like an inconsistency, which in thermodynamical approach is resolved by introducing of chemical potentials. In genuine quantum approach the introduction of thermodynamics quantities is not allowed.

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

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

   The general view about superconductivity in TGD Universe [13, 14] suggests that reconnection can give rise to a Cooper pairs of protons with members at separate flux tubes. Also Cooper pairs of electrons and biologically important ions could form by the same mechanism.

3.3 PAH world hypothesis from TGD point of view

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

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

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

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

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

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

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

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

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

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

4 Some reckless speculation about higher level variants of dark genetic code

A hierarchy of dark nuclear physics with hierarchy of $n = h_{eff}/h = n$ coming as certain powers of two so that the corresponding length scales correspond to p-adic length scales is so attractive idea that I cannot avoid the temptation to speculate about it and I have done it already earlier [11].

4.1 Could cell membrane correspond to dark nuclear physics for $k > 141$?

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

Could cell membranes correspond to a fourth level in the hierarchy of nuclear physics? Or could there be entire hierarchy coming assignable to certain p-adic length scales? One motivation for these speculations is that the Gaussian Mersenne primes $M_{G,k=}(1+i)^k - 1$ for $k \in \{151, 157, 163, 167\}$ define p-adic length scale $L(k) \propto 2^{k/2}$ between 10 nm assignable to the double membrane in mitochondria and 2.5 μm assignable to cell nucleus: so many Gaussian Mersenne in so short length scale range is a number theoretical miracle.

Remark: I have claimed in earlier publications that the lipid double layer defining cell membrane has thickness $L_e(151) = 10$ nm: actually the thickness is $L_e(149) = 5$ nm for ordinary cells and 8-10 nm - roughly $L_e(151)$ - for neuronal membranes. The double cell membrane associated with mitochondria has thickness 22 nm and corresponds to $L_e(153)$: the thickness of the two membranes is about 7 nm. This observation allows to understand in what sense neurons and mitochondria are above ordinary cells in the evolutionary ladder.

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

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

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

   The totally hydrated layer nearest to water is hydrophilic head group, which in the case of phospholipids contains negatively charged phosphate. This phosphate layer has thickness $.7 - 1.0$ nm.

   Below it is a partially hydrated layer of thickness .3 nm, which corresponds to $L(141)$: this of course puts bells ringing!

   Hydrophobic lipid tail layer below it is dehydrated. The thickness of single lipid layer is 1.25-1.75 nm and would correspond to the p-adic length scale $L_e(145) = 1.2$ nm.

3. The phosphate layer analogous to phosphate-ribose backbone and the thickness $L(141)$ of partially hydrated layer suggests that it corresponds to EZ created in Pollack effect so that there would be parallel dark RNA sequence along axon (possibly helical as for microtubules). In the case of cell

membrane would have lattice like system formed from dark protons, and maybe even dark neutrons (as an analog for the neutron halo in some nuclei).

4. If the recent biology is the analog of RNA era for $k > 141$ codes, their manifestations could be seen as analogs of RNAs and the number of different lipids associated with the cell membrane could give some idea about their number. Cell membrane could be seen as a 2-D analog of RNA polymer. Cell division implying membrane replication would correspond to RNA replication (proposed to be catalyzed by tRNA at RNA era). Even the analogs of tRNA and amino-acids but not proteins should be present if one takes the analogy very seriously. Could one identify pairs of lipids and some molecules analogous to proteins appearing in cell division?

5. Both sides of the lipid bilayer would contain cylindrical lattices of dark RNA codons. In the case of axon one could have the analog of dark RNA strand extended to a cylinder containing bundles of these strands at its surface. Lipid layers would be 2-D analogs of 1-D DNA strands in this case.

   Lipids would be analogs of RNA codons and dark RNA codons would code for them: this predicts 64 different lipids in cell membrane. Single dark RNA would correspond to the size scale of single lipid given by $L(143) = 2L(141) = .625$ nm so that the dark nuclear physics would correspond to $k = 143$ and $n = 2^{20}$. The number N of parallel dark RNA strands is roughly the circumference of the axonal lipid layer divided by the size of single lipid about $L(143) = .625$ nm given by $N \sim 2\pi \times L_e(167)/L_e(143) = \pi \times 2^{24} \sim 5 \times 10^6$.

Remark: The flux tubes connecting the dark DNA sequences above lipid layer to those associated with DNA could make possible to realize topological quantum computation [7, 16] in terms of braiding induced by the 2-D liquid flow induced by nerve pulse patterns at nuclear membrane. Flux tubes might be associated with cytoskeleton and define analog of central nervous system. A rough estimate for the numbers of codons for human DNA of length about 1 m and the number of codons allowed by the surface of the nuclear membrane are of order 10^9 so that the proposal might make sense.

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

1. The condition that metabolic energy quantum is not below thermal energy at physiological temperatures suggest that scaling factors λ larger than $\lambda = 16$ in $n = h_{eff}/h$ for $n = 2^{18}$ associated with DNA and RNA cannot be allowed. Single lipid layer would correspond to $L_e(145) = 4L_e(141) = 1.25$ nm and $\lambda = 4$. Single lipid layer with hydrophilic layer included corresponds to $L_e(147) = 8L_e(141) = 1.25$ nm and $\lambda = 8$.

2. The value of $h_{eff}/h = n$ would be $n = 2^{22} \sim 4 \times 10^6$ for $k = 149$ and scaling factor would be $\lambda = 16$. The value of the metabolic energy quantum is now around .04 eV whereas the action potential is around .05 eV. As explained, in TGD Universe the cell membrane can be seen as Josephson junction decomposing in an improved resolution to membrane proteins acting as Josephson junctions [13, 14]. Josephson energy of Cooper pair is twice this - that is $E_J = 0.1$ eV slightly above the maximum $E_{max} = 3T = .09$ eV of the thermal distribution at physiological temperature.

3. For $k = 151$ the metabolic energy quantum would be scaled down to .02 eV (as noticed earlier, the membrane potential for some photoreceptor is .03 eV). The energy at which the intensity of thermal radiation at temperature of 300 K is $E_{max} = .09$ eV. The potential energy gain over cell membrane for a Cooper of charged particles would be $E_J = .045$ eV, which is roughly one half of of the energy of thermal photon at the maximum $E_{max} = 3T = .09$ eV of the thermal distribution. The intensity of the thermal radiation is reduced only by a factor .69 for $E = E_{max}/2$ so that there seems to be a real problem.

4. As far metabolic energy quantum and Josephson radiation are considered, for $k = 149$ membrane would be a quantum critical system. Quantum criticality would give rise to instability making

possible the generation of nerve pulses. During nerve pulse the dark protons at the dark space-time sheet would return to the neuronal membrane and destroy the ionic equilibrium. Also the temperature criticality of consciousness manifesting itself as the generation of hallucinations during fever could be understood. For $k = 151$ the situation would be overcritical and will be discussed separately.

For $k = 151$ Josephson energy of Cooper pair is scaled down to $E_J = .045$ eV considerably below $E_{max} = .09$ eV. Does this mean that Josephson radiation cannot carry information? Or could Nature have found the means to overcome this problem? The notion of generalized Josephson junction central in TGD inspired theory of EEG as communications from brain to MB [15, 6] could save the situation.

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

2. $h_{eff} = h_{gr} = GMm/v_0$ hypothesis [21, 20] guarantees the spectrum of cyclotron energies is universal and does not depend on the mass m of the charged particle being in the range of visible and UV energies of photons (this allows to deduce information about the values of mass M and velocity parameter $v_0 < c$): bio-photons would be produced in energy conserving phase transitions transforming dark photons to ordinary ones [17, 18].

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

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

Remark: In TGD view about information processing in brain [26] active linear neuron groups relate to verbal cognition and 2-D neuronal groups relate to the geometric cognition associated with the decomposition of perceptive field to objects. At cellular level DNA and cell membrane could perhaps be seen as counterparts for these structures. In TGD framework neuronal membrane is proposed to be a constructor of sensory representations communicated to the magnetic body (MB) using generalized Josephson radiation whereas motor control by MB has been assumed to take place via DNA [10].

4.2 Microtubules as quantum critical systems

Also microtubules (see `http://tinyurl.com/y8km9vve`) are 2-D structures having a strong resemblance with the lipid layers of cell membrane. Could a higher level representation of genetic code similar to the one proposed for lipid layers make sense for them.

1. Microtubules are hollow cylinders with outer *resp.* inner diameter equal to 24 *resp.* 12 nm (the scales differ by factor 2) so that their thickness is 12 nm is same as the inner radius and would

correspond to $L(151) = 10$ nm. They decompose to 13 parallel helical filaments consisting of 13 tubulin proteins having size scale of order $L_e(151)$.

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

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

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

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

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

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

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

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

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

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

I have proposed that flux tubes connecting tubulins to the lipids of the axonal lipid layer could give rise to topological quantum computation [7, 7]. The size scale of lipid is about $L_e(141)$ and that of tubulin about $L_e(151) = 32L_e(141)$, and the the radius of axonal membrane is by two orders of magnitude larger than microtubular surface. Hence this proposal does not look realistic unless one assumes that sub-structures of cell membrane with size scale of order $L_e(167)/L_e(151) = 2^8$ larger than tubulin size represented as space-time sheets with cell nucleus size $L(167)$ have flux tube connections to tubulins.

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

References

[1] Shipman B. The geometry of momentum mappings on generalized flag manifolds, connections with a dynamical system, quantum mechanics and the dance of honeybee. Available at: `http://math.cornell.edu/~oliver/Shipman.gif`, 1998.

[2] The Fourth Phase of Water : Dr. Gerald Pollack at TEDxGuelphU. Available at: `https://www.youtube.com/watch?v=i-T7tCMUDXU`, 2014.

[3] Carell T et al. A high-yielding, strictly regioselective prebiotic purine nucleoside formation pathway. *Science.* Available at:`http://science.sciencemag.org/content/352/6287/833`, 352(6287):833–836, 2016.

[4] Ferus M et al. Formation of nucleobases in a millerurey reducing atmosphere. *PNAS.*Available at: `http://tinyurl.com/kxxc7db`, 2017.

[5] Pitkänen M. About the New Physics Behind Qualia. In *Quantum Hardware of Living Matter*. Online book. Available at: `http://tgdtheory.fi/public_html/bioware/bioware.html#newphys`, 2006.

[6] Pitkänen M. Dark Matter Hierarchy and Hierarchy of EEGs. In *TGD and EEG*. Online book. Available at: `http://tgdtheory.fi/public_html/tgdeeg/tgdeeg.html#eegdark`, 2006.

[7] Pitkänen M. DNA as Topological Quantum Computer. In *Genes and Memes*. Online book. Available at: `http://tgdtheory.fi/public_html/genememe/genememe.html#dnatqc`, 2006.

[8] Pitkänen M. Evolution in Many-Sheeted Space-Time. In *Genes and Memes*. Online book. Available at: `http://tgdtheory.fi/public_html/genememe/genememe.html#prebio`, 2006.

[9] Pitkänen M. General Theory of Qualia. In *Bio-Systems as Conscious Holograms*. Online book. Available at: `http://tgdtheory.fi/public_html/hologram/hologram.html#qualia`, 2006.

[10] Pitkänen M. Genes and Memes. In *Genes and Memes*. Online book. Available at: `http://tgdtheory.fi/public_html/genememe/genememe.html#genememec`, 2006.

[11] Pitkänen M. Magnetic Sensory Canvas Hypothesis. In *TGD and EEG*. Online book. Available at: `http://tgdtheory.fi/public_html/tgdeeg/tgdeeg.html#mec`, 2006.

[12] Pitkänen M. Nuclear String Hypothesis. In *Hyper-finite Factors and Dark Matter Hierarchy*. Online book. Available at: `http://tgdtheory.fi/public_html/neuplanck/neuplanck.html#nuclstring`, 2006.

[13] Pitkänen M. Quantum Model for Bio-Superconductivity: I. In *TGD and EEG*. Online book. Available at: http://tgdtheory.fi/public_html/tgdeeg/tgdeeg.html#biosupercondI, 2006.

[14] Pitkänen M. Quantum Model for Bio-Superconductivity: II. In *TGD and EEG*. Online book. Available at: http://tgdtheory.fi/public_html/tgdeeg/tgdeeg.html#biosupercondII, 2006.

[15] Pitkänen M. Quantum Model for Nerve Pulse. In *TGD and EEG*. Online book. Available at: http://tgdtheory.fi/public_html/tgdeeg/tgdeeg.html#pulse, 2006.

[16] Pitkänen M. Three new physics realizations of the genetic code and the role of dark matter in biosystems. In *Genes and Memes*. Online book. Available at: http://tgdtheory.fi/public_html/genememe/genememe.html#dnatqccodes, 2006.

[17] Pitkänen M. Are dark photons behind biophotons. In *TGD based view about living matter and remote mental interactions*. Online book. Available at: http://tgdtheory.fi/public_html/tgdlian/tgdlian.html#biophotonslian, 2013.

[18] Pitkänen M. Comments on the recent experiments by the group of Michael Persinger. In *TGD based view about living matter and remote mental interactions*. Online book. Available at: http://tgdtheory.fi/public_html/tgdlian/tgdlian.html#persconsc, 2013.

[19] Pitkänen M. Cold Fusion Again. In *Hyper-finite Factors and Dark Matter Hierarchy*. Online book. Available at: http://tgdtheory.fi/public_html/neuplanck/neuplanck.html#cfagain, 2014.

[20] Pitkänen M. Criticality and dark matter. In *Hyper-finite Factors and Dark Matter Hierarchy*. Online book. Available at: http://tgdtheory.fi/public_html/neuplanck/neuplanck.html#qcritdark, 2014.

[21] Pitkänen M. Quantum gravity, dark matter, and prebiotic evolution. In *Genes and Memes*. Online book. Available at: http://tgdtheory.fi/public_html/genememe/genememe.html#hgrprebio, 2014.

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

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

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

[25] Pitkänen M. One step further in the understanding the origins of life. Available at: http://tgdtheory.fi/public_htm/articles/purineorigin.pdf, 2016.

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

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

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

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