Exploration

On Dark Variants of DNA, RNA & Amino Acids

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. In this article I restrict the consideration mostly to the dark variants of DNA, RNA, and amino-acids. To make progress one must construct a concrete model for the dark nuclei. The basic question is to what p-adic length scales $L(k)$ dark variants of DNA, RNA and amino-acids identified as flux tubes carrying dark proton sequences with 3 entangled protons defining genetic codons correspond. The original hypothesis was that the p-adic length scale assignable to dark DNA is consistent with the radius of ordinary DNA. It however turned out that this implies that the binding energy scale of corresponding dark nuclear physics is too high for biology. Also the assumption that the dark variant of DNA double strand is horizontally scaled variant of ordinary DNA strand excludes this identification since it requires that the horizontal size scale of dark DNA strand is larger than that of ordinary DNA strand. DNA coil has radius of 10 nm and this suggests that dark DNA radius corresponds to the p-adic length scale $L(151)$, where $k = 151$ corresponds to first Gaussian Mersenne prime belonging to the group $k = 151, 157, 163, 167$. The primes $k > 151$ would correspond to higher level coilings of DNA. From this hypothesis one ends up to the proposal that RNA, tRNA, and amino-acids correspond to $k = 149$.

Keywords: DNA, RNA, amino acid, dark variant, TGD framework.

1 Introduction

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

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

In this article I restrict the consideration mostly to the dark variants of DNA, RNA, and AAs. To make progress one must construct a concrete model for the dark nuclei. The basic question is to what p-adic length scales $L(k)$ dark variants of DNA, RNA and AAs identified as flux tubes carrying dark proton sequences with 3 entangled protons defining genetic codons [27, 24] correspond. The original hypothesis was that the p-adic length scale assignable to dark DNA is consistent with the radius of ordinary DNA. It

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

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

DNA coil has radius of 10 nm and this suggests that dark DNA radius corresponds to the p-adic length scale $L(151)$, where $k = 151$ corresponds to first Gaussian Mersenne prime belonging to the group $k = 151, 157, 163, 167$. The primes $k > 151$ would correspond to higher level coilings of DNA. From this hypothesis one ends up to the proposal that RNA, tRNA, and AAs correspond to $k = 149$.

The recent picture relies strongly on various anomalies to which TGD provides a solution. The TGD inspired model for "cold fusion" leads to the notion of dark nuclear physics - actually hierarchy of them labelled by the values of $h_{eff}/h = n$ and corresponding p-adic length scales: this vision allows to see biology as outcome of evolution of dark nuclear physics characterized by various p-adic length scales $L(k)$ labelled by primes $k = 127, 131, 137, 139, 149, 151, ...$ Second basic idea [4] is that cylindrical variants of EZs discovered by Pollack [4] give rise to the dark counterparts of DNA, RNA, and AAs as dark proton sequences. tRNAs would be analogs of tritium and ^{3}He. Pollack effect serves as a strong constraint for the model. Also the effects of ELF em fields on vertebrate brain [7] combined with the rather recent finding about clustering of RNA II polymerase molecules [5] exhibiting Comorosan effect [6] provide valuable constraints on the model [28]. The outcome of the arguments is that single strand of DNA, mRNA, tRNA and AAs most naturally correspond to $k = 149$ and double stranded DNA to $k = 151$.

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

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

The following considerations try to identify the p-adic length scale of dark variants DNA, RNA, tRNA, and AAs whose existence is predicted by TGD [27, 24].

2.1 Dark variant of DNA

Concerning the identification of the size scale of dark DNA one can consider several options. The first guess was that the scale is same as for ordinary DNA: L(141)=.34 nm obtained by scaling from the distance of protons in the $k = 127$ dark nucleus implicated by the findings of Holmlid et al [2, 3, 23]. It however turns out that the p-adic length scale assignable to dark DNA is most naturally $k = 151$ corresponding to the thickness 10 nm of DNA coil. The hypothesis that the integer k labelling p-adic length scale is prime is attractive working hypothesis leaving very few options under consideration. The options $k = 137$ and $k = 149$ are excluded since the pairing of dark DNA and ordinary DNA would not be possible without the coiling of ordinary RNA around dark DNA. This leaves only options for which $k \geq 149$ for prime values of k.

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

2.1.1 General considerations

Consider first some background.

1. The TGD based model leads to the proposal for a formation of this kind of dark nuclear strings such that the distance between protons is rather precisely electron Compton length $L_e \simeq .4 \times 10^{-12}$ meters explains "cold fusion" in terms of dark nucleosynthesis which should have preceded ordinary nucleosynthesis by heating the material to the temperature required by it [26] [18].

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

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

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

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

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

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

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

   Remark: Scaled up hadron physics would be associated with flux tubes of the magnetic body of the codon at which one would have nucleons as 3-quark color singlets. I have already earlier proposed that scaled variants of hadron physics [10] appear in TGD inspired biology. One motivation comes from honeybee dance [1]!

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

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

   Dark weak interactions correspond to large value of n [26] 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 [26] and lead to a stability by β emission.

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

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

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

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

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

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

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

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

2. The TGD based explanation of Pollack effect provides a consistency test for the idea [4, 22]. In Pollack effect IR light (besides either kinds of energy feeds) induces the formation of negative charged exclusion zones (EZs) in water bounded by gel phase. In TGD based model this would correspond

to the formation of dark proton sequences at magnetic flux tubes. The scale of dark nuclear binding energy would be most naturally in eV scale. The binding energy scale of hydrogen atoms in water molecules is about 5 eV which suggests that the binding energy scale for dark protons sequences is smaller since otherwise energy would be liberated. This would suggest $k = 149$ as will be found.

3. One can imagine that an external perturbation induces

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

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

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

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

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

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

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

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

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

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

1. Cisse et al [5] found that RNA II polymerase molecules cluster during transcription and their dynamics involves multiples of the time scale $\tau = 5$ seconds. Comorosan reported long time ago that just these time scales are universal bio-catalysis [6]. The TGD inspired model [28] for the findings of Cisse et al allows to sharpen the TGD based view about quantum biology considerably.

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

3. The model forces the conclusion that the endogenous magnetic field B_{end} has at its upper bound $B_{end} = .2$ Gauss deduced from the findings of Blackman about effects of ELF em fields on vertebrate brain [7]. The earlier ad hoc hypothesis was that $B_{end} = .2$ Gauss is minimum value of B_{end}. Furthermore, for the required value of h_{gr} $B_{end} = .2$ Gauss corresponds to dark cyclotron energy of .12 keV, which is surprisingly large energy at the upper end of UV band: the earlier intuitive guess was that energy scale is in visible range.

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

   Assume

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

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

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

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

   Could this energy induce an analog of standing em wave in transversal degrees of freedom of DNA perhaps transformable to many phonon state with very large number of photos and thus classical acoustic wave? This would allow to understand how cyclotron harmonics can have non-trivial effects. The effects of ELF radiation on behavior and physiology could be understood as gene expression induced by the irradiation.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

In an earlier article I represented what I called reckless speculations about higher level variants of genetic code (see [27] for the updated version of the original article). The speculations turned out to be not only reckless but to contain besides an unrealistic working hypothesis for p-adic length scale of dark DNA also a numerical error in the estimate of dark nuclear excitation energy scale leading to a wrong track.

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

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

A hierarchy of dark nuclear physics with hierarchy of $n = h_{eff}/h_0 = n$ coming as certain powers of two so that the corresponding length scales correspond to p-adic length scales is an attractive idea. I have speculated with this idea already earlier. A hierarchy of dark nuclear physics with hierarchy of $n = h_{eff}/h = n$ coming as certain powers of two so that the corresponding length scales correspond to p-adic length scales is an attractive idea. I have speculated with this idea already earlier [12].

3.1 Ideas

Consider first the general ideas.

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

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

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

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

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

3. The structures of ordinary bio-matter and also their dark variants assumed to control them are characterized by p-adic length scales. How these p-adic length scales could relate? The natural idea inspired by scaling invariance is that the dark variants of 1-D linear structure and 2-D structures formed from ordinary bio-matter are obtained by radial scaling consistent with p-adic length scale hypothesis, and guaranteeing that the distances between building bricks are scaled to the size scales of dark variants of DNA and other basic molecules. This rule makes sense also for the 2-D structures. For instance, it would scale up the p-adic length scale $L(143)$ characterizing lipid to $L(149)$ assignable to single dark RNA strand or $L(151)$ assignable to dark double DNA strand.

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

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

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

6. I have proposed that the flux tubes connecting the dark DNA sequences above lipid layer to those associated with DNA could make possible to realize topological quantum computation [9, 15] in terms of braiding induced by the 2-D liquid flow induced by nerve pulse patterns at nuclear membrane. Flux tubes might be associated with cytoskeleton and define an analog of central nervous system at the level of cell. A rough estimate for the numbers of codons for human DNA of length about 1 m and the number of codons allowed by the surface of the nuclear membrane are of order 10^9 so that the proposal might make sense.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

3. In the case of cell membrane membrane proteins are the natural candidate for the building bricks. They indeed have an active role and serve as both channels and pumps and in the case of the neural membrane this role is especially important. Membrane proteins are identified in TGD framework as generalized Josephson junctions. In the case of cell membranes mebrane proteins having length of about 5 nm (5 AAs) or 10 nm (10 AAs) going through the membrane are an excellent candidate for the basic building brick. One could see the basic structure either as 2-D structure built from membrane proteins or 3-D structure build from AAs. Membrane proteins would form kind of generalized protein as a 2-D lattice of proteins and accompanied by their dark variants or of 2-D dark variants of RNA or DNA coding for them and identifiable as radial scalings of these proteins to $k = 149$ or $k = 151$.

   The model for topological quantum computation [9] suggesting that DNA codons of are connected to lipids of cell membrane could be modified so that that dark DNA, RNA, or AAs associated with membrane proteins are connected to them by flux tubes which can get braided. This would allow the quantum control of the 2-D protein like structure and make it effectively single quantum coherent Josephson junction as suggested in the quantum model for nerve pulse [K8].

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

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

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

3.2.2 Thermodynamical constraints

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

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

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

2. Note that the action potential assignable to $k = 151$ neuronal membrane is around .05 eV (the membrane potential for some photoreceptors is .03 eV). In TGD Universe the cell membrane can be seen as Josephson junction decomposing in an improved resolution to membrane proteins acting as Josephson junctions [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. As far Josephson radiation are considered, for $k = 151$ membrane would be a quantum critical system. Quantum criticality could give rise to instability making possible the generation of nerve pulses. During nerve pulse the dark protons at the dark space-time sheet would return to the neuronal membrane and destroy the ionic equilibrium. Also the temperature criticality of consciousness manifesting itself as the generation of hallucinations during fever could be understood. For $k = 151$ the situation would be overcritical and will be discussed separately.

The Josephson energy of Cooper pair is scaled down to $E_J = .1$ eV near to $E_{max} = .09$ eV. This is slightly above the thermal energy but one could still argue that Josephson radiation cannot carry information. Or could Nature have found the means to overcome this potential problem? The notion of generalized Josephson junction central in TGD inspired theory of EEG as communications from brain to MB [K8, 8] 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 [20, 19] 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 [16, 17].

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 [25] 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 [11].

3.3 DNA packing problem and p-adic length scales

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

There are 4 levels involved. Could they relate to the Gaussian miracle primes $k = 151, 157, 163, 167$? The general proposal is that the products of powers of small primes define the scale hierarchy. There is evidence that at least the powers of 2 and 3 define p-adic length scales, which would correspond also to dark scales. The simple guess is that the dark scales are identical to the ordinary p-adic scales.

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

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

Consider next nucleosome.

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

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

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

   According to the representation for the hierarchy of packings (see `http://tinyurl.com/ybxv6w4v`), the diameter of the structure is $d = 1.1L(151)$ rather than small and the height of the structure is smaller in the illustration. This width is however not consistent with the helix structure for any value of the height.

2. If the double DNA strand is accompanied by a dark double strand of radius $L(149)$, the situation is like having a band of width $L(151)$ going around the spool. The dark double strand covers an area, which is 4/3 times the spool area. The horizontal thickness of the entire dark structure is about $d_D = (7/4)L(151)$. If the radius of DNA double strand is $r = L(151)$ the area covered by the double strand is roughly twice the area of the spool. This suggests that one should identify the p-adic length scale of DNA double strand as its diameter about $L(151)$ rather than its radius.

Remarks:

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

2. A further interesting finding is that the sequence of 8 quints defines a piece of 12-note scale proceeding by quints as steps between nearest neighbor vertices (using octave equivalence) in the icosahedral model of harmony [21, 29] based on 12-note scale could be interpreted as cubic Hamiltonian cycle giving rise to the notes $F, C, G, D, A, E, H, F\sharp$. This gives the notes of C major scale with 7 notes plus tritonus $F\sharp$ defining half-octave as 8:th note. One could also identify the cycles as consisting of the notes of 8-note scale along cycle in the usual order $C, D, E, F, G, A, H, F\sharp$ based on standard notion of nearness for which neighboring vertices correspond to neighboring notes of the scale. Allowed 3-chords would correspond to triplets containing no neighboring notes. The Hamiltonian cycle for cube is unique apart from isometries as also for tetrahedron and and dodecahedron.

3.4 Microtubules as quantum critical systems

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

code would be in question. In the case of axons a possible identification for the dark scale would be as the radius of the axonal membrane.

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

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

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

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

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

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

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

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

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

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

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

I have proposed that flux tubes connecting tubulins to the lipids of the axonal lipid layer could give rise to topological quantum computation [9, 9]. 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?

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