Three new physics realizations of the genetic code and the role of dark matter in bio-systems

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Abstract

TGD inspired quantum biology leads naturally to the idea that several realizations of genetic code exist. Besides the realizations based on temporal patterns of electromagnetic fields I have considered three different new physics realizations of the genetic code based the notions of many-sheeted space-time, magnetic body, and the hierarchy of Planck constants explaining dark matter in TGD framework.

1. The first realization - proposed in the model for DNA as topological quantum computer (tqc) - maps the nucleotides A,G and T,C to dark quarks u,d and their anti-quarks assignable to the ends of magnetic flux tubes representing braid strands and connecting nucleotides to lipids of cell membrane.
2. Second realization was discovered in the model of dark nuclei as strings of dark baryons. Dark baryons realize codons in terms of quantum entanglement and without decomposition to letters. Dark baryons are strings of 3 quarks connected by two color flux tubes. The neutral states of the dark baryon predicted by the model are in 1-1 correspondence with DNA, RNA, aminoacids. Candidates for the counterparts of tRNA anticodons are also obtained if one accepts that genetic code actually decomposes to 2 steps $64 \to 40 \to 20$ such that there are 40 dark baryon counterparts for tRNA anticodons. The amazing finding is that vertebrate genetic code comes out correctly.
3. The third realization is a physical realization for the divisor code proposed by Khrennikov and Nilsson. The realization relies on two integers labeling magnetic flux tubes containing dark matter. The dark magnetic flux tubes assignable to DNA codons and amino-acids could be labeled by these integers providing a representation of the genetic code consistent with the divisor code. Also a physical mechanism implying the physical equivalence of the dark baryon code and divisor code can be imagined.

The basic proposal is that dark baryon counterparts of basic bio-molecules and genetic code were present from beginning and gave rise to pre-biotic life at the magnetic flux tubes so that the evolution of biological life meant the development of translation and transcription mechanisms allowing to transform dark baryon variants of the codons to their chemical variants. These mechanisms would be still at work inside the living cell and allow the living matter to perform genetic engineering. This proposal is consistent with recent findings about large variations of genomes inside organism.

There is a strange experimental finding giving support for this picture. A water solution containing human cells infected by bacteria is sterilized by a filtering procedure and healthy cells are added to the filtrate. Within few weeks the infected cells re-appear. A possible explanation is that dark baryon variant of the bacterial genome realized as nano-sized particles remains in the solution despite the filtering.

The codes are discussed from the point of view of DNA as tqc hypothesis and the model for protein folding and bio-catalysis. The basic selection rules of bio-catalysis could be based on the two integers assignable to the dark magnetic flux tubes. Only bio-molecules whose dark magnetic bodies contain a layer characterized by same integers can be connected by dark magnetic flux tubes. The reconnection of the dark magnetic flux tubes selecting the bio-molecules participating the catalytic reaction and the contraction of these flux tubes induced by a phase transition reducing Planck constant and forcing the bio-molecules near to each other would represent basic mechanisms of bio-catalysis.

1 Introduction

This chapter represents an attempt to integrate three different models of genetic code [L5, L6, L10] with each other and with DNA as topological quantum computer (tqc) hypothesis [L5] as well as the general ideas behind the model of protein folding and bio-catalysis [L8]. The considerations lead to a modification of the earlier model of protein folding.

1.1 The notions of dark matter and magnetic body

The generalization of the imbedding space to a book like structure (see Appendix) with pages labeled by two non-negative integers (n_a, n_b) characterizing the singular coverings of M^4 (or actually of causal diamond of M^4 defined as intersection of future and past directed light-cones) and of CP_2 together with pages representing singular coverings and represented similarly by a pair of integers (or

equivalently inverses of non-negative integers) provides a possible mathematical realization of dark matter hierarchy. Dark matter is interpreted as phases of ordinary matter at various pages of the book like structure. The pages of the book are partially characterized by a hierarchy of Planck constants. The notion of darkness is only a relative concept in this picture. The phase having $(n_a, n_b) = (1, 1)$ can be identified as ordinary visible matter.

Magnetic body is second key concept in TGD based model of quantum biology. Magnetic body has onion like structure with layers characterized by a spectrum of values of (n_a, n_b) identifiable as orders of the cyclic groups Z_{n_a} *resp.* Z_{n_b} acting in the fiber of singular covering space or factor space assignable M^4 *resp.* CP_2 degrees of freedom. Also the extensions of these groups obtained by adding reflection can be considered. Phase transitions changing the values of (n_a, n_b) and thus also the length of magnetic tubes correspond to a tunneling between two pages of the book and in general change the value of Planck constant. The basic selection rule is familiar from the sub-group rule for phase transitions and means that either n_{a_1} (n_{b_1}) divides n_{a_2} (n_{b_2}) or vice versa. These phase transitions are in a key role in TGD inspired model of bio-catalysis.

The reconnections of flux tubes represents second basic mechanism of bio-catalysis. Together these two mechanisms could be at least partially responsible for the amazing aspects of bio-catalysis such as extreme selectivity and the ability of distant bio-molecules to find each other in the dense soup of bio-molecules.

1.2 Realizations of genetic code

I have proposed several realization of the genetic code during past 15 years. There are three realizations which are especially interesting physically.

1. The first realization is based on the map of G,C *resp.* A,T codons to quarks u,d *resp.* their anti-quarks. This code was proposed to realize DNA as tqc with braid strands represented as flux tubes connecting nucleotides with the lipids of cell membrane [L5]. The quantum states at the ends of braid strands -would be represented by many particle states of quarks and anti-quarks in this model and entanglement of quarks and anti-quarks would be essential for tqc and affected by the braiding induced by the 2-D liquid flow of the lipids.

2. Second realization is based on the observation that the neutral states of dark baryons consisting of u and d quarks in nuclear string model can be regarded as counterparts of DNA, RNA, amino-acids and perhaps even tRNA [L6, K5]. Nuclear strings would represent DNA and other polymers at the level of dark matter.

3. Third realization is based on the interpretation of divisor code discovered by Khrennikov and Nilsson [34] in terms of the sub-group rule for phase transitions [L6]. Second realization and this one are in 1-1 correspondence under certain prerequisites. The magnetic- interaction energy of the dark baryon depends on the projections of the total quark spin and total color flux tube spin to the direction of the magnetic field labeling both DNA codons and amino-acids. This interaction energy is a function of (n_a, n_b) and minimized for some pair (n_a, n_b). This gives 1-1 correspondence the states of dark baryon and page of the book and since the page numbering allows to interpret physically the divisor code, one might hope that this correspondence is consistent with both codes.

4. I have also proposed number theory based thermodynamical models for the genetic code [L9, L10] discussed also by others [19, 21], and a suitable modification of this kind of model could allow to model the thermodynamics based on magnetic interaction energy.

I have also suggested realizations of the genetic code in terms of electromagnetic field patterns and computer metaphor encourages to think that standard genetic code is just one possible realization among many.

1.3 Questions

These ideas raise a bundle of questions.

1. There are three candidates for the realization of the genetic code. Are all these realizations needed? Are the realizations based on dark baryons and divisor code equivalent?

2. The realization based on correspondence with DNA nucleotides and quarks and anti-quarks works nicely for DNA as tqc hypothesis. Can one consider also a realization of DNA as tqc in terms of dark baryons?

3. How dark baryon realization relates with ordinary chemical realizations and to evolution of prebiotic life forms? Could it be that the life based on nuclear string genetic code gradually moved from the dark pages of the book to the page containing visible matter as chemical realizations of the analogs of DNA, RNA, amino-acids and even tRNA gradually developed? Note that the process bears formal similarity to the transition of life from sea to land. Is it possible to transcribe the counterparts of DNA,RNA, and amino-acids to their real counterparts? Is prebiotic era continuing still inside dark magnetic flux tubes and could it make possible genetic engineering?

2 A vision about evolution and codes

The fact is that the only thing we really know about dark matter is that 95 percent of matter is dark (matter or dark matter and energy depending on theoretical framework used). Therefore the ideas about dark baryon code are necessarily speculative. One can however base the speculations to some vision in order achieve internal consistency if nothing else.

2.1 Basic insights

The idea that biological life was preceded by dark life with subset for the counterparts of DNA, RNA, amino-acids and tRNA dominating the scene looks like a plausible starting point. Second attractive assumption is that this era still continues at magnetic bodies and makes possible genetic engineering based on experimentation and transcription of at least dark baryon analog of DNA to ordinary DNA.

The transformations for RNA and amino-acids to dark matter and vice versa seems necessary if the experimentation with new variants of genes is to be carried out unless one is satisfied with the testing of the modified genes in a small scale. Reconnection and $\hbar$ changing phase transitions of flux tubes would serve as the basic mechanism of bio-catalysis in TGD Universe. One can imagine two basic mechanisms involving reconnection of flux tube and transforming dark nuclear strings to polymers.

1. Given bio-molecule could be accompanied by a closed flux tube of the magnetic field containing dark matter and extending to some page of the book characterized by two numbers x_a *resp.* x_b, which are integers for singular coverings of M^4 *resp.* CP_2 and inverse integers for singular factor spaces of M^4 *resp.* CP_2. For bio-molecules for which x_a and x_b are identical these closed loops could reconnect to form a pair of flux tubes connecting bio-molecules (see Fig. 2.1). A phase transition reducing Planck constant would bring the molecules close to each other. This would provide a general recognition mechanism central in the reactions of bio-molecules.

2. These flux tube connections between two molecules could also involve only single *permanently* existing flux tube (this is a rather strong prediction which might be used to kill this option). In this case the reconnection for the flux tubes connecting molecules X and Y *resp.* U and V would give rise to connections $X-U$ and $Y-V$ for instance. The general recipe for achieving these transformations is based on the assumption that molecule and its dark conjugate connected by flux tubes can be present and that reconnection process given exchange of particles describable in terms of diagrams analogous to stringy diagrams is possible. This means that pairings $X-dY$ and $U-dV$ can be transformed to pairings $X-U$ and $dY-dV$ and $X-dV$ and $U-dY$ (see Fig. 2.1). This process would extend the variety of possible transcription like processes to allow also transcription of dark variants of DNA, RNA and amino-acids to visible ones and vice versa.

Genetic engineering would be possible by the fact that the dark nuclear string variants of genes could be easily transferred around the biological body unlike modified DNAs. In particular, modified dark genes could be transferred to the nuclei of germ cells. Essentially the TGD inspired mechanism of homeopathy would be in question [K5].

Figure 1: Illustration of the reconnection by magnetic flux loops.

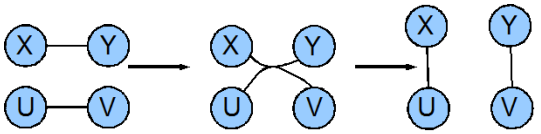

Figure 2: Illustration of the reconnection by flux tubes connecting pairs of molecules.

There is analogy with the evolution of language. Both DNA codons and representation of nucleotides in terms of quarks and anti quarks (perhaps accompanying the intronic portions of DNA) mean a representation of codons as three-letter sequences. Since dark baryons represent genetic codons as indecomposable structures in terms of quantum entanglement, the emergence of both representations would be analogous to the emergence of written language when spoken words forming indecomposable units decomposed into letters having no meaning as such. The findings that there are major differences between the genomes of blood and tissue cells [35] and that the genetic variation due to jumping genes is highest in brain and germ cells [36] is consistent with the view about dark evolution modifying at least intron portion of the genome.

RNA world [37, 38, 39] represents a dominating vision about pre-biotic evolution. The idea is RNA era was first and that somehow DNA and amino-acids emerged in some later stage. It has not been possible yet to reproduce replicating RNA sequences in laboratory so that there is still room for alternatives. Dark baryon realization of the genetic code predicts that the analogs of DNA, RNA, amino-acids and even tRNA anticodons might have been there all the time. This might apply also to the primitive chemical representations of DNA, RNA, tRNA, and amino-acids. It is of course possible that the chemical representation of RNA evolved first. This era could still continue inside cell nuclei and make possible genetic engineering as experimentation with dark baryon genes producing amino-acids and RNA and then possibly transforming the resulting RNAs to DNA by reverse transcription. Also a direct transcription to DNA could take place.

2.2 The simplest scenario

The evolution could might have proceed as a gradual transition of life from dark pages to the visible page allowing chemical realization of the genetic code.

1. Dark matter era would replace RNA and already this era involved at least the dark counterparts of DNA, RNA, amino-acids and perhaps even $64-40 \to 40-20$ two-step realization of the genetic code with tRNA anticodons representing a particular example of 40-D realization intermediate between DNA and amino-acids. Maximum number of different tRNA codons is indeed around 40 [40]. Without further assumptions the pairing of all dark DNA and RNA codons coding for the same amino-acid was possible. The situation changes if one assumes 1-1 correspondence between dark baryon realization and the realization of the divisor code in terms of dark magnetic flux tubes to be discussed later. This era could still continue at magnetic bodies and make genetic experimentation and genetic engineering possible.

2. Dark nuclear strings became gradually associated with the magnetic bodies of DNA, RNA and amino-acids and a machinery transforming DNA to mRNA to tRNA to amino-acids developed. Flux tube connections could have formed between nuclear strings and the magnetic bodies of the bio-molecules. A stronger condition is that dark nuclear strings became part of the magnetic bodies of DNA, RNA and amino-acids forming helical structures running parallel to the corresponding molecular structures. For this option base pairing could have made the

dark counterparts of DNA-DNA and DNA-mRNA pairings unique (also the equivalence of dark baryon and divisor codes could have guaranteed this). mRNA-tRNA base is pairing is not unique but wobble base pairing made possible for all mRNA codons except stopping codons to pair to tRNA anticodons. Whether RNA appeared first or whether the counterparts of the basic bio-molecules were present from the beginning remains an open question.

3. Topological quantum computation based on the map of A,G *resp.* T,C to quarks *resp.* anti-quarks emerged later as something analogous to written language and would naturally correspond to the intron portions of genome for which the decomposition into triplets is not essential and the nucleotide composition is not too essential since it is braiding which defines topological quantum computation (the 4 different colors of the braid strands are not necessary).

2.3 How dark baryon code could be involved with transcription and translation mechanisms?

In the following it is assumed that one can talk about magnetic flux tubes containing dark nucleon strings as independent objects and therefore not identified as a helical string parallel to DNA, RNA or amino-acid sequence as one might also imagine. Therefore it is not necessary to assume that dark baryons have the same size scale as corresponding molecular units. One can also assume that one can connect flux tubes associated with nuclear strings by magnetic flux tubes.

Genetic engineering makes sense if the transcription of nuclear string counterparts of DNA, RNA, tRNA, and amino-acids to their chemical counterparts is possible.

1. One can classify flux tube connections by introducing the notion of order of flux tube connection expected to characterize the probability of flux tube connection. First order means a flux tube entirely in given page of the book like structure defined by the generalized imbedding space, second order to a flux tube between two different pages, third order a flux tube traversing through an intermediate page between two pages, and so on. Reconnection of the magnetic flux tubes provides a general mechanism for this transformations and as already explained there are two general recipes for the formation of reconnection.

2. **Option I** - the simpler one - involves a reconnection of the closed flux tubes associated with the molecules to be paired. This mechanism would make it possible for a bio-molecule X to catch a partner Y if the corresponding closed flux tubes reside at same page of the book s(see Fig. 2.1). This mechanism provides a straightforward description of replication, transcription and translation as well as their generalizations allowing to transform dark nuclear strings to their molecular counterparts and vice.

3. **Option II** is more complex (see Fig. 2.1) and can be formulated in terms of two stringy diagrams with two strings connecting objects X and Y *resp.* U and V at their ends touch and transform to strings with X and V *resp.* U and V or X and U *resp.* Y and V at their ends. The process can be visualized as exchange of half strings and stringy diagrams represent various processes. Denote by dX the dark matter counterpart of X which can be DNA,RNA, or amino-acid and assume that all combinations obtained by the reconnection process are possible so that one would has pairings $X-Y, X-dY, dX-Y$, and $dX-dY$ defined by flux tube connections. All these variants present and $X-Y$ and $dX-dY$ can be first order connections whereas $X-dY$ and $dX-Y$ are second or higher order connections. This option requires permanent flux tube connections.

4. These are the simplest options. One can wonder whether the hydrogen bonds associated with base pairs correspond to a pair $(A-T)$ or triplet $(G-C)$ of contracted flux tubes. It is of course possible to have more than two flux tubes. If the third hydrogen bond for $G-C$ corresponds to a flux tube a permanent flux tube connection between G and C nucleotides would exist.

One could think that only few bio-molecules can have flux tubes at the page at which the particular dark nuclear string typically resides (minimization of the magnetic interaction energy could fix the most probable candidate for this page and imply connection between dark baryon code and divisor code) and that bio-molecules are gradually selected from these particular molecules. The process would be still in progress. Vertebrate nuclear code would be however identical with the dark baryon code. For tRNA anti-codons the situation would be far from ideal.

2.3.1 Replication

In the following $'\circ'$ means one or two bonds depending on whether Option I or II is in question.

Option I: Let $(X \circ Y)$ denote DNA double helix with two flux tubes connecting them and U a V DNA nucleotides. The opening of DNA double strand means reconnection of these flux tubes so that two closed loops are obtained. These flux tubes transform to dark flux tubes and reconnect with dark flux tubes associated with U and V respectively and a phase transition reducing $\hbar$ brings U and V near sequences X and Y where they combine with already existing new sequence.

Option II: Let $(X \circ Y)$ denote DNA double helix and $(U \circ V)$ to a pair of codon and anticodon assumed to be connected by a long flux tube (this should be a testable prediction). Replication of DNA would correspond to $(X \circ Y) + (U \circ V) \to X \circ U \to Y \circ V$ with reconnection taking place for the flux tubes.

With the same conventions the transcription of dark DNA to ordinary DNA and vice versa would correspond to a process $dX \circ dY + U + V \to dX \circ U \to V \circ dY$ giving rise to ordinary-dark DNA double strand. This process would be followed by $(dX \circ U) + (dV \circ Y) \to dX \circ dV \to U \circ Y$ proceeding like DNA replication.

2.3.2 $DNA \to mRNA$ transcription

Let $X \circ Y$ denote DNA double helix in the sequel. For Option I the transcription process would occur in straightforward manner by the transformation of double connection between X and Y to loops and the reconnection of loop associated with Y with that assignable to $mRNA$ codon followed by $\hbar$ reducing phase transition leading to a generation of DNA and mRNA sequences with nucleotides connected by flux tube pairs. The third step would be reconnection transforming double flux tube bonds between DNA and mRNA nucleotides to loops.

Consider next Option II:

1. Let $U \circ V$ denote mRNA-cmRNA that is pair of mRNA codon and its conjugate assumed to be connected by a long flux tube. Ordinary transcription $DNA \to mRNA$ could correspond to the $(X \circ Y) + (U \circ V) \to X \circ U \to Y \circ V$ followed by its reversal but mRNAs arranged to a sequence. Note that every mRNA would have long flux tube connection with the conjugate mRNA.

2. Let $U \circ V$ could denote mRNA-dcmRNA. The same process would give mRNA sequence with each codon connected by a long flux tube to dcmRNA codon.

3. For a third realization $U - V$ would denote the pair $mRNA - dtRNA$. The same process as above would give mRNA sequence with each mRNA codon connected by a long flux tube to $dtRNA$ anticodon.

This process has also variants allowing to assign mRNA to dDNA and to DNA dmRNA.

2.3.3 Translation as a sequence of reconnections

For Option I the description of translation should be obvious on basis of previous examples. For Option II translation could be realized as a sequence of reconnections in several manners. The basic idea is that the reconnections and their reversals transform the tRNA_1-AA pairs with $tRNA_1$ denotes $tRNA$ without amino-acid AA to a sequence of them but $tRNA_1$ connected to amino-acid by a long flux tube. In the decay of the amino-acid this long tRNA would reduce to ordinary tRNA: this serves as a killer prediction.

For instance, let $X - Y = mRNA - dmRNA$ mRNA sequence with dark mRNA codons connected to mRNA codons and let $U - V = tRNA_1 - AA$ denote tRNA. Reconnection would allow to arrange tRNAs to sequence of "long" tRNAs while keeping $X - Y$ as such. One could also replace Y by $dtRNA$. Obviously the process has several variants. When amino-acid sequence decays ordinary "short" tRNAs are formed again. Also the translation of dark mRNA to ordinary amino-acid sequence with long flux tubes to either dark tRNA or ordinary tRNA.

3 DNA as topological quantum computer: realization of the genetic code in terms of quarks and anti-quarks

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Large values of Planck constant makes possible all kinds of quantum computations [23, 24, 25, 26]. What makes topological quantum computation (tqc) [27, 29, 28, 30, 31] so attractive is that the computational operations are very robust and there are hopes that external perturbations do not spoil the quantum coherence in this case. The basic problem is how to create, detect, and control the dark matter with large $\hbar$. The natural looking strategy would be to assume that living matter, say a system consisting of DNA and cell membranes, performs tqc and to look for consequences.

There are many questions. How the tqc could be performed? Does tqc hypothesis might allow to understand the structure of living cell at a deeper level? What does this hypothesis predict about DNA itself? One of the challenges is to fuse the vision about living system as a conscious hologram with the DNA as tqc vision. The experimental findings of Peter Gariaev [43, 42] might provide a breakthrough in this respect. In particular, the very simple experiment in which one irradiates DNA sample using ordinary light in UV-IR range and photographs the scattered light seems to allow an interpretation as providing a photograph of magnetic flux tubes containing dark matter. If this is really the case, then the bottle neck problem of how to make dark matter visible and how to manipulate it would have been resolved in principle. The experiment of Gariaev and collaborators [42] also show that the photographs are obtained only in the presence of DNA sample. This leaves open the question whether the magnetic flux tubes associated with instruments are there in absence of DNA and only made visible by DNA or generated by the presence of DNA.

3.1 Basic ideas of tqc

The basic idea of topological quantum computation (tqc) is to code tqc programs to braiding patterns (analogous to linking and knotting). A nice metaphor for tqc is as dance. Dancing pattern in time direction defines the tqc program. This kind of patterns are defined by any objects moving around so that the Universe might be performing topological quantum computation like activities in all scales.

One assigns to the strands of the braid elementary particles. The S-matrix coding for tqc is determined by purely topological consideration as a representation for braiding operation. It is essential that the particles are in anyonic phase: this means in TGD framework that the value of Planck constant differs from its standard value. Tqc as any quantum computation halts in state function reduction which corresponds to the measurement of say spins of the particles involved.

As in the case of ordinary computers one can reduce the hardware to basic gates. The basic 2-gate is represented by a purely topological operation in which two neighboring braid strands are twisted by π. 1-particle gate corresponds to a phase multiplication of the quantum state associated with braid strand. This operation is not purely topological and requires large Planck constant to overcome the effects of thermal noise.

In TGD framework tqc differs somewhat from the ordinary one.

1. Zero energy ontology means that physical states decompose into pairs of positive and negative energy states at boundaries of causal diamond formed by future and past directed lightcones containing the particles at their light-like boundaries. The interpretation is as an event, say particle scattering, in positive energy ontology. The time like entanglement coefficients define S-matrix, or rather M-matrix, and this matrix can be interpreted as coding for physical laws in the structure of physical state as quantum superposition of statements "A implies B" with A and B represented as positive and negative energy parts of quantum state. The halting of topological quantum computation would select this kind of statement.

2. The new view about quantum state as essentially 4-D notion implies that the outcome of tqc is expressed as a four-dimensional pattern at space-time sheet rather than as time=constant final state. All kinds of patterns would provide a representation of this kind. In particular, holograms formed by large $\hbar$ photons emitted by Josephson currents, including EEG as a special case, would define particular kind of representation of outcome.

3.2 Identification of hardware of tqc and tqc programs

One challenge is to identify the hardware of tqc and realization of tqc programs.

1. Living cell is an excellent candidate in this respect. The lipid layers of the cell membrane is 2-D liquid crystal and the 2-D motion of lipids would define naturally the braiding if the lipids are connected to DNA nucleotides. This motion might be induced by the self organization patterns of metabolically driven liquid flow in the vicinity of lipid layer both in interior and exterior of cell membrane and thus self-organization patters of the water flow would define the tqc programs.

2. This identification of braiding implies that tqc as dancing pattern is coded automatically to memory in the sense that lipids connected to nucleotides are like dancers whose feet are connected to the wall of the dancing hall define automatically space-like braiding as the threads connected to their feet get braided. This braiding would define universal memory realized not only as tissue memory but related also to water memory [L7].

3. It is natural to require that the genetic code is somehow represented as property of braids strands. This is achieved if strands are "colored" so that A,T,C,G correspond to four different "colors". This leads to the hypothesis that flux tubes assignable to nucleotides are wormhole magnetic flux tubes such that the ends of the two sheets carry quark and anti-quark (*resp.* anti-quark and quark) quantum numbers. This gives mapping A,T,C,G to u, u_c, d, d_c. These quarks are not ordinary quarks but their scaled variants predicted by the fractal hierarchy of color and electro-weak physics. Chiral selection in living matter could be explained by the hierarchy of weak physics. The findings of topologist Barbara Shipman about mathematical structure of honeybee dance led her to proposed that the color symmetries of quarks are in some mysterious manner involved with honeybee cognition and this model would justify her intuition [22].

4. One should identify the representation of qubit. Ordinary spin is not optimal since the representation of 1-gates would require a modification of direction of magnetic field in turn requiring modification of direction of flux tubes. A more elegant representation is based on quark color which means effectively 3-valued logic: true, false, and undefined, also used in ordinary computers and is natural in a situation in which information is only partial. In this case 1-gates would correspond to color rotations for space-time sheets requiring no rotation of the magnetic field.

In this framework genes define the hardware of tqc rather than genetic programs. This means that the evolution takes place also at the level of tqc programs meaning that strict genetic determinism fails. There are also good reasons to believe that these tqc programs can be inherited to some degree. This could explain the huge differences between us and our cousins in spite of almost the identical genetic codes and explains also cultural evolution and the observation that our children seem to learn more easily those things that we have already learned [44]. It must be added that DNA as tqc paradigm seems to generalizedDNA, lipids, proteins, water molecules,... can have flux tubes connecting them together and this is enough to generate braidings and tqc programs. Even water could be performing simple tqc or at least building memory representations based on braiding of flux tubes connecting water molecules.

3.3 How much tqc resembles ordinary computation?

If God made us to his own image one can ask whether we made computers images of ourselves in some respects. Taking this seriously one ends up asking whether facts familiar to us from ordinary computers and world wide web might have counterparts in DNA as tqc paradigm.

1. Can one identify program files as space-like braiding patterns. Can one differentiate between program files and data files?

2. In ordinary computers electromagnetic signalling is in key role. The vision about living matter as conscious holograms suggests that this is the case also now. In particular, the idea that entire biosphere forms a tqc web communicating electromagnetically information and control signals looks natural. Topological light rays (MEs) make possible precisely targeted communications with light velocity without any change in pulse shape. Gariaev's findings [43] that the irradiation

of DNA by laser light induces emission of radio wave photons having biological effects on living matter at distances of tens of kilometers supports this kind of picture. Also the model of EEG in which the magnetic body controls the biological body also from astrophysical distances conforms with this picture.

3. The calling of computer programs by simply clicking the icon or typing the name of program followed by return is an extremely economic manner to initiate complex computer programs. This also means that one can construct arbitrarily complex combinations from given basic modules and call this complex by a single name if the modules are able to call each other. This kind of program call mechanism could be realized at the level of tqc by DNA. Since the intronic portion of genome increases with the evolutionary level and is about 98 per cent for humans, one can ask whether introns would contain representations for names of program modules. If so, introns would express themselves electromagnetically by transcribing the nucleotide to a temporal pattern of electromagnetic radiation activating desired subprogram call, presumably the conjugate of intronic portion as DNA sequence. A hierarchical sequence of subprogram calls proceeding downwards at intronic level and eventually activating the tqc program leading to gene expression is suggestive.

   Gariaev [43] has found that laser radiation scattering from given DNA activates only genomes which contain an address coded as temporal pattern for the direction of polarization plane. If flux tubes are super-conducting and there is strong parity breaking (chiral selection) then Faraday rotation for photons traveling through the wormhole flux tube code nucleotide to an angle characterizing the rotation of polarization plane. User id and password would be kind of immune system against externally induced gene expression.

4. Could nerve pulses establish only the connection between receiver and sender neurons as long magnetic flux tubes? Real communication would take place by electromagnetic signals along the flux tube, using topological light ray (ME) attached to flux tube, and by entanglement. Could neural transmitters specify which parts of genomes are in contact and thus serve as a kind of directory address inside the receiving genome?

3.4 Basic predictions of DNA as tqc hypothesis

DNA as tqc hypothesis leads to several testable predictions about DNA itself.

3.4.1 Anomalous em charge

The model for DNA as tqc assigns to flux tubes starting from DNA an anomalous em charge. This means that the total charge of DNA nucleotide using e as unit is $Q = -2+Q(q)$, where -2 is the charge of phosphate group and $Q(q) = -/+2/3, +/-1/3$ is the electromagnetic charge of quark associated with "upper" sheet of wormhole magnetic flux tube. If the phosphate group is not present one has $Q = Q(q)$. In the presence of phosphate bonds the anomalous charge makes possible the coding of nucleotides to the rotation of angle of polarization plane resulting as photon travels along magnetic flux tube. The anomalous em charge should be visible as an anomalous voltage created by DNA. It would be relatively easy to test this prediction by using various kinds of DNA:s.

3.4.2 Does breaking of matter antimatter and isospin symmetries happen at the level of DNA and mRNA?

The nice feature of the model is that it allows to interpret the slightly broken A-G and T-C symmetries of genetic code with respect to the third nucleotide Z of codon XYZ in terms of the analog of strong isospin symmetry at quark level at wormhole magnetic flux tubes. Also matter-antimatter dichotomy has a chemical analog in the sense that if the letter Y of codon corresponds to quark u, d (anti-quark u_c, d_c), the codon codes for hydrophobic (hydrophilic) amino-acid. It is also known that the first letter X of the codon codes for the reaction path leading from a precursor to an amino-acid. These facts play a key role in the model for code of protein folding and catalysis. The basic assumption generalizing base pairing for DNA nucleotides is that wormhole flux tubes can connect an amino-acid inside protein only to molecules (amino-acids, DNA, mRNA, or tRNA) for which Y letter is conjugate to that associated with the amino-acid. This means that the reduction of Planck constant leading to

the shortening of the flux tube can bring only these amino-acids together so that only these molecules can find each other in biocatalysis: this would mean kind of code of bio-catalysis.

The fact that matter-antimatter and isospin symmetries are broken in Nature suggests that the same occurs at the level of DNA for quarks and anti-quarks coding for nucleotides. One would expect that genes and other parts of genome differ in the sense that the anomalous em charge, isospin, and net quark number (vanishes for matter antimatter symmetric situation) differ for them. From Wikipedia [41] one learns that there are rules about distribution of nucleotides which cannot be understood on basis of chemistry. The rules could be understood in terms of new physics. Chargaff's rules state that these symmetries hold true in one per cent approximation at the level of entire chromosomes. Szybalski's rules [41] state that they fail for genes. There is also a rule stating that in good approximation both strands contain the same portion of DNA transcribed to mRNA. This implies that at mRNA level the sign of matter antimatter asymmetry is always the same: this is analogous to the breaking of matter antimatter asymmetry in cosmology (only matter is observed).

It would be interesting to study systematically the breaking of these symmetries for a sufficiently large sample of genes and also other in parts of genome where a compensating symmetry breaking must occur. that the irradiation of DNA by laser light induces emission of radio wave photons having biological effects on living matter at distances of tens of kilometers supports this kind of picture. Also the model of EEG in which magnetic body controls biological body from astrophysical distances conforms with this picture.

4 Realization of genetic code in terms of dark baryons

Either dark baryon code or code based on u,d and their anti-quarks could be involved with various pairings. For dark baryon code DNA would not decompose into codons. For latter code this would be the case. One could also consider the possibility that the regions genes realized the dark baryon code and the regions between them are realized in terms of ududbardbar code. The latter code could be also involved with tqc.

4.1 Dark nuclear strings as analogs of DNA-, RNA- and amino-acid sequences and baryonic realization of genetic code?

Water memory is one of the ugly words in the vocabulary of a main stream scientist. The work of pioneers is however now carrying fruit. The group led by Jean-Luc Montagnier, who received Nobel prize for discovering HIV virus, has found strong evidence for water memory and detailed information about the mechanism involved [32, L6, K5, F9]. The work leading to the discovery was motivated by the following mysterious finding. When the water solution containing human cells infected by bacteria was filtered in purpose of sterilizing it, it indeed satisfied the criteria for the absence of infected cells immediately after the procedure. When one however adds human cells to the filtrate, infected cells appear within few weeks. If this is really the case and if the filter does what it is believed to do, this raises the question whether there might be a representation of genetic code based on nano-structures able to leak through the filter with pores size below 200 nm.

The question is whether dark nuclear strings might provide a representation of the genetic code. In fact, I posed this question year before the results of the experiment came with motivation coming from attempts to understand water memory. The outcome was a totally unexpected finding: the states of dark nucleons formed from three quarks can be naturally grouped to multiplets in one-one correspondence with 64 DNAs, 64 RNAS, and 20 amino-acids and there is natural mapping of DNA and RNA type states to amino-acid type states such that the numbers of DNAs/RNAs mapped to given amino-acid are same as for the vertebrate genetic code.

The basic idea is simple. Since baryons consist of 3 quarks just as DNA codons consist of three nucleotides, one might ask whether codons could correspond to baryons obtained as open strings with quarks connected by two color flux tubes. This representation would be based on entanglement rather than letter sequences. The question is therefore whether the dark baryons constructed as string of 3 quarks using color flux tubes could realize 64 codons and whether 20 amino-acids could be identified as equivalence classes of some equivalence relation between 64 fundamental codons in a natural manner.

The following model indeed reproduces the genetic code directly from a model of dark neutral baryons as strings of 3 quarks connected by color flux tubes.

1. Dark nuclear baryons are considered as a fundamental realization of DNA codons and constructed as open strings of 3 dark quarks connected by two colored flux tubes, which can be also charged. The baryonic strings cannot combine to form a strictly linear structure since strict rotational invariance would not allow the quark strings to have angular momentum with respect to the quantization axis defined by the nuclear string. The independent rotation of quark strings and breaking of rotational symmetry from SO(3) to SO(2) induced by the direction of the nuclear string is essential for the model.

   Baryonic strings could form a helical nuclear string (stability might require this) locally parallel to DNA, RNA, or amino-acid) helix with rotations acting either along the axis of the DNA or along the local axis of DNA along helix. The rotation of a flux tube portion around an axis parallel to the local axis along DNA helix requires that magnetic flux tube has a kink in this portion. An interesting question is whether this kink has correlate at the level of DNA too. Notice that color bonds appear in two scales corresponding to these two strings. The model of DNA as topological quantum computer [L5] allows a modification in which dark nuclear string of this kind is parallel to DNA and each codon has a flux tube connection to the lipid of cell membrane or possibly to some other bio-molecule.

2. The new element as compared to the standard quark model is that between both dark quarks and dark baryons can be charged carrying charge $0, \pm 1$. This is assumed also in nuclear string model and there is empirical support for the existence of exotic nuclei containing charged color bonds between nuclei.

3. The net charge of the dark baryons in question is assumed to vanish to minimize Coulomb repulsion:

$$\sum_q Q_{em}(q) = -\sum_{flux\ tubes} Q_{em}(flux\ tube) \ . \tag{4.1}$$

   This kind of selection is natural taking into account the breaking of isospin symmetry. In the recent case the breaking cannot however be as large as for ordinary baryons (implying large mass difference between Δ and nucleon states).

4. One can classify the states of the open 3-quark string by the total charges and spins associated with 3 quarks and to the two color bonds. Total em charges of quarks vary in the range $Z_B \in \{2, 1, 0, -1\}$ and total color bond charges in the range $Z_b \in \{2, 1, 0, -1, -2\}$. Only neutral states are allowed. Total quark spin projection varies in the range $J_B = 3/2, 1/2, -1/2, -3/2$ and the total flux tube spin projection in the range $J_b = 2, 1, -1, -2$. If one takes for a given total charge assumed to be vanishing one representative from each class (J_B, J_b), one obtains $4 \times 5 = 20$ states which is the number of amino-acids. Thus genetic code might be realized at the level of baryons by mapping the neutral states with a given spin projection to single representative state with the same spin projection. The problem is to find whether one can identify the analogs of DNA, RNA and amino-acids as baryon like states.

4.1.1 States in the quark degrees of freedom

One must construct many-particle states both in quark and flux tube degrees of freedom. These states can be constructed as representations of rotation group SU(2) and strong isospin group SU(2) by using the standard tensor product rule $j_1 \times j_2 = j_1 + j_2 \oplus j_1 + j_2 - 1 \oplus ... \oplus |j_1 - j_2|$ for the representation of SU(2) and Fermi statistics and Bose-Einstein statistics are used to deduce correlations between total spin and total isospin (for instance, $J = I$ rule holds true in quark degrees of freedom). Charge neutrality is assumed and the breaking of rotational symmetry in the direction of nuclear string is assumed.

Consider first the states of dark baryons in quark degrees of freedom.

1. The tensor product $2 \otimes 2 \otimes 2$ is involved in both cases. Without any additional constraints this tensor product decomposes as $(3 \oplus 1) \otimes 2 = 4 \oplus 2 \oplus 2$: 8 states altogether. This is what one should have for DNA and RNA candidates. If one has only identical quarks *uuu* or *ddd*,

Pauli exclusion rule allows only the 4-D spin 3/2 representation corresponding to completely symmetric representation -just as in standard quark model. These 4 states correspond to a candidate for amino-acids. Thus RNA and DNA should correspond to states of type uud and ddu and amino-acids to states of type *uuu* or ddd. What this means physically will be considered later.

2. Due to spin-statistics constraint only the representations with $(J, I) = (3/2, 3/2)$ (Δ resonance) and the second $(J, I) = (1/2, 1/2)$ (proton and neutron) are realized as free baryons. Now of course a dark -possibly p-adically scaled up - variant of QCD is considered so that more general baryonic states are possible. By the way, the spin statistics problem which forced to introduce quark color strongly suggests that the construction of the codons as sequences of 3 nucleons - which one might also consider - is not a good idea.

3. Second nucleon like spin doublet - call it 2_{odd} - has wrong parity in the sense that it would require $L = 1$ ground state for two identical quarks (*uu* or *dd* pair). Dropping 2_{odd} and using only $4 \oplus 2$ for the rotation group would give degeneracies $(1, 2, 2, 1)$ and 6 states only. All the representations in $4 \oplus 2 \oplus 2_{odd}$ are needed to get 8 states with a given quark charge and one should transform the wrong parity doublet to positive parity doublet somehow. Since open string geometry breaks rotational symmetry to a subgroup SO(2) of rotations acting along the direction of the string and since the boundary conditions on baryonic strings force their ends to rotate with light velocity, the attractive possibility is to add a baryonic stringy excitation with angular momentum projection $L_z = -1$ to the wrong parity doublet so that the parity comes out correctly. $L_z = -1$ orbital angular momentum for the relative motion of *uu* or *dd* quark pair in the open 3-quark string would be in question. The degeneracies for spin projection value $J_z = 3/2, ..., -3/2$ are $(1, 2, 3, 2)$. Genetic code means spin projection mapping the states in $4 \oplus 2 \oplus 2_{odd}$ to 4.

4.1.2 States in the flux tube degrees of freedom

Consider next the states in flux tube degrees of freedom.

1. The situation is analogous to a construction of mesons from quarks and anti-quarks and one obtains the analogs of π meson (pion) with spin 0 and ρ meson with spin 1 since spin statistics forces $J = I$ condition also now. States of a given charge for a flux tube correspond to the tensor product $2 \otimes 2 = 3 \oplus 1$ for the rotation group.

2. Without any further constraints the tensor product $3 \otimes 3 = 5 \oplus 3 \oplus 1$ for the flux tubes states gives 8+1 states. By dropping the scalar state this gives 8 states required by DNA and RNA analogs. The degeneracies of the states for DNA/RNA type realization with a given spin projection for $5 \oplus 3$ are $(1, 2, 2, 2, 1)$. $8\times$ 8 states result altogether for both *uud* and *udd* for which color bonds have different charges. Also for *ddd* state with quark charge -1 one obtains $5 \oplus 3$ states giving 40 states altogether.

3. If the charges of the color bonds are identical as the are for *uuu* type states serving as candidates for the counterparts of amino-acids bosonic statistics allows only 5 states ($J = 2$ state). Hence 20 counterparts of amino-acids are obtained for *uuu*. Genetic code means the projection of the states of $5 \oplus 3$ to those of 5 with the same spin projection and same total charge.

4.1.3 Analogs of DNA,RNA, amino-acids, and of translation and transcription mechanisms

Consider next the identification of analogs of DNA, RNA and amino-acids and the baryonic realization of the genetic code, translation and transcription.

1. The analogs of DNA and RNA can be identified dark baryons with quark content *uud*, *ddu* with color bonds having different charges. There are 3 color bond pairs corresponding to charge pairs $(q_1, q_2) = (-1, 0), (-1, 1), (0, 1)$ (the order of charges does not matter). The condition that the total charge of dark baryon vanishes allows for *uud* only the bond pair $(-1, 0)$ and for *udd* only the pair $(-1, 1)$. These thus only single neutral dark baryon of type *uud resp. udd*: these would

be the analogous of DNA and RNA codons. Amino-acids would correspond to uuu states with identical color bonds with charges $(-1,-1)$, $(0,0)$, or $(1,1)$. uuu with color bond charges (-1,-1) is the only neutral state. Hence only the analogs of DNA, RNA, and amino-acids are obtained, which is rather remarkable result.

2. The basic transcription and translation machinery could be realized as processes in which the analog of DNA can replicate, and can be transcribed to the analog of mRNA in turn translated to the analogs of amino-acids. In terms of flux tube connections the realization of genetic code, transcription, and translation, would mean that only dark baryons with same total quark spin and same total color bond spin can be connected by flux tubes. Charges are of course identical since they vanish.

3. Genetic code maps of $(4 \oplus 2 \oplus 2) \otimes (5 \oplus 3)$ to the states of 4×5. The most natural map takes the states with a given spin to a state with the same spin so that the code is unique. This would give the degeneracies $D(k)$ as products of numbers $D_B \in \{1,2,3,2\}$ and $D_b \in \{1,2,2,2,1\}$: $D = D_B \times D_b$. Only the observed degeneracies $D = 1,2,3,4,6$ are predicted. The numbers $N(k)$ of amino-acids coded by D codons would be

$$[N(1),N(2),N(3),N(4),N(6)] = [2,7,2,6,3] \ .$$

The correct numbers for vertebrate nuclear code are $(N(1),N(2),N(3),N(4),N(6)) = (2,9,1,5,3)$. Some kind of symmetry breaking must take place and should relate to the emergence of stopping codons. If one codon in second 3-plet becomes stopping codon, the 3-plet becomes doublet. If 2 codons in 4-plet become stopping codons it also becomes doublet and one obtains the correct result $(2,9,1,5,3)$!

4. Stopping codons would most naturally correspond to the codons, which involve the $L_z = -1$ relative rotational excitation of uu or dd type quark pair. For the 3-plet the two candidates for the stopping codon state are $|1/2,-1/2\rangle \otimes \{|2,k\rangle\}$, $k = 2,-2$. The total spins are $J_z = 3/2$ and $J_z = -7/2$. The three candidates for the 4-plet from which two states are thrown out are $|1/2,-3/2\rangle \otimes \{|2,k\rangle,|1,k\rangle\}$, $k = 1,0,-1$. The total spins are now $J_z = -1/2,-3/2,-5/2$. One guess is that the states with smallest value of J_z are dropped which would mean that $J_z = -7/2$ states in 3-plet and $J_z = -5/2$ states 4-plet become stopping codons.

5. One can ask why just vertebrate code? Why not vertebrate mitochondrial code, which has unbroken $A-G$ and $T-C$ symmetries with respect to the third nucleotide. And is it possible to understand the rarely occurring variants of the genetic code in this framework? One explanation is that the baryonic realization is the fundamental one and biochemical realization has gradually evolved from non-faithful realization to a faithful one as kind of emulation of dark nuclear physics. Also the role of tRNA in the realization of the code is crucial and could explain the fact that the code can be context sensitive for some codons.

If the pairing is based on the assumption that total quark spins and total flux tube spins are identical, the pairing of dark variants of DNA and its conjugate and DNA and mRNA are are not unique at the level of dark matter but respect the genetic code. Divisor code to be discussed later and equivalent with dark baryon code in realization based on magnetic flux tubes predicts similar non-uniqueness.

4.1.4 Is the genetic code a composite of $64 \to 40$ and $40 \to 20$ codes?

As found, dark baryon counterpart of tRNA could correspond to the multiplet of states containing 40 states. According to [33] most organisms have fewer the 45 species of tRNA. Typical value of anticodons is around 30 and in some organisms the number is as low as 22. This means that the number of different anticodons in tRNA is not larger than 45 and could be at most 40. Unfortunately I do not know what the real situation is. The realization of mRNA-tRNA pairing is known to be based on wobble base pairing [33]. This means that the pairing is not unique for the third nucleotide of the anticodon so that all mRNA codons can pair with tRNA in a manner consistent with the genetic code.

This finding suggests that tRNA could correspond to a 40-plet of anticodons at the level of dark matter then for tRNA-amino-acid genetic code the numbers of codons $N(k)$ with given degeneracy k would be $(N(1), N(2), N(3)) = \{5, 10, 5\}$. The interpretation would be as $DNA \to tRNA$ dark baryon genetic code projection of states of $4 \oplus 2 \oplus 2$ to states of 4 with the same spin in color bond degrees of freedom to a state with same spin in $J = 2$ multiplet with 5 states. Numbers of dark aminocids with given degeneracy k would $(N(1), N(2)) = \{16, 24\}$. Ordinary genetic code would result as a composite of the projections associated with these codes. If the identification in terms of 40-plet makes sense one might consider the possibility that the evolution for tRNA-dtRNA correspondence has not yet achieved the ideal situation in which tRNA anti-codons would be in 1-1 correspondence with their dark counterparts.

4.1.5 Objections

Consider next some particle physicist's objections against this picture.

1. The realization of the code requires the dark scaled variants of spin 3/2 baryons known as Δ resonance and the analogs (and only the analogs) of spin 1 mesons known as ρ mesons. The lifetime of these states is very short in ordinary hadron physics. Now one has a scaled up variant of hadron physics: possibly in both dark and p-adic senses with latter allowing arbitrarily small overall mass scales. Hence the lifetimes of states can be scaled up.

2. Both the absolute and relative mass differences between Δ and N *resp.* ρ and π are large in ordinary hadron physics and this makes the decays of Δ and ρ possible kinematically. This is due to color magnetic spin-spin splitting proportional to the color coupling strength $\alpha_s \sim .1$, which is large. In the recent case α_s could be considerably smaller - say of the same order of magnitude as fine structure constant 1/137 - so that the mass splittings could be so small as to make decays impossible.

3. Dark hadrons could have lower mass scale than the ordinary ones if scaled up variants of quarks in p-adic sense are in question. Note that the model for cold fusion that inspired the idea about genetic code requires that dark nuclear strings have the same mass scale as ordinary baryons. In any case, the most general option inspired by the vision about hierarchy of conscious entities extended to a hierarchy of life forms is that several dark and p-adic scaled up variants of baryons realizing genetic code are possible.

4. A heavy objection relates to the addition of $L_z = -1$ excitation to $S_z = |1/2, \pm 1/2\rangle_{odd}$ states which transforms the degeneracies of the quark spin states from $(1, 3, 3, 1)$ to $(1, 2, 3, 2)$. The most plausible answer is that the breaking of the full rotation symmetry induced by nuclear string reduces $SO(3)$ to $SO(2)$. Also the fact that the states of massless particles are labeled by the representation of $SO(2)$ might be of some relevance.

The conclusion is that genetic code can be understand as a map of stringy baryonic states induced by the projection of all states with same spin projection to a representative state with the same spin projection. Genetic code would be realized at the level of dark nuclear physics and biochemical representation would be only one particular higher level representation of the code. A hierarchy of dark baryon realizations corresponding to p-adic and dark matter hierarchies can be considered. Translation and transcription machinery would be realized by flux tubes connecting only states with same quark spin and flux tube spin. Charge neutrality is essential for having only the analogs of DNA, RNA and amino-acids and would guarantee the em stability of the states.

4.2 DNA as tqc hypothesis and dark baryon code

The coding of DNA codons by assigning to A,G *resp.* T,C of u and d quarks *resp.* their anti-quarks works nicely in the model of DNA as topological quantum computer. One can however consider also the option for which dark baryons code for entire DNA codons.

1. DNA as tqc using dark baryons to represent DNA codons would require that DNA strand is accompanied by a nuclear string parallel to it. If the pairing of baryons at the ends of string requires only opposite total quark spins and total flux tube spins the map would obey genetic

code rather than being 1-1. The situation changes if dark baryon states are in 1-1 correspondence with the integers (n_a, n_b) labeling the page of book at which magnetic body of the codon resides.

2. The condition that the other end of flux tube beginning from the DNA codon contains nuclear string made from anti-baryons is natural but matter antimatter asymmetry if present also for dark matter does not favor this while mesonic strings with quarks at their ends are natural.

3. Rotating kinks assignable to 16 codons might be problematic from the point of tqc unless they represent codons with some special significance and play some special role - perhaps representing control commands in tqc program.

4. The flux tubes assignable to codons -instead of nucleotides as for earlier realization - would be basic units connected to lipids. The entanglement between dark baryon states of dark nuclear string would replaced the entanglement between quarks and anti-quarks at the ends of the flux tubes.

5. Only the portions of DNA having interpretation as gene have a natural decomposition to codons. Hence the dark baryon representation of codons is not attractive idea in intronic portions of the genome forming the most plausible candidates for quantum computing part of DNA since the portion of introns has been increasing during evolution and highest variation of this portion is encountered in human brain [36]. Hence one might think that tqc as relatively late outcome of the evolution and that only this part of genome is responsible for tqc so that the mpa of nucleotides to quarks would realize genetic code. Furthermore, braiding matters in tqc much more than the colors of braid strands determined by nucleotides so that intronic portions could quite well be repeating sequences without any obvious as information carriers in standard sense and therefore interpreted as junk DNA. There would be also an analogy between emergence of written language meaning that words as holistic entities were replaced with sequences of letters having as such no meaning.

5 Flux tube realization of the divisor code

Divisor code discovered by Khrennikov and Nilsson [L10] allows a flux tube realization and a close connection with dark baryon code seems to be possible.

5.1 Divisor code

The idea of divisor code discussed in [34] is inspired by the following observations.

1. Consider the number $N(n)$ of integer divisors for integers n in the range $[1, 21]$ corresponding to amino-acids with stopping sign counted as amino-acid.

2. Denote the number of integers $n \leq 21$ for which the number of divisors is k by $B(k)$. Also stopping sign is counted as an amino-acid and $n = 0$ corresponds to amino-acid also. This number $N(k)$ varies in the range $[1, 6]$. $B(k)$ has the values $(1, 8, 2, 5, 1, 3)$ where k runs from 1 to 6.

3. Denote by $A(k)$ the number of amino-acids coded by k DNA codons. $A(k)$ has the values $2, 9, 2, 5, 0, 3$.

The spectrum of $A(k)$ is very similar to that of $B(k)$ and this raises the question whether one could understand genetic code as a divisor code in the sense that the degeneracy of amino-acid would be dictated by the number of the integers $1 \leq n \leq 21$ coding it. One might also ask whether the amino-acids which are abundant and thus important are coded by integers with a large number of divisors. Also one can ask whether the divisor structure possibly correlates with the structure of the amino-acid.

Divisor code in this form would be only approximate and one can wonder could try to imagine some simple symmetry breaking mechanism. In this respect the crucial observations might be following.

1. The number of DNAs needed to realize divisor code would be 70 instead of 64. One must drop 6 codons and by choosing them suitably one might hope of getting correct degeneracies.

2. The most natural manner to break the symmetry is to drop the 4 codons from the codons coding for 5-plet which would thus become 1-plet. 5-plet corresponds to integer $n = 16$ and its product compositions $(16, 1), (1, 16), (2, 8), (8, 2), (4, 4)$ correspond to the DNAs coding for it. $(4, 4)$ would naturally correspond to singlet.

3. By dropping 2 codons from some 4-plet one obtains 2-plet and correct degeneracies. One candidate for 4-plet corresponds to $n = 8$ and its product decompositions $(1, 8), (8, 1), (2, 4), (4, 2)$. By dropping two of these one obtains correct degeneracies. It might that power of 2 property of $n = 8$ and $n = 16$ somehow relates to 2-adicity and to the special role of these amino-acids.

4. A possible interpretation is in terms of symmetry based on cyclic group $Z(n)$ serving as a symmetry of DNA codons coding for amino-acid labeled n. Z_n allows decompositions $Z_n = Z_{n_1} \times Z_{n_2}$, $n = n_1 \times n_2$ and if the representations are invariant under Z_{n_2} and thus reduce to those of Z_{n_1} codons coding for a given amino-acid correspond to the product decompositions. Symmetry breaking would be due to the lacking 6 codons and would mean that only Z_4 invariant states would be realized for Z_{16} and Z_1 and Z_8 of Z_2 and Z_4 invariant states are realized for $n = 8$. $n = 4$ could correspond to triplet of stopping codons so that powers of 2 would be in special role for vertebrate code suggesting 4-adicity. 4-adicity is also suggests by the almost exact A-G and T-C symmetries of the last nucleotide.

5.2 Topological interpretation of the divisor code in TGD framework

The most concrete physical interpretation of the divisor code found in TGD framework is topological and based on TGD inspired vision about the role of dark matter in biology [L10].

1. The generalized 8-D imbedding space has a book like structure with pages glued together along back which is 4-D surface of $H = M^4 \times CP_2$ [C3, C4]. Particles at different pages are dark relative to each other since they cannot have local interactions (appear in the same vertex of Feynman diagram). The pages are partially characterized by the value of Planck constant which can be arbitrary large. This explains the macroscopic quantum coherence of living matter. Matter can leak between different pages meaning a phase transition changing Planck constant.

2. The notion of magnetic body with flux tubes carrying dark matter and connecting different bio-molecules central for the TGD inspired model of living matter [L5]. Magnetic bodies of bio-molecules can be also connected by magnetic flux tubes, even those in different pages of the book. For instance, the phase transition reducing $\hbar$ reduces the distance between two bio-molecules connected in this manner and forces them near to each other. This explains the extreme selectivity of bio-catalysis and the miraculous ability of two bio-molecules to find each other in the dense soup of bio-molecules. In particular, DNA and its conjugate codons, mRNA codons, and tRNA would be connected by this kind of flux tubes. Also amino-acids would be connected to tRNA codons in this manner since tRNA molecules catch the amino-acids and bring them to the mRNA-amino-acid translation site. Genetic code could reduce to the selection rules for the flux tube connections connecting in general situation magnetic bodies belonging to different pages of the book.

3. The pages of book are almost copies of $M^4 \times CP_2$. This means that M^4 is replaced with n_a-fold singular covering and CP_2 with n_b-fold singular covering. The coverings have cyclic groups Z_{n_a} and Z_{n_b} act as discrete symmetries for the wave functions of particles in the covering. A given page is thus labeled by two pager numbers (n_a, n_b). Two pages contain common points and thus a direct tunneling of 3-surfaces between these pages is possible only if the number n_{a_1} of the sheets of covering divides n_{a_2} or vice versa. Same holds true for n_{b_1} and n_{b_2}. This rule is just the basic rule about how symmetries of system can change in phase transition. This number theoretic rule could be behind genetic code and the extreme selectivity of bio-catalysis.

4. Suppose that both bio-molecules correspond to ordinary matter with $n_a = n_b = 1$ but that the magnetic body of a given amino-acid corresponds to $(n_a(A), n_b(A))$ and DNA, RNA, and tRNA codon to $(r_a(DNA), r_b(DNA))$. Since the flux tube from tRNA codon to the amino-acid page is essential for the process in which amino-acid is attached to tRNA, only tRNA for with $r_a(tRNA)$ divides $n_a(A)$ can catch an amino-acid labeled by n_a. Same applies to r_b and n_b.

5. Without the presence of the integer n_b the code would fail since DNA codon labeled by r_a would code for all amino-acids for which n_a has r_a as a factor. n_b can indeed save the situation. Suppose that one has $r_b(tRNA) = n_b(A)$ if DNA codes for an amino-acid. Assume also that $n_b(a)$ is prime: $n_b(A) = p_b(A)$, and different for each amino-acid. This prime does not correspond to p-adic prime, which is expected to be very large in the length scales of atomic physics (electron corresponds to $M_{127} = 2^{127} - 1$). Note that the assumption that amino-acids are labeled by small primes was made in both TGD inspired number theoretical models of the genetic code.

6. The assumptions mean that tRNA and amino-acid can be connected by a magnetic flux tube only if one has

$$p_b(tRNA) = p_b(A)$$

and $r_a(tRNA)$ divides $n_a(A)$. If the pages numbers n_a vary in the range $[1, 21]$ the divisor code follows from the argument of the previous section. Taking the previous argument seriously, one should also understand why there is no amino-acid labeled by $n_a = 4$ and why corresponding DNAs correspond to prime characterizing $n_a = 4$, why the number of DNA codons labeled by the factors of $n_a = 8$ is two, and why the number of codons associated with $n_a = 16$ only one.

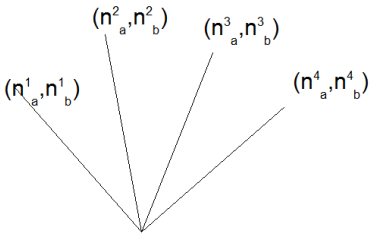

Figure 3: Illustration of the book-like structure of the generalized imbedding space.

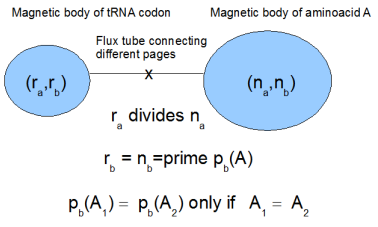

Figure 4: Illustration of the selection rules for magnetic flux tubes connecting magnetic bodies of tRNA and amino-acid.

Some further comments are in order.

1. The realization of the genetic code is not unique since the integers r_a and n_a could be replaced with Nn_a, where N is a product of primes larger than $p = 19$. It is also enough that the integers characterizing amino-acids are relative primes (have not common factors).

2. The quantum states of dark baryons realize vertebrate genetic code with very general assumptions group theoretically [L6, K5, F9]. Since dark matter is involved in both cases, one might wonder whether these codes could be related somehow. A one-one correspondence between the quantum states of dark nucleons representing codon and the integers r_a, p_b is required in order to have this connection. The simplest possibility is that that energy minimization implies that given dark nucleon resides with high probability at aflux tube labeled by unique value of r_a. Same applies to amino-acids.

3. The model in principle allows infinite number of analogous codes and an interesting question is whether the bio-catalysis involves this kind of codes.

5.3 About detailed correspondence between DNA codons, dark baryon codons, and their divisor code counterparts

One can make some conclusions also about the detailed correspondence between DNA codons and dark baryon codons as well as their divisor code counterparts. $L_z = -1$ requires that there is a rotating kink in flux tube representing nuclear string. One can ask whether also the corresponding DNA codons could be somehow special.

1. Maximal spin projections for both quarks ($J_z^q = 3/2$) and flux tube $J_z^f = \pm 2$ correspond to amino-acids met and trp coded by single codon. For the proposed interpretation of the divisor code these codons would correspond to $n = 1$ and $n = 16$.

2. Amino-acids coded by two codons correspond to $(J_z^q = 3/2, J_z^f \in \{1, 0, -1\})$ and $(J_z^q \in \{1/2, -1/2\}, J_z^f \in \{2, -2\})$. For the divisor code these amino-acids correspond to 8 primes plus lacking 9:th doublet results when one drops two codons from one 4-plet ($n = 8$ 4-plet is a good candidate).

3. For the baryonic realization 2 3-plets $J_z^q = -3/2, J_z^f \in \{2, -2\}$) contain one member corresponding to rotating kink. The first corresponds to ile and the DNA codon coding for met if T-C symmetry of the third nucleotide were exact. Second corresponds to stop codon coding for trp if T-C symmetry were exact. In divisor code triplets corresponds to $n = 4$ (stop codon?) and $n = 9$.

4. Three 6-plets correspond to $(J_z^q = -3/2, J_z \in \{1, 0, -1\}$ contain one anomalous member each and the corresponding codon would naturally belong to the doublet part of 6-plet in the code table. In divisor code 6-plets correspond to $n \in \{12, 18, 20\}$.

5. Three of the six 4-plets $(J_z^q = 1/2, -3/2, J_z \in \{1, 0, -1\}$ contain 2 anomalous members. From one 4-plet 2 codes for nothing or formally stop codon so that it becomes 2-plet: naturally these codons correspond to $L_z = -1$ and a rotating kink in the helix model of the nuclear string. From second 3-plet one $L_1 = -1$ codon would codes for nothing becoming formally stop codon and one obtains second 2-plet.

6. The only regularity which comes in mind is that the 3 anomalous 4-plets and 2 anomalous doublets could populate the lowest row of the code table. The 16 oddballs would reside at the boundaries of the code table. In divisor code these would correspond to $n \in \{6, 8, 10, 14, 15, 21\}$. Dropping from $n = 8$ 4-plet 2 codons one would obtain 5 4-plets and 9 2-plets as required. Besides this one must drop 4 codons from $n = 16$ 5-plet to get singlet. As already noticed, 2-adicity suggests that $n = 2^k$ represents something special.

6 A model for protein folding and catalytic action

It would be fascinating if the vision about the role of flux tube connections would generalize to interactions of all molecules in living matter. The mere selection rules would mean hidden simplicity behind extremely complex looking interactions in living matter. The model for protein folding and

catalytic action discussed in [L8] is the first attempt in this direction. In the following this model is briefly summarized and the improvement of the model inspired by recent considerations is suggested.

6.1 Earlier model for the folding code

The model for the evolution of the genetic code led [L7] to the idea that the folding of proteins obeys a code inherited from the genetic code. One can imagine several variants of this code. One of the is that amino-acid behaves like the conjugate Y_c of the middle nucleotide of the codon XYZ coding for it. Conjugation for amino-acids would correspond to the hydrophilic-hydrophobic dichotomy. Also catalyst action could reduce to effective base pairing in this picture chemically and at the level of quarks associated with the flux tube to matter antimatter conjugation. The guess that amino-acid and its conjugate form pairs turned out to be wrong however and after various twists and turns I ended up with the hypothesis that the amino-acid in protein behaves like Y_cZ_c where Z corresponds to third nucleotide for some codon coding for the amino-acid.

It however turned that the model as such is probably too restrictive and not fully consistent in the particular cases studied. In the following this model is discussed briefly and later an improved model for protein folding is proposed.

6.1.1 Flux tubes as correlates of directed attention at molecular level

After some trials one ends up with a general conceptualization of the situation with the identification of ("wormhole") magnetic flux tubes as correlates for attention at molecular level so that a direct connection with TGD inspired theory of consciousness emerges at quantitative level. Whether wormhole flux tubes or ordinary flux tubes are needed is not a completely settled question yet and the attribute "wormhole" will not be used in the sequel. This allows a far reaching generalization of the DNA as topological quantum computer paradigm and makes it much more detailed. The final outcome is very simple quantitative model for both protein folding and catalyst action based on minimization of energy, which seems to be consistent with basic experimental facts as well as general ideas.

6.1.2 What kind of atoms can be connected by flux tubes?

1. Hydrogen bonds play a key role in bio-catalysis but are not understood completely satisfactorily in the standard chemistry. Hence the basic question is whether hydrogen bonds can be regarded as or are accompanied by short (wormhole) magnetic flux tubes: note that the subject-object asymmetry of directed attention would correspond to donor-acceptor asymmetry of they hydrogen bond. If this is the case, the identification of the magnetic flux tube connection as a prerequisite for a hydrogen bond or as hydrogen bond becomes natural. At least the atoms able to form hydrogen bonds could form flux tube contacts so that the model would be very predictive and would conform with the known important role of hydrogen bonds in bio-catalysis.

2. The fact that hydrogen bonds connect base pairs suggests a generalization of the notion of base pairing stating that under some conditions amino-acids coded by XYZ and UY_cV can behave like base pairs. These amino-acic pairs correspond to pairs of amino-acid residues which are hydrophilic *resp*. hydrophobic and hydrophobic residue do not form hydrogen bonds in general. These flux tubes would thus be more general and in general long. The model for DNA as topological quantum computer requires this kind of flux tubes and they would in general connect atoms or molecules which act as acceptors in hydrogen bonding: O = atom in amino-acid and aromatic ring are basic examples.

3. If one assumes that both $N-H$ and $O=$ associated with the constant part of the amino-acid can act as flux tube terminals and represent Z and Y nucleotides of the codon XYZ coding for the amino-acid, one obtains $Y=Z$ pairing of $O=-O=$ flux tubes are allowed and $Y=Z_c$ pairing if only hydrogen bond like pairings are allowed.

6.1.3 Color inheritance by a reconnection of flux tubes

1. There should exist some mechanism allowing amino-acids to inherit the base pairing property from the tRNAs associated with them so that one can identify amino-acid with the middle

nucleotide of the codon coding it. If tRNA middle nucleotide is connected to $O=$ of the amino-acid, this becomes possible since the reconnection of flux tubes preserves the "color" of the flux tubes coded by (A,T,G,C) that is by the quark or anti-quark coding for the nucleotide. The temporary formation of a hydrogen bond between $N-H$ and $O=$ of two amino-acids as in the case of alpha helix would allow $N-H$ to inherit the conjugate of the color associated with $O=$. Alternative interpretation is that this hydrogen bond is possible only if the predetermined color of $N-H$ is consistent with the inherited one. The inheritance of flux tube color would be a completely general mechanism and even the donor atoms in the residues of amino-acids could inherit the color of $O=$ in this manner.

2. A possible interpretation for the fixing of the flux tube color is in terms of quantum measurement selecting one color from quantum superposition in the reconnection process. This would mean that the unitary process can bring superposition back and reconnection process can change the inherited color. The hydrogen bonds between water molecules could correspond to quantum superpositions of different colors. This superposition property might relate to the wobble base pairing phenomenon for the third nucleotide in tRNA.

6.1.4 Folding code

The identification of $N-H$ as a representation for the conjugate of the third nucleotide Z means that amino-acids would remember which codon coded them. If only hydrogen bond like flux tubes are allowed, flux tubes can connect only amino-acids satisfying $Y=Z_c$. If $=O-O=$ flux tubes are allowed $Y=Z$ rule favored by the model of DNA as topological quantum computer follows. The isospin symmetry of the third nucleotide implies that both rules are quite flexible. If one identifies hydrogen bond with flux tube ($Y(n)=Z(n+k)$) the model works badly for both options. If one assumes only that the presence of a flux tube connecting amino-acids in either direction ($Y(n)=Z(n+k)$ or $Z(n)=Y(n+k)$) is a prerequisite for the formation of hydrogen bond, the model works. $Y=Z$ rule is favored by the study of five enzymes: the possible average length of alpha helix is considerably longer than the average length of alpha helix if gene is the unique gene allowing to satisfy $Y=Z$ rule. The explicit study of alpha helices and beta sheets for these enzymes demonstrates that the failure to satisfy the condition for the existence of hydrogen bond fails rarely and at most for two amino-acids (for 2 amino-acids in single case only).

$Y=Z$ rule could mean a solution of the basic problem of proteonics: Do genes determine the folding of proteins and how this would take place? The interpretation would be that the information loss suggested by the many-to-one character of the genetic code is only apparent. The apparently lost information which corresponds to the $A-G$ and $T-C$ symmetries of the third nucleotide codes for the hydrogen bonding and hence for the folding of the protein. The model in its most stringent form is easy to kill since in the case of alpha helices and beta sheets the hydrogen bonding fixes completely the DNA sequence coding for the protein. A weaker variant of the model based on quantum variant of wobble base pairing: in this case there are no conditions on DNA sequence. It turns out that only this variant works. Hence hydrogen bonded amino-acid behave as if they were coded by the unique codon consistent with $Y=Z$ rule.

6.1.5 Quantitative model

The quantitative model relies on the assumption that the contribution of a flux tube connecting two amino-acids to the potential energy depends only on the distance between the molecules in question. The extremals of the total interaction energy are same for any choice of the potential and only the absolute minimum of the interaction energy depends on the choice of the potential. The simplest potential corresponds to harmonic oscillator potential and would explain formation of alpha helices and beta sheets and with the fact that hydrophilic and hydrophobic residues tend to have a large distance and only few flux tube contacts. For large Planck constant also long flux tubes could correspond to attractive harmonic oscillator potential. Also the contribution of other interactions between neighboring amino-acids are expected to be present but are neglected in the simplest model. The model predicts alpha helices and beta sheets, and more generally, periodic structures, as solutions to energy minimization equations.

The model fails to catch completely the basic rules of protein folding, and the predictions are not fully consistent with empirical facts in the cases studied. A model in which the hydrophilic and

hydrophobic interactions are mediated by flux tubes between magnetic bodies of the molecule and water molecule and in this manner induce long range interactions between amino-acids - somewhat like the attractive interactions of electrons with ions induce attractive interaction between the members of a Cooper pair - looks more attractive. This model is however computationally much heavier and is not discussed in [L8]. In the sequel a formulation of this model is discussed.

6.2 Hydrophily and hydrophoby number theoretically

Amino-acids can be classified to hydrophilic and hydrophobic ones whereas all DNA codons are hydrophilic. Hydrophily and hydrophoby are believed to relate to the standard chemistry alone and this might be the case. One can however just for fun ask whether hydrophily and hydrophoby could have a connection with divisor code, formation of flux tubes connecting the molecule to water molecules, and phase transitions changing the value of Planck constant and changing the length of flux tube. I have discussed this idea already in the model of protein folding [L8].

To simplify the model assume that only single dark page is associated with water molecule and labeled by (n_a^W, n_b^W). Of course, several levels characterized by different integers are also possible and this would bring in additional flexibility. Both hydrophoby and hydrophily would mean interaction mediated by the flux tubes to the magnetic body of water with the sign of the force differing for hydrophilic and hydrophobic amino-acids. There is no need to assume that quarks and anti-quarks generate the interaction. Gly for which the residue is just hydrogen atom does not allow classification as a hydrophilic or hydrophobic which would suggest that it does not have any flux tube connections with the magnetic body of the water. The interaction mediated by flux tubes between amino-acids and water molecules would be analogous to the interaction induced by the interaction between electrons and ions inducing attractive interaction between the members of Cooper pair. It would induce attractive interaction between hydrophilic amino-acids and repulsive interaction between hydrophilic and hydrophobic amino-acids favoring the formation of hydrophilic outer surfaces and hydrophobic inner surfaces.

One could understand hydrophily/hydrophoby dichotomy number theoretically for both options. The discussion of the first option makes clear that also second option is possible to realize.

1. Assume that n_a^W is divisible by all integers n_a^{DNA} associated with DNA codons and thus involves suitable powers of primes $p \leq 19$. It could contain also an integer factor which is product of primes larger than $p = 19$. This is necessary for achieving hydrophily of DNA codons.

2. Hydrophily of DNA codons also requires n_b^W must be proportional to the product of coprime integers n_b^W (primes for the simplest option) assignable to DNA codons. n_b^W could involve also a factor proportional to second integer expressible as product of primes $p > 19$. The simplest option is that this integer equals to 1.

3. For hydrophobic amino-acids integers n_b^A must be of form $mn_b^A = n_b^{DNA} m_b$ such that m_a does not divide n_b^W and n_b^W. This is enough to guarantee that magnetic flux tubes in either direction are impossible so that hydrophoby is guaranteed in the proposed sense. This definition extends also to other molecules and can be expressed in terms of the integers (n_a, n_b) labeling the magnetic body of the molecule.

4. Second option is obtained by assigning the integer m_b only to *Gly* which is neither hydrophilic nor hydrophobic.

6.3 Could there be new physics behind hydrophily and hydrophoby

One could accept just as a fact that magnetic flux tubes to the magnetic body of water mediate an interaction which is attractive or repulsive between water molecules and amino-acids and attractive between DNA molecules and water. Accepting that this induces interaction between amino-acids one could proceed to model building without any mention about TGD.

One could also try to dig deeper and ask what might be the origin of this interaction.

1. **Option I**: Could one understand the interaction in terms of phase transitions changing the Planck constant of the magnetic flux tube. The interaction would be repulsive (attractive) would result if the interaction energy increases (decreases) when Planck constant is reduced.

Magnetic interaction energy is certainly the best candidate and could also imply the equivalence of the divisor code and dark baryon code.

2. **Option II**: Could hydrophily and hydrophoby be described in terms of em interactions of quarks representing nucleotides in the model of DNA as tqc. For instance, could amino-acids and water molecules be characterized by charges which are of opposite sign for water molecules and hydrophilic molecules and of same sign for water molecules and hydrophobic molecules.

For **Option I**, which represents completely new physics (using the standards of TGD!), the situation looks promising. The magnetic interaction energy assignable to the flux tube is a function of the integers (n_a, n_b) -in particular of the Planck constant of the flux tube- and the minimization is performed by keeping the charges of the quarks possibly at its ends fixed. This new physics fits also nicely with the idea that magnetic body controls the living matter by utilizing phase transitions changing Planck constant.

What comes in mind in the case of **Option II** is that the ends of the flux tube carry opposite charges correlating with the codon coding for the amino-acid and giving rise to ordinary gauge interactions. Unfortunately this scenario does not seem to work.

1. In [L8] it was found that (denoting codons by XYZ) only $Y = A, G$ type amino-acid residue can form hydrogen bonds and is hydrophilic and thus interacts strongly with water and DNA and RNA. If water end of flux tube corresponds to anti-quarks the attractive interaction between quark and anti-quark at the ends of flux tube could relate to hydrophily. For hydrophobic amino-acids one would have interaction between identical quarks and already Fermi statistics would cause repulsion. In DNA as tqc model based on the coding of A,G and T,C in terms of quarks u,d and their anti-quarks hydrophily-hydrophoby dichotomy corresponds to matter-antimatter dichotomy for quark assigned to the ends of the flux tube. Quarks and anti-quark have opposite charges. Hence the flux tube ends of hydrophilic amino-acids could correspond to quarks and water and hydrophobic ends of flux tubes to anti-quarks. Therefore the DNA as tqc model would predict the needed behavior of the forces. In the case of Gly containing only hydrogen as residue the flux tube might be simply absent.

2. DNA codons A,T,C,G are bases and thus polar and hydrophilic. In the case of DNA charge conjugation for quarks corresponds to the puridine-pyrimidine complementarity corresponding to conjugation of nucleotides. The rule applying in the case of amino-acids would predict T,C to be hydrophobic nucleotides which does not make sense. Therefore it seems that hydrophily and hydrophoby cannot reduce to the interactions of dark quarks and that they only represent conjugation of nucleotides symbolically.

6.4 An improved model for protein folding

To begin with let us summarize some basic facts about protein folding.

1. Hydrophily and hydrophoby play a key role in protein folding and dictate to a high degree the resulting folding patterns. This suggests that one cannot neglect the role of water in the process.

2. Protein folding proceeds from short to long length scales starting with the formation of secondary structures such as alpha helices, beta sheets, and random coil portions and is followed by the formation of tertiary and higher structures.

3. The formation of hydrogen bonds is in a decisive role in the formation of secondary structures. The mechanism leading to their formation might be contraction of magnetic flux tube by a phase transition changing Planck constant.

4. The folding patterns do not depend strongly on the precise primary structure, that is precise amino-acid decomposition which suggests that instead of the detailed chemistry the forces between quarks and anti-quarks mediated by flux tubes is what matter so that hydrophily and hydrophoby would become the basic characterizers of the interaction. The phase transitions changing Planck constant would indeed represent this kind of universal interactions independent of the chemistry.

5. In the first approximation amino-acids could be labeled by a variable telling whether it is hydrophobic, hydrophilic, or neither or these (Gly). This approximation would be broken by special amino-acids which appear in edges if beta sheets (Pro) and Cys which often appear as S-S boded pair in junctions. By bringing in forces depending on the angles between tangent vectors of successive amino-acids and on amino-adics themselves this tendency could be modeled.

The earlier approach to protein folding inspired by DNA as tqc idea did not start from this picture but assumed that direct flux tube connections between amino-acids rather than the interactions induced by flux tube connections with the magnetic bodies of water molecules were responsible for the folding. The model did not lead to any spectacular results and the proposed rules were not fully consistent in the cases studied.

6.5 The model for which the magnetic body of water is involved

The improved approach to protein folding starts from the general vision about magnetic body containing dark matter as a controller of visible matter in living system. The protein and its magnetic body would be regarded as a living system in itself.

1. Magnetic body must have large number of flux tube contacts to the visible matter. An excellent candidate for the magnetic body is that assignable with water and having flux tube connections to DNA and both hydrophilic and hydrophobic amino-acids. The magnetic body could control and at least fasten the self-organization process leading to the folding pattern which - by applying standard argument - would otherwise take astronomical time otherwise. The two-step attractive connections between all hydrophilic amino-acids would be possible via the magnetic body of water. The non-hydrophilic amino-acids not in direct contact with water are known to be more like passive structural stuff responsible for a fixed structure but not so relevant for the functioning of the bio-molecule. Hydrophily and hydrophoby would reflect the dependence of interaction energy on the value of Planck constant associated with the flux tube mediating the interaction.

2. This picture implies a straightforward modification of the earlier model. The simplest model would minimize a potential function V expressible as a sum $V = V_1 + V_2 + V_3$ of three terms. V_1 would be sum of the values of a universal two-particle potential function $V_{phi,phi}(r)$ for arguments $r_{ij} = |r_i - r_j|$ varying over all hydrophilic amino-acid pairs and giving rise to an attractive force. V_2 would be a sum of a universal two-particle potential function $V_{pho,pho}(r)$ for arguments $r_{ij} = |r_i - r_j|$ varying over all hydrophobic amino-acid pairs. V_3 would be would be sum of the values of a universal potential function $V_{phi,pho}(r)$ for arguments $r_{ij} = |r_i - r_j|$ varying over all pairs of hydrophilic and hydrophobic amino-acids. This potential function would induce a repulsive force. Besides this a constraint force due to the fact that amino-acids form a sequence would be present.

3. The resultant of the forces along lines connecting amino-acids would be parallel to the amino-acid sequence in the mechanical equilibrium. Hydrogen bonds and other bonds are indeed formed between neighboring hydrophilic amino-acids and the contraction of the flux tubes connecting the amino-acids in question to the magnetic body of water could be the mechanism. The model seems to be consistent with the basic qualitative facts about folding. The quantitative testing of the model would require determination of the conformations minimizing the potential function subject to the constraint provided by amino-acid sequence. Here of course the freedom to choose the three functions provides a considerable flexibility and symmetry arguments might allow to pose conditions on the form of these functions.

4. One could also include to the potential function describing a direct interaction with water molecules depending on parameters like pH affecting the folding pattern. The resultant for a given amino-acid would be sum of forces directed from a hydrophilic amino-acids to neighboring water molecules. It is not clear whether the normal component of this force could be compensated by the induced forces between amino-acids in a typical equilibrium configuration and the formation of hydrogen bonds involving the contraction of the flux tube could be the manner to achieve this.

6.5.1 Could one regard amino-acids and DNAs of given type as analog of species?

An interesting idea raised by the work with the model for protein folding is that the magnetic bodies amino-acids or DNA codon of a given type could behave like single phase on their respective page of the book so that the mutual interactions of their magnetic bodies could affect considerably the behavior of this phase to first order although amino-acids themselves are at different positions and one might expect only small correlations between their motions. Whether the dynamics of amino-acids of given type in protein folding are strongly correlated could be tested.

In certain sense one could speak of single species formed by amino-acids of given type and folding as long range interaction could be seen as an outcome of self-organizing interaction between members of various species and between species themselves plus short range constraints due to the fact that amino-acids form a sequence. The question applies to DNA and RNA codons and also to larger units such as genes formed to which one could assign their own page of the book. Water would represent the page to which all DNAs can send flux tubes. Even the notion of biological species could involve common dark space-time sheet(s) where the magnetic bodies of the members of species are and interact making the members of species to behave like single coherent unit.

7 Appendix: Generalization of the notion of imbedding space

This section summarizes the the attempt to understand how the hierarchy of Planck constants is realized at the level of imbedding space and what quantum criticality for phase transitions changing Planck constant means.

7.1 Generalization of the notion of imbedding space

The original idea was that the proposed modification of the imbedding space could explain naturally phenomena like quantum Hall effect involving fractionization of quantum numbers like spin and charge. This does not however seem to be the case. $G_a \times G_b$ implies just the opposite if these quantum numbers are assigned with the symmetries of the imbedding space. For instance, quantization unit for orbital angular momentum becomes n_a where Z_{n_a} is the maximal cyclic subgroup of G_a.

One can however imagine of obtaining fractionization at the level of imbedding space for space-time sheets, which are analogous to multi-sheeted Riemann surfaces (say Riemann surfaces associated with $z^{1/n}$ since the rotation by 2π understood as a homotopy of M^4 lifted to the space-time sheet is a non-closed curve. Continuity requirement indeed allows fractionization of the orbital quantum numbers and color in this kind of situation.

7.1.1 Both covering spaces and factor spaces are possible

The observation above stimulates the question whether it might be possible in some sense to replace H or its factors by their multiple coverings.

1. This is certainly not possible for M^4, CP_2, or H since their fundamental groups are trivial. On the other hand, the fixing of quantization axes implies a selection of the sub-space $H_4 = M^2 \times S^2 \subset M^4 \times CP_2$, where S^2 is a geodesic sphere of CP_2. $\hat{M}^4 = M^4 \backslash M^2$ and $\hat{CP}_2 = CP_2 \backslash S^2$ have fundamental group Z since the codimension of the excluded sub-manifold is equal to two and homotopically the situation is like that for a punctured plane. The exclusion of these sub-manifolds defined by the choice of quantization axes could naturally give rise to the desired situation.

2. H_4 represents a straight cosmic string. Quantum field theory phase corresponds to Jones inclusions with Jones index $\mathcal{M} : \mathcal{N} < 4$. Stringy phase would by previous arguments correspond to $\mathcal{M} : \mathcal{N} = 4$. Also these Jones inclusions are labeled by finite subgroups of $SO(3)$ and thus by Z_n identified as a maximal Abelian subgroup.

   One can argue that cosmic strings are not allowed in QFT phase. This would encourage the replacement $\hat{M}^4 \times \hat{CP}_2$ implying that surfaces in $M^4 \times S^2$ and $M^2 \times CP_2$ are not allowed. In particular, cosmic strings and CP_2 type extremals with M^4 projection in M^2 and thus light-like geodesic without zitterwebegung essential for massivation are forbidden. This brings in mind instability of Higgs=0 phase.

3. The covering spaces in question would correspond to the Cartesian products $\hat{M}^4{}_{n_a} \times C\hat{P}_{2n_b}$ of the covering spaces of $\hat{M}^4$ and $C\hat{P}_2$ by Z_{n_a} and Z_{n_b} with fundamental group is $Z_{n_a} \times Z_{n_b}$. One can also consider extension by replacing M^2 and S^2 with its orbit under G_a (say tedrahedral, octahedral, or icosahedral group). The resulting space will be denoted by $\hat{M}^4 \hat{\times} G_a$ *resp.* $C\hat{P}_2 \hat{\times} G_b$.

4. One expects the discrete subgroups of $SU(2)$ emerge naturally in this framework if one allows the action of these groups on the singular sub-manifolds M^2 or S^2. This would replace the singular manifold with a set of its rotated copies in the case that the subgroups have genuinely 3-dimensional action (the subgroups which corresponds to exceptional groups in the ADE correspondence). For instance, in the case of M^2 the quantization axes for angular momentum would be replaced by the set of quantization axes going through the vertices of tedrahedron, octahedron, or icosahedron. This would bring non-commutative homotopy groups into the picture in a natural manner.

5. Also the orbifolds $\hat{M}^4/G_a \times C\hat{P}_2/G_b$ can be allowed as also the spaces $\hat{M}^4/G_a \times (C\hat{P}_2 \hat{\times} G_b)$ and $(\hat{M}^4 \hat{\times} G_a) \times C\hat{P}_2/G_b$. Hence the previous framework would generalize considerably by the allowance of both coset spaces and covering spaces.

There are several non-trivial questions related to the details of the gluing procedure and phase transition as motion of partonic 2-surface from one sector of the imbedding space to another one.

1. How the gluing of copies of imbedding space at $M^2 \times CP_2$ takes place? It would seem that the covariant metric of M^4 factor proportional to $\hbar^2$ must be discontinuous at the singular manifold since only in this manner the idea about different scaling factor of M^4 metric can make sense. This is consistent with the identical vanishing of Chern-Simons action in $M^2 \times S^2$.

2. One might worry whether the phase transition changing Planck constant means an instantaneous change of the size of partonic 2-surface in M^4 degrees of freedom. This is not the case. Light-likeness in $M^2 \times S^2$ makes sense only for surfaces $X^1 \times D^2 \subset M^2 \times S^2$, where X^1 is light-like geodesic. The requirement that the partonic 2-surface X^2 moving from one sector of H to another one is light-like at $M^2 \times S^2$ irrespective of the value of Planck constant requires that X^2 has single point of M^2 as M^2 projection. Hence no sudden change of the size X^2 occurs.

3. A natural question is whether the phase transition changing the value of Planck constant can occur purely classically or whether it is analogous to quantum tunnelling. Classical non-vacuum extremals of Chern-Simons action have two-dimensional CP_2 projection to homologically non-trivial geodesic sphere S^2_I. The deformation of the entire S^2_I to homologically trivial geodesic sphere S^2_{II} is not possible so that only combinations of partonic 2-surfaces with vanishing total homology charge (Kähler magnetic charge) can in principle move from sector to another one, and this process involves fusion of these 2-surfaces such that CP_2 projection becomes single homologically trivial 2-surface. A piece of a non-trivial geodesic sphere S^2_I of CP_2 can be deformed to that of S^2_{II} using 2-dimensional homotopy flattening the piece of S^2 to curve. If this homotopy cannot be chosen to be light-like, the phase transitions changing Planck constant take place only via quantum tunnelling. Obviously the notions of light-like homotopies (cobordisms) and classical light-like homotopies (cobordisms) are very relevant for the understanding of phase transitions changing Planck constant.

7.1.2 Do factor spaces and coverings correspond to the two kinds of Jones inclusions?

What could be the interpretation of these two kinds of spaces?

1. Jones inclusions appear in two varieties corresponding to $\mathcal{M} : \mathcal{N} < 4$ and $\mathcal{M} : \mathcal{N} = 4$ and one can assign a hierarchy of subgroups of $SU(2)$ with both of them. In particular, their maximal Abelian subgroups Z_n label these inclusions. The interpretation of Z_n as invariance group is natural for $\mathcal{M} : \mathcal{N} < 4$ and it naturally corresponds to the coset spaces. For $\mathcal{M} : \mathcal{N} = 4$ the interpretation of Z_n has remained open. Obviously the interpretation of Z_n as the homology group defining covering would be natural.

2. $\mathcal{M} : \mathcal{N} = 4$ should correspond to the allowance of cosmic strings and other analogous objects. Does the introduction of the covering spaces bring in cosmic strings in some controlled manner? Formally the subgroup of $SU(2)$ defining the inclusion is $SU(2)$ would mean that states are $SU(2)$ singlets which is something non-physical. For covering spaces one would however obtain the degrees of freedom associated with the discrete fiber and the degrees of freedom in question would not disappear completely and would be characterized by the discrete subgroup of $SU(2)$.

   For anyons the non-trivial homotopy of plane brings in non-trivial connection with a flat curvature and the non-trivial dynamics of topological QFTs. Also now one might expect similar non-trivial contribution to appear in the spinor connection of $\hat{M}^2 \hat{\times} G_a$ and $\hat{CP}_2 \hat{\times} G_b$. In conformal field theory models non-trivial monodromy would correspond to the presence of punctures in plane.

3. For factor spaces the unit for quantum numbers like orbital angular momentum is multiplied by n_a *resp.* n_b and for coverings it is divided by this number. These two kind of spaces are in a well defined sense obtained by multiplying and dividing the factors of $\hat{H}$ by G_a *resp.* G_b and multiplication and division are expected to relate to Jones inclusions with $\mathcal{M} : \mathcal{N} < 4$ and $\mathcal{M} : \mathcal{N} = 4$, which both are labeled by a subset of discrete subgroups of SU(2).

4. The discrete subgroups of $SU(2)$ with fixed quantization axes possess a well defined multiplication with product defined as the group generated by forming all possible products of group elements as elements of $SU(2)$. This product is commutative and all elements are idempotent and thus analogous to projectors. Trivial group G_1, two-element group G_2 consisting of reflection and identity, the cyclic groups Z_p, p prime, and tedrahedral, octahedral, and icosahedral groups are the generators of this algebra.

   By commutativity one can regard this algebra as an 11-dimensional module having natural numbers as coefficients ("rig"). The trivial group G_1, two-element group G_2¡ generated by reflection, and tedrahedral, octahedral, and icosahedral groups define 5 generating elements for this algebra. The products of groups other than trivial group define 10 units for this algebra so that there are 11 units altogether. The groups Z_p generate a structure analogous to natural numbers acting as analog of coefficients of this structure. Clearly, one has effectively 11-dimensional commutative algebra in 1-1 correspondence with the 11-dimensional "half-lattice" N^{11} (N denotes natural numbers). Leaving away reflections, one obtains N^7. The projector representation suggests a connection with Jones inclusions. An interesting question concerns the possible Jones inclusions assignable to the subgroups containing infinitely manner elements. Reader has of course already asked whether dimensions 11, 7 and their difference 4 might relate somehow to the mathematical structures of M-theory with 7 compactified dimensions. One could introduce generalized configuration space spinor fields in the configuration space labeled by sectors of H with given quantization axes. By introducing Fourier transform in N^{11} one would formally obtain an infinite-component field in 11-D space.

5. How do the Planck constants associated with factors and coverings relate? One might argue that Planck constant defines a homomorphism respecting the multiplication and division (when possible) by G_i. If so, then Planck constant in units of $\hbar_0$ would be equal to n_a/n_b for $\hat{H}/G_a \times G_b$ option and n_b/n_a for $\hat{H} \hat{\times} (G_a \times G_b)$ with obvious formulas for hybrid cases. This option would put M^4 and CP_2 in a very symmetric role and allow much more flexibility in the identification of symmetries associated with large Planck constant phases.

7.2 Phase transitions changing the value of Planck constant

There are two basic kinds of phase transitions changing the value of Planck constant inducing a leakage between sectors of imbedding space. There are three cases to consider corresponding to

1. leakage in M^4 degrees of freedom changing G_a: the critical manifold is $R_+ \times CP_2$;

2. leakage in CP_2 degrees of freedom changing G_b: the critical manifold is $\delta M^4_+ \times S^2_{II}$;

3. leakage in both degrees of freedom changing both G_a and G_b: the critical manifold is $R_+ \times S^2_{II}$. This is the non-generic case

For transitions of type 2) and 3) X^2 must go through vacuum extremal in the classical picture about transition.

Covering space can also change to a factor space in both degrees of freedom or vice versa and in this case G can remain unchanged as a group although its interpretation changes.

The phase transitions satisfy also strong group theoretical constraints. For the transition $G_1 \to G_2$ either $G_1 \subset G_2$ or $G_2 \subset G_1$ must hold true. For maximal cyclic subgroups Z_n associated with quantization axes this means that n_1 must divide n_2 or vice versa. Hence a nice number theoretic view about transitions emerges.

One can classify the points of critical manifold according to the degree of criticality. Obviously the maximally critical points corresponds to fixed points of G_i that its points $z = 0, \infty$ of the spheres S_r^2 and S_{II}^2. In the case of δM_+^4 the points $z = 0$ and ∞ correspond to the light-like rays R_+ in opposite directions. This ray would define the quantization direction of angular momentum. Quantum phase transitions changing the value of M^4 Planck constant could occur anywhere along this ray (partonic 2-surface would have 1-D projection along this ray). At the level of cosmology this would bring in a preferred direction. Light-cone dip, the counterpart of big bang, is the maximally quantum critical point since it remains invariant under entire group $SO(3,1)$.

Interesting questions relate to the groups generated by finite discrete subgroups of $SO(3)$. As noticed the groups generated as products of groups leaving R_+ invariant and three genuinely 3-D groups are infinite discrete subgroups of SO(3) and could also define Jones inclusions. In this case orbifold is replaced with orbifold containing infinite number of rotated versions of R_+. These phases could be important in elementary particle length scales or in early cosmology.

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