DNA as Topological Quantum Computer

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Abstract

This chapter represents a vision about how DNA might act as a topological quantum computer (tqc). Tqc means that the braidings of braid strands define tqc programs and M-matrix (generalization of S-matrix in zero energy ontology) defining the entanglement between states assignable to the end points of strands define the tqc usually coded as unitary time evolution for Schrödinger equation. One can end up to the model in the following manner.

1. Darwinian selection for which the standard theory of self-organization provides a model, should apply also to tqc programs. Tqc programs should correspond to asymptotic self-organization patterns selected by dissipation in the presence of metabolic energy feed. The spatial and temporal pattern of the metabolic energy feed characterizes the tqc program - or equivalently - sub-program call.
2. Since braiding characterizes the tqc program, the self-organization pattern should correspond to a hydrodynamical flow or a pattern of magnetic field inducing the braiding. Braid strands must correspond to magnetic flux tubes of the magnetic body of DNA. If each nucleotide is transversal magnetic dipole it gives rise to transversal flux tubes, which can also connect to the genome of another cell. As a matter fact, the flux tubes would correspond to what I call wormhole magnetic fields having pairs of space-time sheets carrying opposite magnetic fluxes.
3. The output of tqc sub-program is probability distribution for the outcomes of state function reduction so that the sub-program must be repeated very many times. It is represented as four-dimensional patterns for various rates (chemical rates, nerve pulse patterns, EEG power distributions,...) having also identification as temporal densities of zero energy states in various scales. By the fractality of TGD Universe there is a hierarchy of tqcs corresponding to p-adic and dark matter hierarchies. Programs (space-time sheets defining coherence regions) call programs in shorter scale. If the self-organizing system has a periodic behavior each tqc module defines a large number of almost copies of itself asymptotically. Generalized EEG could naturally define this periodic pattern and each period of EEG would correspond to an initiation and halting of tqc. This brings in mind the periodically occurring sol-gel phase transition inside cell near the cell membrane. There is also a connection with hologram idea: EEG rhythm corresponds to reference wave and nerve pulse patters to the wave carrying the information and interfering with the reference wave.
4. Fluid flow must induce the braiding which requires that the ends of braid strands must be anchored to the fluid flow. Recalling that lipid mono-layers of the cell membrane are liquid crystals and lipids of interior mono-layer have hydrophilic ends pointing towards cell interior, it is easy to guess that DNA nucleotides are connected to lipids by magnetic flux tubes and hydrophilic lipid ends are stuck to the flow.
5. The topology of the braid traversing cell membrane cannot be affected by the hydrodynamical flow. Hence braid strands must be split during tqc. This also induces the desired magnetic isolation from the environment. Halting of tqc reconnects them and make possible the communication of the outcome of tqc.

There are several problems related to the details of the realization.

1. How nucleotides A,T,C,G are coded to the strand color and what this color corresponds to physically? There are two options which could be characterized as fermionic and bosonic.

   i) Magnetic flux tubes having quark and anti-quark at their ends with u,d and u_c, d_c coding for A,G and T,C. CP conjugation would correspond to conjugation for DNA nucleotides.

   ii) Wormhole magnetic flux tubes having wormhole contact and its CP conjugate at its ends with wormhole contact carrying quark and anti-quark at its throats. The latter are predicted to appear in all length scales in TGD Universe.
2. How to split the braid strands in a controlled manner? High T_c super conductivity provides a possible mechanism: braid strand can be split only if the supra current flowing through it vanishes. A suitable voltage pulse induces the supra-current and its negative cancels it. The conformation of the lipid controls whether it it can follow the flow or not.
3. How magnetic flux tubes can be cut without breaking the conservation of the magnetic flux? The notion of wormhole magnetic field could save the situation now: after the splitting the flux returns back along the second space-time sheet of wormhole magnetic field. An alternative solution is based on reconnection of flux tubes. Since only flux tubes of same color can reconnect this process can induce transfer of color: "color inheritance": when applied at the level of amino-acids this leads to a successful model of protein folding. Reconnection

makes possible breaking of flux tube connection for both the ordinary magnetic flux tubes and wormhole magnetic flux tubes.

4. How magnetic flux tubes are realized? The interpretation of flux tubes as correlates of directed attention at molecular level leads to concrete picture. Hydrogen bonds are by their asymmetry natural correlates for a directed attention at molecular level. Also flux tubes between acceptors of hydrogen bonds must be allowed and acceptors can be seen as the subjects of directed attention and donors as objects. Examples of acceptors are aromatic rings of nucleotides, O = atoms of phosphates, etc.. A connection with metabolism is obtained if it is assumed that various phosphates XMP, XDP, XTP, $X = A, T, G, C$ act as fundamental acceptors and plugs in the connection lines. The basic metabolic process $ATP \to ADP + P_i$ allows an interpretation as a reconnection splitting flux tube connection, and the basic function of phosphorylating enzymes would be to build flux tube connections as also of breathing and photosynthesis.

The model makes several testable predictions about DNA itself. In particular, matter-antimatter asymmetry and slightly broken isospin symmetry have counterparts at DNA level induced from the breaking of these symmetries for quarks and antiquarks associated with the flux tubes. DNA cell membrane system is not the only possible system that could perform tqc like activities and store memories in braidings: flux tubes could connect biomolecules and the braiding could provide an almost definition for what it is to be living. Even water memory might reduce to braidings.

The model leads also to an improved understanding of other roles of the magnetic flux tubes containing dark matter. Phase transitions changing the value of Planck constant for the magnetic flux tubes could be key element of bio-catalysis and electromagnetic long distance communications in living matter. For instance, one ends up to what might be called code for protein folding and bio-catalysis. There is also a fascinating connection with Peter Gariaev's work suggesting that the phase transitions changing Planck constant have been observed and wormhole magnetic flux tubes containing dark matter have been photographed in his experiments.

1 Introduction

Large values of Planck constant makes possible all kinds of quantum computations [19, 20, 21, 22]. What makes topological quantum computation (tqc) [23, 25, 24, 26, 27] 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 [120, 124] 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 [124] 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.

1.1 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.

1.2 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 [N4].

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 antiquark (*resp.* antiquark 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 [18].

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 [133]. 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.

1.3 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 [120] 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 [120] 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?

1.4 Basic predictions of DNA as tqc hypothesis

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

1.4.1 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.

1.4.2 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 (antiquark u_c, d_c), the codon codes for hydrophobic (hydrophilic) aminoacid. It is also known that the first letter X of the codon codes for the reaction path leading from a precursor to an aminoacid. 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 aminoacid inside protein only to molecules (aminoacids, DNA, mRNA, or tRNA) for which Y letter is conjugate to that associated with the aminoacid. This means that the reduction of Planck constant leading to the shortening of the flux tube can bring only these aminoacids 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 [78] 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 [78] 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.

2 How quantum computation in TGD Universe differs from standard quantum computation?

Many problems of quantum computation in standard sense might relate to a wrong view about quantum theory. If TGD Universe is the physical universe, the situation would improve in many respects. There is the new fractal view about quantum jump and observer as "self"; there is p-adic length scale hierarchy and hierarchy of Planck constants as well as self hierarchy; there is a new view about entanglement and the possibility of irreducible entanglement carrying genuine information and making possible quantum superposition of fractal quantum computations and quantum parallel dissipation; there is zero energy ontology, the notion of M-matrix allowing to understand quantum theory as a square root of thermodynamics, the notion of measurement resolution allowing to identify M-matrix

in terms of Connes tensor product; there is also the notion of magnetic body providing one promising realization for braids in tqc, etc... This section gives a short summary of these aspects of TGD.

There is also a second motivation for this section. Quantum TGD and TGD inspired theory of consciousness involve quite a bundle of new ideas and the continual checking of internal consistency by writing it through again and again is of utmost importance. This section can be also seen as this kind of checking. I can only represent apologies to the benevolent reader: this is a work in rapid progress.

2.1 General ideas related to topological quantum computation

Topological computation relies heavily on the representation of tqc program as a braiding. There are many kinds of braidings. Number theoretic braids are defined by the orbits of minima of vacuum expectation of Higgs at lightlike partonic 3-surfaces (and also at space-like 3-surfaces). There are braidings defined by Kähler gauge potential (possibly equivalent with number theoretic ones) and by Kähler magnetic field. Magnetic flux tubes and partonic 2-surfaces interpreted as strands of define braidings whose strands are not infinitely thin. A very concrete and very complex time-like braiding is defined by the motions of people at the surface of globe: perhaps this sometimes purposeless-looking fuss has a deeper purpose: maybe those at the higher levels of dark matter hierarchy are using us to carry out complex topological quantum computations)!

2.1.1 General vision about quantum computation

In TGD Universe the hierarchy of Planck constants gives excellent prerequisites for all kinds of quantum computations. The general vision about quantum computation (tqc) would result as a special case and would look like follows.

1. Time-like entanglement between positive and negative energy parts of zero energy states would define the analogs of qc-programs. Space-like quantum entanglement between ends of strands whose motion defines time-like braids would provide a representation of q-information.

2. Both time- and space-like quantum entanglement would correspond to Connes tensor product expressing the finiteness of the measurement resolution between the states defined at ends of space-like braids whose orbits define time like braiding. The characterization of the measurement resolution would thus define both possible q-data and tq-programs as representations for "laws of physics".

3. The braiding between DNA strands with each nucleotide defining one strand transversal to DNA realized in terms of magnetic flux tubes was my first bet for the representation of space-like braiding in living matter. It turned out that the braiding is more naturally defined by flux tubes connecting nucleotides to the lipids of nuclear-, cell-, and endoplasma membranes. Also braidings between other microtubules and axonal membrane can be considered. The conjectured hierarchy of genomes giving rise to quantum coherent gene expressions in various scales would correspond to computational hierarchy.

2.1.2 About the relation between space-like and time-like number theoretic braidings

The relationship between space- and time-like braidings is interesting and there might be some connections also to 4-D topological gauge theories suggested by geometric Langlands program discussed in the previous posting and also in [E11].

1. The braidings along light-like surfaces modify space-like braiding if the moving ends of the space-like braids at partonic 3-surfaces define time-like braids. From tqc point of view the interpretation would be that tqc program is written to memory represented as the modification of space-like braiding in 1-1 correspondence with the time-like braiding.

2. The orbits of space-like braids define codimension two sub-manifolds of 4-D space-time surface and can become knotted. Presumably time-like braiding gives rise to a non-trivial "2-braid". Could also the "2-braiding" based on this knotting be of importance? Do 2-connections of n-category theorists emerge somehow as auxiliary tools? Could 2-knotting bring additional structure into the topological QFT defined by 1-braidings and Chern-Simons action?

3. The strands of dynamically evolving braids could in principle go through each other so that time evolution can transform braid to a new one also in this manner. This is especially clear from standard representation of knots by their planar projections. The points where intersection occurs correspond to self-intersection points of 2-surface as a sub-manifold of space-time surface. Topological QFT:s are also used to classify intersection numbers of 2-dimensional surfaces understood as homological equivalence classes. Now these intersection points would be associated with "braid cobordism".

2.1.3 Quantum computation as quantum superposition of classical computations?

It is often said that quantum computation is quantum super-position of classical computations. In standard path integral picture this does not make sense since between initial and final states represented by classical fields one has quantum superposition over *all* classical field configurations representing classical computations in very abstract sense. The metaphor is as good as the perturbation theory around the minimum of the classical action is as an approximation.

In TGD framework the classical space-time surface is a preferred extremal of Kähler action so that apart from effects caused by the failure of complete determinism, the metaphor makes sense precisely. Besides this there is of course the computation associated with the spin like degrees of freedom in which one has entanglement and which one cannot describe in this manner.

For tqc a particular classical computation would reduce to the time evolution of braids and would be coded by 2-knot. Classical computation would be coded to the manipulation of the braid. Note that the branching of strands of generalized number theoretical braids has interpretation as classical communication.

2.1.4 The identification of topological quantum states

Quantum states of tqc should correspond to topologically robust degrees of freedom separating neatly from non-topological ones.

1. The generalization of the imbedding space inspired by the hierarchy of Planck constants suggests an identification of this kind of states as elements of the group algebra of discrete subgroup of $SO(3)$ associated with the group defining covering of M^4 or CP_2 or both in large $\hbar$ sector. One would have wave functions in the discrete space defined by the homotopy group of the covering transforming according to the representations of the group. This is by definition something robust and separated from non-topological degrees of freedom (standard model quantum numbers). There would be also a direct connection with anyons.

2. An especially interesting group is dodecahedral group corresponding to the minimal quantum phase $q = exp(2\pi/5)$ (Golden Mean) allowing a universal topological quantum computation: this group corresponds to Dynkin diagram for E_8 by the ALE correspondence. Interestingly, neuronal synapses involve clathrin molecules [53] associated with microtubule ends possessing dodecahedral symmetry.

2.1.5 Some questions

A conjecture inspired by the inclusions of HFFs is that these states can be also regarded as representations of various gauge groups which TGD dynamics is conjectured to be able to mimic so that one might have connection with non-Abelian Chern-Simons theories where topological S-matrix is constructed in terms of path integral over connections: these connections would be only an auxiliary tool in TGD framework.

1. Do these additional degrees of freedom give only rise to topological variants of gauge- and conformal field theories? Note that if the earlier conjecture that entire dynamics of these theories could be mimicked, it would be best to perform tqc at quantum criticality where either M^4 or CP_2 dynamical degrees of freedom or both disappear.

2. Could it be advantageous to perform tqc near quantum criticality? For instance, could one construct magnetic braidings in the visible sector near q-criticality using existing technology and then induce phase transition changing Planck constant by varying some parameter, say temperature.

2.2 Fractal hierarchies

Fractal hierarchies are the essence of TGD. There is hierarchy of space-time sheets labelled by preferred p-adic primes. There is hierarchy of Planck constants reflecting a book like structure of the generalized imbedding space and identified in terms of a hierarchy of dark matters. These hierarchies correspond at the level of conscious experience to a hierarchy of conscious entities - selves: self experiences its sub-selves as mental images.

Fractal hierarchies mean completely new element in the model for quantum computation. The decomposition of quantum computation to a fractal hierarchy of quantum computations is one implication of this hierarchy and means that each quantum computation proceeds from longer to shorter time scales $T_n = T_0 2^{-n}$ as a cascade like process such that at each level there is a large number of quantum computations performed with various values of input parameters defined by the output at previous level. Under some additional assumptions to be discussed later this hierarchy involves at a given level a large number of replicas of a given sub-module of tqc so that the output of single fractal sub-module gives automatically probabilities for various outcomes as required.

2.3 Irreducible entanglement and possibility of quantum parallel quantum computation

The basic distinction from standard measurement theory is irreducible entanglement not reduced in quantum jump.

2.3.1 NMP and the possibility of irreducible entanglement

Negentropy Maximimization Principle (NMP) states that entanglement entropy is minimized in quantum jump. For standard Shannon entropy this would lead to a final state which corresponds to a ray of state space. If entanglement probabilities are rational - or even algebraic - one can replace Shannon entropy with its number theoretic counterpart in which p-adic norm of probability replaces the probability in the argument of logarithm: $log(p_n) \to log(|p_n|_p)$. This entropy can have negative values. It is not quite clear whether prime p should be chosen to maximize the number theoretic negentropy or whether p is the p-adic prime characterizing the light-like partonic 3-surface in question.

Obviously NMP favors generation of irreducible entanglement which however can be reduced in U process. Irreducible entanglement is something completely new and the proposed interpretation is in terms of experience of various kinds of conscious experiences with positive content such as understanding.

Quantum superposition of unitarily evolving quantum states generalizes to a quantum superposition of quantum jump sequences defining dissipative time evolutions. Dissipating quarks inside quantum coherent hadrons would provide a basic example of this kind of situation.

2.3.2 Quantum parallel quantum computations and conscious experience

The combination of quantum parallel quantum jump sequences with the fractal hierarchies of scales implies the possibility of quantum parallel quantum computations. In ordinary quantum computation halting selects single computation but in the recent case arbitrarily large number of computations can be carried out simultaneously at various branches of entangled state. The probability distribution for the outcomes is obtained using only single computation.

One would have quantum superposition of space-time sheets (assignable to the maxima of Kähler function) each representing classically the outcome of a particular computation. Each branch would correspond to its own conscious experience but the entire system would correspond to a self experiencing consciously the outcome of computation as intuitive and holistic understanding, and abstraction. Emotions and emotional intellect could correspond to this kind of non-symbolic representation for the outcome of computation as analogs for collective parameters like temperature and pressure.

2.3.3 Delicacies

There are several delicacies involved.

1. The above argument works for factors of type I. For HFFs of type II_1 the finite measurement resolution characterized in terms of the inclusion $\mathcal{N} \subset \mathcal{M}$ mean is that state function reduction takes place to $\mathcal{N}$-ray. There are good reasons to expect that the notion of number theoretic entanglement negentropy generalizes also to this case. Note that the entanglement associated with $\mathcal{N}$ is below measurement resolution.

2. In TGD inspired theory of consciousness irreducible entanglement makes possible sharing and fusion of mental images. At space-time level the space-time sheets corresponding to selves are disjoint but the space-time sheets topologically condensed at them are joined typically by what I call join along boundaries bonds identifiable as braid strands (magnetic flux quanta). In topological computation with finite measurement resolution this kind of entanglement with environment would be below the natural resolution and would not be a problem.

3. State function reduction means quantum jump to an eigen state of density matrix. Suppose that density matrix has rational elements. Number theoretic vision forces to ask whether the quantum jump to eigen state is possible if the eigenvalues of ρ do not belong to the algebraic extension of rationals and p-adic numbers used. If not, then one would have number theoretically irreducible entanglement depending on the algebraic extension used. If the eigenvalues actually define the extension there would be no restrictions: this option is definitely simpler.

4. Fuzzy quantum logic [A8] brings also complications. What happens in the case of quantum spinors that spin ceases to be observable and one cannot reduce the state to spin up or spin down. Rather, one can measure only the eigenvalues for the probability operator for spin up (and thus for spin down) so that one has fuzzy quantum logic characterized by quantum phase. Inclusions of HFFs are characterized by quantum phases and a possible interpretation is that the quantum parallelism related to the finite measurement resolution could give rise to fuzzy qubits. Also the number theoretic quantum parallelism implied by number theoretic NMP could effectively make probabilities as operators. The probabilities for various outcomes would correspond to outcomes of quantum parallel state function reductions.

2.4 Connes tensor product defines universal entanglement

Both time-like entanglement between quantum states with opposite quantum numbers represented by M-matrix and space-like entanglement reduce to Connes tensor dictated highly uniquely by measurement resolution characterized by inclusion of HFFs of type II_1

2.4.1 Time-like and space-like entanglement in zero energy ontology

If hyper-finite factors of II_1 are all that is needed then Connes tensor product defines universal S-matrix and the most general situation corresponds to a direct sum of them. M-matrix for each summand is product of Hermitian square root of density matrix and unitary S-matrix multiplied by a square root of probability having interpretation as analog for Boltzmann weight or probability defined by density matrix (note that it is essential to have $Tr(Id) = 1$ for factors of type II_1. If factor of type I_∞ are present situation is more complex. This means that quantum computations are highly universal and M-matrices are characterized by the inclusion $\mathcal{N} \subset \mathcal{M}$ in each summand defining measurement resolution. Hermitian elements of $\mathcal{N}$ act as symmetries of M-matrix. The identification of the reducible entanglement characterized by Boltzmann weight like parameters in terms of thermal equilibrium would allow to interpret quantum theory as square root of thermodynamics.

If the entanglement probabilities defined by S-matrix and assignable to $\mathcal{N}$ rays do not belong to the algebraic extension used then a full state function reduction is prevented by NMP. Ff the generalized Boltzmann weights are also algebraic then also thermal entanglement is irreducible. In p-adic thermodynamics for Virasoro generator L_0 and using some cutoff for conformal weights the Boltzmann weights are rational numbers expressible using powers of p-adic prime p.

2.4.2 Effects of finite temperature

Usually finite temperature is seen as a problem for quantum computation. In TGD framework the effect of finite temperature is to replace zero energy states formed as pairs of positive and negative energy states with a superposition in which energy varies.

One has an ensemble of space-time sheets which should represent nearly replicas of the quantum computation. There are two cases to be considered.

1) If the thermal entanglement is reducible then each space-time sheet gives outcome corresponding to a well defined energy and one must form an average over these outcomes.

2) If thermal entanglement is irreducible each space-time sheet corresponds to a quantum superposition of space-time sheets, and if the outcome is represented classically as rates and temporal field patterns, it should reflect thermal average of the outcomes as such.

If the degrees of freedom assignable to topological quantum computation do not depend on the energy of the state, thermal width does not affect at all the relevant probabilities. The probabilities are actually affected even in the case of tqc since 1-gates are not purely topological and the effects of temperature in spin degrees of freedom are unavoidable. If T grows the probability distribution for the outcomes flattens and it becomes difficult to select the desired outcome as that appearing with the maximal probability.

2.5 Possible problems related to quantum computation

At least following problems are encountered in quantum computation.

1. How to preserve quantum coherence for a long enough time so that unitary evolution can be achieved?

2. The outcome of calculation is always probability distribution: for instance, the output with maximum probability can correspond to the result of computation. The problem is how to replicate the computation to achieve the desired accuracy. Or more precisely, how to produce replicas of the hardware of quantum computer defined in terms of classical physics?

3. How to isolate the quantum computer from the external world during computation and despite this feed in the inputs and extract the outputs?

2.5.1 The notion of coherence region in TGD framework

In standard framework one can speak about coherence in two senses. At the level of Schrödinger amplitudes one speaks about coherence region inside which it makes sense to speak about Schrödinger time evolution. This notion is rather defined.

In TGD framework coherence region is identifiable as a region inside which the modified Dirac equation holds true. Strictly speaking, this region corresponds to a light-like partonic 3-surface whereas 4-D space-time sheet corresponds to coherence region for classical fields. p-Adic length scale hierarchy and hierarchy of Planck constants means that arbitrarily large coherence regions are possible.

The precise definition for the notion of coherence region and the presence of scale hierarchies imply that the coherence in the case of single quantum computation is not a problem in TGD framework. De-coherence time or coherence time correspond to the temporal span of space-time sheet and a hierarchy coming in powers of two for a given value of Planck constant is predicted by basic quantum TGD. p-Adic length scale hypothesis and favored values of Planck constant would naturally reflect this fundamental fractal hierarchy.

2.5.2 De-coherence of density matrix and replicas of tqc

Second phenomenological description boils down to the assumption that non-diagonal elements of the density matrix in some preferred basis (involving spatial localization of particles) approach to zero. The existence of more or less faithful replicas of space-time sheet in given scale allows to identify the counterpart of this notion in TGD context. De-coherence would mean a loss of information in the averaging of M-matrix and density matrix associated with these space-time sheets.

Topological computations are probabilistic. This means that one has a collection of space-time sheets such that each space-time sheet corresponds to more or less the same tqc and therefore the same M-matrix. If M is too random (in the limits allowed by Connes tensor product), the analog of generalized phase information represented by its "phase" - S-matrix - is useless.

In order to avoid de-coherence in this sense, the space-time sheets must be approximate copies of each other. Almost copies are expected to result by dissipation leading to asymptotic self-organization

patterns depending only weakly on initial conditions and having also space-time correlates. Obviously, the role of dissipation in eliminating effects of de-coherence in tqc would be something new. The enormous symmetries of M-matrix, the uniqueness of S-matrix for given resolution and parameters characterizing braiding, fractality, and generalized Bohr orbit property of space-time sheets, plus dissipation give good hopes that almost replicas can be obtained.

2.5.3 Isolation and representations of the outcome of tqc

The interaction with environment makes quantum computation difficult. In the case of topological quantum computation this interaction corresponds to the formation of braid strands connecting the computing space-time sheet with space-time sheets in environment. The environment is four-dimensional in TGD framework and an isolation in time direction might be required. The space-time sheets responsible for replicas of tqc should not be connected by light-like braids strands having time-like projections in M^4.

Length scale hierarchy coming in powers of two and finite measurement resolution might help considerably. Finite measurement resolution means that those strands which connect space-time sheets topologically condensed to the space-time sheets in question do not induce entanglement visible at this level and should not affect tqc in the resolution used.

Hence only the elimination of strands responsible for tqc at given level and connecting computing space-time sheet to space-time sheets at same level in environment is necessary and would require magnetic isolation. Note that super-conductivity might provide this kind of isolation. This kind of elimination could involve the same mechanism as the initiation of tqc which cuts the braid strands so the initiation and isolation might be more or less the same thing.

Strands reconnect after the halting of tqc and would make possible the communication of the outcome of computation along strands by using say em currents in turn generating generalized EEG, nerve pulse patterns, gene expression, etc... halting and initiation could be more or less synonymous with isolation and communication of the outcome of tqc.

2.5.4 How to express the outcome of quantum computation?

The outcome of quantum computation is basically a representation of probabilities for the outcome of tqc. There are two representations for the outcome of tqc. Symbolic representation which quite generally is in terms of probability distributions represented in terms "classical space-time" physics. The rates for various processes having basically interpretation as geometro-temporal densities would represent the probabilities just as in the case of particle physics experiment. For tqc in living matter this would correspond to gene expression, neural firing, EEG patterns,...

A representation as a conscious experience is another (and actually the ultimate) representation of the outcome. It need not have any symbolic counterpart since it is felt. Intuition, emotions and emotional intelligence would naturally relate to this kind of representation made possible by irreducible entanglement. This representation would be based on fuzzy qubits and would mean that the outcome would be true or false only with certain probability. This unreliability would be felt consciously.

The proposed model of tqc combined with basic facts about theta waves [54, 55] to be discussed in the subsection about the role of supra currents in tqc suggests that EEG rhythm (say theta rhythm) and correlated firing patterns correspond to the isolation at the first half period of tqc and random firing at second half period to the sub-sequent tqc:s at shorter time scales coming as negative powers of 2. The fractal hierarchy of time scales would correspond to a hierarchy of frequency scales for generalized EEG and power spectra at these scales would give information about the outcome of tqc. Synchronization would be obviously an essential element in this picture and could be understood in terms of classical dynamics which defines space-time surface as a generalized Bohr orbit.

Tqc would be analogous to the generation of a dynamical hologram or "conscious hologram" [K4]. EEG rhythm would correspond to reference wave generated by magnetic body as control and coordination signal and the contributions of spikes to EEG generated by neurons would correspond to the incoming wave interfering with the reference wave.

2.5.5 How data is feeded into submodules of tqc?

Scale hierarchy obviously gives tqc a fractal modular structure and the question is how data is feeded to submodules at shorter length scales. There are certainly interactions between different levels

of scale hierarchy. The general ideas about master-slave hierarchy assigned with self-organization support the hypothesis that these interactions are directed from longer to shorter scales and have interpretation as a specialization of input data to tqc sub-modules represented by smaller space-time sheets of hierarchy. The call of submodule would occur when the tqc of the calling module halts and the result of computation is expressed as a 4-D pattern. The lower level module would start only after the halting of tqc (with respect to subjective time at least) and the durations of resulting tqc's would come as $T_n = 2^{-n}T_0$ that geometric series of tqc's would become possible. There would be entire family of tqc's at lower level corresponding to different values of input parameters from calling module.

One of the ideas assigned to hyper-computation [28] is that one can have infinite series of computations with durations comings as negative powers of 2 (Zeno paradox obviously inspires this idea). In TGD framework there can be however only a finite series of these tqc's since CP_2 time scale poses a lower bound for the duration of tqc. One might of course ask whether the spectrum of Planck constant could help in this respect.

2.5.6 The role of dissipation and energy feed

Dissipation plays key role in the theory of self-organizing systems [132]. Its role is to serve as a Darwinian selector. Without an external energy feed the outcome is a situation in which all organized motions disappear. In presence of energy feed highly unique self-organization patterns depending only very weakly on the initial conditions emerge.

In the case of tqc one function of dissipation would be to drive the braidings to static standard configurations, and perhaps even effectively eliminate fluctuations in non-topological degrees of freedom. Note that magnetic fields are important for 1-gates. Magnetic flux conservation however saves magnetic fields from dissipation.

External energy feed is needed in order to generate new braidings. For the proposed model of cellular tqc the flow of intracellular water induces the braiding and requires energy feed. Also now dissipation would drive this flow to standard patterns coding for tqc programs. Metabolic energy would be also needed in order to control whether lipids can flow or not by generating cis type unsaturated bonds. Obviously, energy flows defining self organization patterns would define tqc programs.

2.5.7 Is it possible to realize arbitrary tqc?

The 4-D spin glass degeneracy of TGD Universe due to the enormous vacuum degeneracy of Kähler action gives good hopes that the classical dynamics for braidings allows to realize every possible tqc program. As a consequence, space-time sheets decompose to maximal non-deterministic regions representing basic modules of tqc. Similar decomposition takes place at the level of light-like partonic 3-surfaces and means decomposition to 3-D regions inside which conformal invariance eliminates light-like direction as dynamical degree of freedom so that the dynamics is effectively that of 2-dimensional object. Since these 3-D regions behave as independent units as far as longitudinal conformal invariance is considered, one can say that light-like 3-surfaces are 3-dimensional in discretized sense. In fact, for 2-D regions standard conformal invariance implies similar effective reduction to 1-dimensional dynamics realized in terms of a net of strings and means that 2-dimensionality is realized only in discretized sense.

3 DNA as topological quantum computer

Braids [17] code for topological quantum computation. One can imagine many possible identifications of braids but this is not essential for what follows. What is highly non-trivial is that the motion of the ends of strands defines both time-like and space-like braidings with latter defining in a well-defined sense a written version of the tqc program, kind of log file. The manipulation of braids is a central element of tqc and if DNA really performs tqc, the biological unit modifying braidings should be easy to identify. An obvious signature is the 2-dimensional character of this unit.

3.1 Conjugate DNA as performer of tqc and lipids as quantum dancers

In this section the considerations are restricted to DNA as tqc. It is however quite possible that also RNA and other biomolecules could be involved with tqc like process.

3.1.1 Sharing of labor

The braid strands must begin from DNA double strands. Precisely which part of DNA does perform tqc? Genes? Introns[56]? Or could it be conjugate DNA which performs tqc? The function of conjugate DNA has indeed remained a mystery and sharing of labor suggests itself.

Conjugate DNA would do tqc and DNA would "print" the outcome of tqc in terms of RNA yielding amino-acids in the case of exons. RNA could the outcome in the case of introns. The experience about computers and the general vision provided by TGD suggests that introns could express the outcome of tqc also electromagnetically in terms of standardized field patterns. Also speech would be a form of gene expression. The quantum states braid would entangle with characteristic gene expressions. This hypothesis will be taken as starting point in the following considerations.

3.1.2 Cell membranes as modifiers of braidings defining tqc programs?

The manipulation of braid strands transversal to DNA must take place at 2-D surface. The ends of the space-like braid are dancers whose dancing pattern defines the time-like braid, the running of classical tqc program. Space-like braid represents memory storage and tqc program is automatically written to memory during the tqc. The inner membrane of the nuclear envelope and cell membrane with entire endoplasmic reticulum included are good candidates for dancing hall. The 2-surfaces containing the ends of the hydrophobic ends of lipids could be the parquets and lipids the dancers. This picture seems to make sense.

1. Consider first the anatomy of membranes. Cell membrane [58] and membranes of nuclear envelope [59] consist of 2 lipid [60] layers whose hydrophobic ends point towards interior. There is no water here nor any direct perturbations from the environment or interior milieu of cell. Nuclear envelope consists of two membranes having between them an empty volume of thickness 20-40 nm. The inner membrane consists of two lipid layers like ordinary cell membrane and outer membrane is connected continuously to endoplasmic reticulum [62], which forms a highly folded cell membrane. Many biologists believe that cell nucleus is a prokaryote, which began to live in symbiosis with a prokaryote defining the cell membrane.

2. What makes dancing possible is that the phospholipid layers of the cell membrane are liquid crystals [63]: the lipids can move freely in the horizontal direction but not vertically. "Phospho" could relate closely to the metabolic energy needs of dancers. If these lipids are self-organized around braid strands, their dancing patterns along the membrane surface would be an ideal manner to modify braidings since the lipids would have standard positions in a lattice. This would be like dancing on a chessboard. Note that the internal structure of lipid does not matter in this picture since it is braid color dicated by DNA nucleotide which matters. As a matter fact, living matter is full of self-organizing liquid crystals and one can wonder whether the deeper purpose of their life be running and simultaneous documentation of tqc programs?

3. Ordinary computers have an operating system [64]: a collection of standard programs - the system - and similar situation should prevail now. The "printing" of outputs of tqc would represent example of this kind of standard program. This tqc program should not receive any input from the environment of the nucleus and should therefore correspond to braid strands connecting conjugate strand with strand. Braid strands would go only through the inner nuclear membrane and return back and would not be affected much since the volume between inner and outer nuclear membranes is empty. This assumption looks ad hoc but it will be found that the requirement that these programs are inherited as such in the cell replication necessitates this kind of structure (see the section "Cell replication and tqc").

4. The braid strands starting from the conjugate DNA could traverse several time through the highly folded endoplasmic reticulum but without leaving cell interior and return back to nucleus and modify tqc by intracellular input. Braid strands could also traverse the cell membrane and

thus receive information about the exterior of cell. Both of these tqc programs could be present also in prokaryotes [65] but the braid strands would always return back to the DNA, which can be also in another cell. In multicellulars (eukaryotes [66]) braid strands could continue to another cell and give rise to "social" tqc programs performed by the multicellular organisms. Note that the topological character of braiding does not require isolation of braiding from environment. It might be however advantageous to have some kind of sensory receptors amplifying sensory input to standardized re-braiding patterns. Various receptors in cell membrane would serve this purpose.

5. Braid strands can end up at the parquet defined by ends of the inner phospholipid layer: their distance of inner and outer parquet is few nanometers. They could also extend further.

   i) If one is interested in connecting cell nucleus to the membrane of another cell, the simpler option is the formation of hole defined by a protein attached to cell membrane. In this case only the environment of the second cell affects the braiding assignable to the first cell nucleus.

   ii) The bi-layered structure of the cell membrane could be essential for the build-up of more complex tqc programs since the strands arriving at two nearby hydrophobic 2-surfaces could combine to form longer strands. The formation of longer strands could mean the fusion of the two nearby hydrophobic two-surfaces in the region considered. In fact, tqc would begin with the cutting of the strands so that non-trivial braiding could be generated via lipid dance and tqc would halt when strands would recombine and define a modified braiding. This would allow to connect cell nucleus and cell membrane to a larger tqc unit and cells to multicellular tqc units so that the modification of tqc programs by feeding the information from the exteriors of cells - essential for the survival of multicellulars - would become possible.

3.1.3 Gene expression and other basic genetic functions from tqc point of view

It is useful to try to imagine how gene expression might relate to the halting of tqc. There are of course myriads of alternatives for detailed realizations, and one can only play with thoughts to build a reasonable guess about what might happen.

1. Qubits for transcription factors and other regulators

Genetics is consistent with the hypothesis that genes correspond to those tqc moduli whose outputs determine whether genes are expressed or not. The naive first guess would be that the value of single qubit determines whether the gene *is* expressed or not. Next guess replaces "*is* " with "*can be*".

Indeed, gene expression involves promoters, enhancers and silencers [67]. Promoters are portions of the genome near genes and recognized by proteins known as transcription factors [68]. Transcription factors bind to the promoter and recruit RNA polymerase, an enzyme that synthesizes RNA. In prokaryotes RNA polymerase itself acts as the transcription factor. For eukaryotes situation is more complex: at least seven transcription factors are involved with the recruitment of the RNA polymerase II catalyzing the transcription of the messenger RNA. There are also transcription factors for transcription factors and transcription factor for the transcription factor itself.

The implication is that several qubits must have value "Yes" for the actual expression to occur since several transcription factors are involved with the expression of the gene in general. In the simplest situation this would mean that the computation halts to a measurement of single qubit for subset of genes including at least those coding for transcription factors and other regulators of gene expression.

2. Intron-exon qubit

Genes would have very many final states since each nucleotide is expected to correspond to at least single qubit. Without further measurements that state of nucleotides would remain highly entangled for each gene. Also these other qubits are expected to become increasingly important during evolution.

For instance, eukaryotic gene expression involves a transcription of RNA and splicing out of pieces of RNA which are not translated to amino-acids (introns). Also the notion of gene is known to become increasingly dynamical during the evolution of eukaryotes so that the expressive power of genome increases. A single qubit associated with each codon telling whether it is spliced out or not would allow maximal flexibility. Tqc would define what genes are and the expressive power of genes would be due to the evolution of tqc programs: very much like in the case of ordinary computers.

Stopping sign codon and starting codon would automatically tell where the gene begins and ends if the corresponding qubit is "Yes". In this picture the old fashioned static genes of prokaryotes without splicings would correspond to tqc programs for which the portions of genome with a given value of splicing qubit are connected.

3. What about braids between DNA, RNA, tRNA and amino-acids

This simplified picture might have created the impression that amino-acids are quantum outsiders obeying classical bio-chemistry. For instance, transcription factors would in this picture end up to the promoter by a random process and "Print" would only increase the density of the transcription factor. If DNA is able to perform tqc, it would however seem very strange if it would be happy with this rather dull realization of other central functions of the genetic apparatus.

One can indeed consider besides the braids connecting DNA and its conjugate - crucial for the success of replication - also braids connecting DNA to mRNA and other forms of RNA, mRNA to tRNA, and tRNA to amino-acids. These braids would provide the topological realization of the genetic code and would increase dramatically the precision and effectiveness of the transcription and translation if these processes correspond to quantum transitions at the level of dark matter leading more or less deterministically to the desired outcome at the level of visible matter be it formation of DNA doublet strand, of DNA-mRNA association, of mRNA-tRNA association or tRNA-amino-acid association.

For instance, a temporary reduction of the value of Planck constant for these braids would contract these to such a small size that these associations would result with a high probability. The increase of Planck constant for braids could in turn induce the transfer of mRNA from the nucleus, the opening of DNA double strand during transcription and mitosis.

Also DNA-amino-acid braids might be possible in some special cases. The braiding between regions of DNA at which proteins bind could be a completely general phenomenon. In particular, the promoter region of gene could be connected by braids to the transcription factors of the gene and the halting of tqc computation to printing command could induce the reduction of Planck constant for these braids inducing the binding of the transcription factor binds to the promoter region. In a similar manner, the region of DNA at which RNA polymerase binds could be connected by braid strands to the RNA polymerase.

3.1.4 How braid color is represented?

If braid strands carry 4-color (A,T,C,G) then also lipid strands should carry this kind of 4-color. The lipids whose hydrophobic ends can be joined to form longer strand should have same color. This color need not be chemical in TGD Universe.

Only braid strands of the same color can be connected as tqc halts. This poses strong restrictions on the model.

1. Do braid strands appear as patches possessing same color?

Color conservation is achieved if the two lipid layers decompose in a similar manner into regions of fixed color and the 2-D flow is restricted inside this kind of region at both layers. A four-colored map of cell membrane would be in question! Liquid crystal structure [58] applies only up to length scale of $L(151) = 10$ nm and this suggests that lipid layer decomposes into structural units of size $L(151)$ defining also cell membrane thickness. These regions might correspond to minimal regions of fixed color containing $N \sim 10^2$ lipids.

The controversial notion of lipid raft [61] was inspired by the immiscibility of ordered and disordered liquid phases in a liquid model of membrane. The organization to connected regions of particular phase could be a phenomenon analogous to a separation of phases in percolation. Many cell functions implicate the existence of lipid rafts. The size of lipid rafts has remained open and could be anywhere between 1 and 1000 nm. Also the time scale for the existence of a lipid raft is unknown. A line tension between different regions is predicted in hydrodynamical model but not observed. If the decomposition into ordered and disordered phases is time independent, ordered phases could correspond to those involved with tqc and possess a fixed color. If disordered phases contain no braid strands the mixing of different colors is avoided. The problem with this option is that it restricts dramatically the possible braidings.

If one takes this option seriously, the challenge is to make patches and patch color (A,T,C,G) visible. Perhaps one could try to mark regions of portions of lipid layer by some marker to find whether the lipid layer decomposes to non-mixing regions.

Quantum criticality suggests that that the patches of lipid layer have a fractal structure corresponding to a hierarchy of tqc program modules. The hydrodynamics would be thus fractal: patches containing patches.... moving with respect to each other would correspond to braids containing braids containing ... such that sub-braids behave as braid strands. In principle this is also a testable prediction.

2. Does braid color corresponds to some chemical property?

The conserved braid color is not necessary for the model but would imply genetic coding of the tqc hardware so that sexual reproduction would induce an evolution of tqc hardware. Braid color would also make the coupling of foreign DNA to the tqc performed by the organism difficult and realize an immune system at the level of quantum information processing.

The conservation of braid color poses however considerable problems. The concentration of braid strands of the same color to patches would guarantee the conservation but would restrict the possible braiding dramatically. A more attractive option is that the strands of same color find each other automatically by energy minimization after the halting of tqc. Electromagnetic Coulomb interaction would be the most natural candidate for the interaction in question. Braid color would define a faithful genetic code at the level of nucleotides. It would induce long range correlation between properties of DNA strand and the dynamics of cell immediately after the halting of tqc.

The idea that color could be a chemical property of phospholipids does not seem plausible. The lipid asymmetry of the inner and outer monolayers excludes the assignment of color to the hydrophilic groups PS, PI, PE, PCh. Fatty acids have $N = 14, ..., 24$ carbon atoms and $N = 16$ and 18 are the most common cases so that one could consider the possibility that the 4 most common feet pairs could correspond to the resulting combinations. It is however extremely difficult to understand how long range correlation between DNA nucleotide and fatty acid pair could be created.

3. Does braid color correspond to neutral quark pairs?

It seems that the color should be a property of the braid strand. In TGD inspired model of high T_c super-conductivity [J1] wormhole contacts having u and $\overline{d}$ and d and $\overline{u}$ quarks at the two wormhole throats feed electron's gauge flux to larger space-time sheet. The long range correlation between electrons of Cooper pairs is created by color confinement for an appropriate scaled up variant of chromo-dynamics which are allowed by TGD. Hence the neutral pairs of colored quarks whose members are located the ends of braid strand acting like color flux tube connecting the nucleotide to the lipid could code DNA color to QCD color.

For the pairs $u\overline{d}$ with net em charge the quark and anti-quark have the same sign of em charge and tend to repel each other. Hence the minimization of electro-magnetic Coulomb energy favors the neutral configurations $u\overline{u}$, $d\overline{d}$ and $u\overline{u}$, and $d\overline{d}$ coding for A,T,C,G in some order.

After the halting of tqc only these pairs would form with a high probability. The reconnection of the strands would mean a formation of a short color flux tube between the strands and the annihilation of quark pair to gluon. Note that single braid strand would connect DNA color and its conjugate rather than identical colors so that braid strands connecting two DNA strands (conjugate strands) should always traverse through an even (odd) number of cell membranes. The only plausible looking option is that nucleotides A,T,G,C are mapped to pairs of quark and anti-quarks at the ends of braid strand. Symmetries pose constraints on this coding.

1. By the basic assumptions charge conjugation must correspond to DNA conjugation so that one A and T would be coded to quark pair, say $q\overline{q}$ and its conjugate $\overline{q}q$. Same for C and G.

2. An additional aesthetically appealing working hypothesis is that *both* A and G with the same number of aromatic cycles (three) correspond to $q\overline{q}$ (or its conjugate).

   This would leave four options:

$$\begin{array}{ll} (A,G) \to (u\overline{u}, d\overline{d}) \ , & (T,C) \to (\overline{u}u, \overline{d}d) \ , \\ (A,G) \to (d\overline{d}, u\overline{u}) \ , & (T,C) \to (\overline{d}d), \overline{u}u) \ , \\ (T,C) \to (u\overline{u}, d\overline{d}) \ , & (A,G) \to (\overline{u}u, \overline{d}d) \ , \\ (T,C) \to (d\overline{d}, u\overline{u}) \ , & (A,G) \to (\overline{d}d), \overline{u}u) \ . \end{array} \tag{3.1}$$

It is an experimental problem to deduce which of these correspondences - if any - is realized.

3.1.5 Some general predictions

During tqc the lipids of the two lipid layers should define independent units of lipid hydrodynamics whereas after halting of tqc they should behave as single dynamical unit. Later it will be found that these two phases should correspond to high T_c superconductivity for electrons (Cooper pairs would bind the lipid pair to form single unit) and its absence. This prediction is testable.

The differentiation of cells should directly correspond to the formation of a mapping of a particular part of genome to cell membrane. For neurons the gene expression is maximal which conforms with the fact that neurons can have very large size. Axon might be also part of the map. Stem cells represent the opposite extreme and in this case minimum amount of genome should be mapped to cell membrane. The prediction is that the evolution of cell should be reflected in the evolution of the genome-membrane map.

3.1.6 Quantitative test for the proposal

There is a simple quantitative test for the proposal. A hierarchy of tqc programs is predicted, which means that the number of lipids in the nuclear inner membrane should be larger or at least of the same order of magnitude that the number of nucleotides. For definiteness take the radius of the lipid molecule to be about 5 Angstroms (probably somewhat too large) and the radius of the nuclear membrane about 2.5 μm.

For our own species the total length of DNA strand is about one meter and there are 30 nucleotides per 10 nm. This gives 6.3×10^7 nucleotides: the number of intronic nucleotides is only by few per cent smaller. The total number of lipids in the nuclear inner membrane is roughly 10^8. The number of lipids is roughly twice the number nucleotides. The number of lipids in the membrane of a large neuron of radius of order 10^{-4} meters is about 10^{11}. The fact that the cell membrane is highly convoluted increases the number of lipids available. Folding would make possible to combine several modules in sequence by the proposed connections between hydrophobic surfaces.

3.2 How quantum states are realized?

Quantum states should be assigned to the ends of the braid strands and therefore to the nucleotides of DNA and conjugate DNA. The states should correspond to many-particle states of anyons and fractional electrons and quarks and anti-quarks are the basic candidates.

3.2.1 Anyons represent quantum states

The multi-sheeted character of space-time surface as a 4-surface in a book like structure having as pages covering spaces of the imbedding space (very roughly, see the appendix) would imply additional degrees of freedom corresponding to the group algebra of the group $G \supset Z_n$ defining the covering. Especially interesting groups are tedra-hedral, octahedral, and icosahedral groups whose action does not map any plane to itself. Group algebra would give rise to $n(G)$ quantum states. If electrons are labeled by elements of group algebra this gives $2^{n(G)}$-fold additional degeneracy corresponding to many-electron states at sheets of covering. The vacuum state would be excluded so that $2^{n(G)} - 1$ states would result. If only Cooper pairs are allowed one would have $m_n = 2^{n(G)-1} - 1$ states.

This picture suggests the fractionization of some fermionic charges such as em charge, spin, and fermion number. This aspect is discussed in detail in the Appendix. Single fermion state would be replaced by a set of states with fractional quantum numbers and one would have an analogy with the full electronic shell of atom in the sense that a state containing maximum number of anyonic fermions with the same spin direction would have the quantum numbers of the ordinary fermion.

One can consider two alternative options.

1. The fractionization of charges inspired the idea that catalytic hot spots correspond to "half" hydrogen bonds containing dark fractionally charged electron meaning that the Fermi sea for electronic anyons is not completely filled [J7]. The formation of hydrogen bond would mean a fusion of "half hydrogen bond" and its conjugate having by definition a compensating fractional charges guaranteing that the net em charge and electron number of the resulting state are those of the ordinary electron pair and the state is stable as an analog of the full electron shell. Half hydrogen bonds would assign to bio-molecules "names" as sequences of half hydrogen bonds and only molecules whose "names" are conjugates of each other would form stable hydrogen bonded pairs. Therefore symbolic dynamics would enter the biology via bio-catalysis. Concerning quantum computation the problem is that the full shell assigned to hydrogen bond corresponds to only single state and cannot carry information.

2. The assignment of braids and fractionally charged anyonic quarks and anti-quarks would realize very similar symbolic dynamics. One cannot exclude the possibility that leptonic charges fractionize to same values as quark charges.

This suggest the following picture.

1. One could assign the fractional quantum numbers to the quarks and anti-quarks at the ends of the flux tubes defining the braid strands. This hypothesis is consistent with the correspondence between nucleotides and quarks and assigns anyonic quantum states to the ends of the braid. Wormhole magnetic fields would distinguish between matter in vivo and in vitro. This option is certainly favored by Occam's razor in TGD Universe.

2. Hydrogen bonds connect the DNA strands which suggests that fractionally charged quantum states at the ends of braids might be assignable to the ends of hydrogen bonds. The model for plasma electrolysis of Kanarev [F9] leads to a proposal that new physics is involved with hydrogen bonds. The presence of fractionally charged particles at the ends of bond might provide alternative explanation for the electrostatic properties of hydrogen bonds usually explained in terms of a modification electronic charge distribution by donor-acceptor mechanism. There would exists entire hierarchy of hydrogen bonds corresponding to the increasing values of Planck constant. DNA and even hydrogen bonds associated with water might correspond to a larger value of Planck constant for mammals than for bacteria.

3. The model for protein folding code [L7] leads to a cautious conclusion that flux tubes are prerequisites for the formation of hydrogen bonds although not identifiable with them. The model predicts also the existence of long flux tubes between acceptors of hydrogen bonds (such as $O=$, and aromatic rings assignable to DNA nucleotides, amino-acid backbone, phosphates, XYP, $X = A, T, G, C$, $Y = M, D, T$). This hypothesis would allow detailed identification of places to which quantum states are assigned.

3.2.2 Hierarchy of genetic codes defined by Mersenne primes

The model for the hierarchy of genetic codes inspires the question whether the favored values of $n(G) - 1$ correspond to Mersenne primes [16]. The table below lists the lowest hierarchies. Most of them are short.

$\{M_n\}$	$\{n(G)\}$	
	$\{n_b\}$	
$\{2, 7, 127, 2^{127} - 1, ?\}$	$\{4, 8, 128, 2^{127}, ?\}$	$\{2, 6, 126, 2^{126}, ?\}$
$\{5, 31, 2^{31} - 1\}$	$\{6, 32, 2^{31}\}$	$\{4, 30, 2^{30}\}$
$\{13, 2^{13} - 1\}$	$\{14, 2^{13}\}$	$\{12, 2^{12}\}$
$\{17, 2^{17} - 1\}$	$\{18, 2^{17}\}$	$\{16, 2^{16}\}$
$\{19, 2^{19} - 1\}$	$\{20, 2^{19}\}$	$\{18, 2^{18}\}$
$\{61, 2^{61} - 1\}$	$\{62, 2^{61}\}$	$\{60, 2^{60}\}$
$\{89, 2^{89} - 1\}$	$\{90, 2^{89}\}$	$\{88, 2^{88}\}$
$\{107, 2^{107} - 1\}$	$\{108, 2^{107}\}$	$\{106, 2^{106}\}$

(3.2)

The number of states assignable to M_n is $M_n = 2^n - 1$ which does not correspond to full n bits: the reason is that one of the states is not physically realizable. 2^{n-1} states have interpretation as maximal number of mutually consistent statements and to $n_b = n - 1$ bits. The table above lists the values of n_b for Mersenne primes.

Notice that micro-tubules decompose into 13 parallel helices consisting of 13 tubulin dimers. Could these helices with the conformation of the last tubulin dimer serving as a kind of parity bit realize M_{13} code?

There would be a nice connection with the basic phenomenology of ordinary computers. The value of the integer $n-1$ associated with Mersenne primes would be analogous to the number of bits of the basic information unit of processor. During the evolution of PCs it has evolved from 8 to 32 and is also power of 2.

3.3 The role of high T_c superconductivity in tqc

A simple model for braid strands leads to the understanding of how high T_c super conductivity assigned with cell membrane [M3] could relate to tqc. The most plausible identification of braid strands is as magnetic or wormhole magnetic flux tubes consisting of pairs of flux tubes connected by wormhole contacts whose throats carry fermion and anti-fermion such that their rotational motion at least partially generates the antiparallel magnetic fluxes at the two sheets of flux tube. The latter option is favored by the model of tqc but one must of course keep mind open for variants of the model involving only ordinary flux tubes. Both kinds of flux tubes can carry charged particles such as protons, electrons, and biologically important ions as dark matter with large Planck constant and the model for nerve pulse and EEG indeed relies on this assumption [M2].

3.3.1 Currents at space-like braid strands

If space-like braid strands are identified as idealized structures obtained from 3-D tube like structures by replacing them with 1-D strands, one can regard the braiding as a purely geometrical knotting of braid strands.

The simplest realization of the braid strand as magnetic flux tube would be as a hollow cylindrical surface connecting conjugate DNA nucleotide to cell membrane and going through 5- and/or 6- cycles associated with the sugar backbone of conjugate DNA nucleotides. The free electron pairs associated with the aromatic cycles would carry the current creating the magnetic field needed.

For wormhole magnetic flux one would have pair of this kind of hollow cylinders connected by wormhole contacts and carrying opposite magnetic fluxes. In this case the currents created by wormhole contacts would give rise to the antiparallel magnetic fluxes at the space-time sheets of wormhole contact and could serve as controllers of tqc. I have indeed proposed long time ago that so called wormhole Bose-Einstein condensates might be fundamental for the quantum control in living matter [J5]. In this case the presence of supra currents at either sheet would generate asymmetry between the magnetic fluxes.

There are two extreme options for both kinds of magnetic fields. For B-option magnetic field is parallel to the strand and vector potential rotates around it. For A-option vector potential is parallel to the strand and magnetic field rotates around it. The general case corresponds to the hybrid of these options and involves helical magnetic field, vector potential, and current.

1. For B-option current flowing around the cylindrical tube in the transversal direction would generate the magnetic field. The splitting of the flux tube would require that magnetic flux vanishes requiring that the current should go to zero in the process. This would make possible selection of a part of DNA strand participating to tqc.

2. For A-option the magnetic field lines of the braid would rotate around the cylinder. This kind of field is created by a current in the direction of cylinder. In the beginning of tqc the strand would split and the current of electron pairs would stop flowing and the magnetic field would disappear. Also now the initiation of computation would require stopping of the current and should be made selectively at DNA.

   The control of the tqc should rely on currents of electron pairs (perhaps Cooper pairs) associated with the braid strands. Supra currents would have quantized values and they are therefore very

attractive candidates. The (supra) currents could also bind lipids to pairs so that they would define single dynamical unit in 2-D hydrodynamical flow. One can also think that Cooper pairs with electrons assignable to different members of lipid pair bind it to a single dynamical unit.

3.3.2 Do supra currents generate magnetic fields?

Energetic considerations favor the possibility that supra currents create the magnetic fields associated with the braid strands defined by magnetic flux tubes. In the case of wormhole magnetic flux tubes supra currents could generate additional magnetic fields present only at the second sheet of the flux tube.

Supra current would be created by a voltage pulse ΔV, which gives rise to a constant supra current after it has ceased. Supra current would be destroyed by a voltage pulse of opposite sign. Therefore voltage pulses could define an elegant fundamental control mechanism allowing to select the parts of genome participating to tqc. This kind of voltage pulse could be collectively initiated at cell membrane or at DNA. Note that constant voltage gives rise to an oscillating supra current.

Josephson current through the cell membrane would be also responsible for dark Josephson radiation determining that part of EEG which corresponds to the correlate of neuronal activity [M3]. Note that TGD predicts a fractal hierarchy of EEGs and that ordinary EEG is only one level in this hierarchy. The pulse initiating or stopping tqc would correspond in EEG to a phase shift by a constant amount

$$\Delta\Phi = Ze\Delta VT/\hbar \ ,$$

where T is the duration of pulse and ΔV its magnitude.

The contribution of Josephson current to EEG responsible for beta and theta bands interpreted as satellites of alpha band should be absent during tqc and only EEG rhythm would be present. The periods dominated by EEG rhythm should be observed as EEG correlates for problem solving situations (say mouse in a maze) presumably involving tqc. The dominance of slow EEG rhythms during sleep and meditation would have interpretation in terms of tqc.

3.3.3 Topological considerations

The existence of supra current requires that the flow allows for a complex phase $exp(i\Psi)$ such that supra current is proportional to $\nabla\Psi$. This requires integrability in the sense that one can assign to the flow lines of A or B (combination of them in the case of A-B braid) a coordinate variable Ψ varying along the flow lines. In the case of a general vector field X this requires $\nabla\Psi = \Phi X$ giving $\nabla \times X = -\nabla\Phi/\Phi$ as an integrability condition. This condition defines what is known as Beltrami flow [D1].

The perturbation of the flux tube, which spoils integrability in a region covering the entire cross section of flux tube means either the loss of super-conductivity or the disappearance of the net supra current. In the case of the A-braid, the topological mechanism causing this is the increase in the dimension of the CP_2 projection of the flux tube so that it becomes 3-D [D1], where I have also considered the possibility that 3-D character of CP_2 projection is what transforms the living matter to a spin glass type phase in which very complex self-organization patterns emerge. This would conform with the idea that in tqc takes place in this phase.

3.3.4 Fractal memory storage and tqc

If Josephson current through cell membrane ceases during tqc, tqc manifests itself as the presence of only EEG rhythm characterized by an appropriate cyclotron frequency. Synchronous neuron firing might therefore relate to tqc. The original idea that a phase shift of EEG is induced by the voltage initiating tqc - although wrong - was however useful in that it inspired the question whether the initiation of tqc could have something to do with what is known as a place coding by phase shifts performed by hippocampal pyramidal cells [54, 55]. The playing with this idea provides important insights about the construction of quantum memories and demonstrates the amazing explanatory power of the paradigm once again.

The model also makes explicit important conceptual differences between tqc a la TGD and in the ordinary sense of wordin particular those related to different view about the relation between subjective and geometric time.

1. In TGD tqc corresponds to the unitary process U taking place following by a state function reduction and preparation. It replaces configuration space ("world of classical worlds") spinor field with a new one. Configuration space spinor field represent generalization of time evolution of Schrödinger equation so that a quantum jump occurs between entire time evolutions. Ordinary tqc corresponds to Hamiltonian time development starting at time $t = 0$ and halting at $t = T$ to a state function reduction.

2. In TGD the expression of the result of tqc is essentially 4-D pattern of gene expression (spiking pattern in the recent case). In usual tqc it would be 3-D pattern emerging as the computation halts at time t. Each moment of consciousness can be seen as a process in which a kind of 4-D statue is carved by starting from a rough sketch and proceeding to shorter details and building fractally scaled down variants of the basic pattern. Our life cycle would be a particular example of this process and would be repeated again and again but of course not as an exact copy of the previous one.

1. Empirical findings

The place coding by phase shifts was discovered by O'Reefe and Recce [54]. In [55] Y. Yamaguchi describes the vision in which memory formation by so called theta phase coding is essential for the emergence of intelligence. It is known that hippocampal pyramidal cells have "place property" being activated at specific "place field" position defined by an environment consisting of recognizable objects serving as landmarks. The temporal change of the percept is accompanied by a sequence of place unit activities. The theta cells exhibit change in firing phase distributions relative to the theta rhythm and the relative phase with respect to theta phase gradually increases as the rat traverses the place field. In a cell population the temporal sequence is transformed into a phase shift sequence of firing spikes of individual cells within each theta cycle.

Thus a temporal sequence of percepts is transformed into a phase shift sequence of individual spikes of neurons within each theta cycle along linear array of neurons effectively representing time axis. Essentially a time compressed representation of the original events is created bringing in mind temporal hologram. Each event (object or activity in perceptive field) is represented by a firing of one particular neuron at time τ_n measured from the beginning of the theta cycle. τ_n is obtained by scaling down the real time value t_n of the event. Note that there is some upper bound for the total duration of memory if scaling factor is constant.

This scaling down - story telling - seems to be a fundamental aspect of memory. Our memories can even abstract the entire life history to a handful of important events represented as a story lasting only few seconds. This scaling down is thought to be important not only for the representation of the contextual information but also for the memory storage in the hippocampus. Yamaguchi and collaborators have also found that the gradual phase shift occurs at half theta cycle whereas firings at the other half cycle show no correlation [55]. One should also find an interpretation for this.

2. TGD based interpretation of findings

How this picture relates to TGD based 4-D view about memory in which primary memories are stored in the brain of the geometric past?

1. The simplest option is the initiation of tqc like process in the beginning of each theta cycle of period T and having geometric duration $T/2$. The transition $T \to T/2$ conforms nicely with the fundamental hierarchy of time scales comings as powers defining the hierarchy of measurement resolutions and associated with inclusions of hyperfinite factors of type II_1 [A8]. That firing is random at second half of cycle could simply mean that no tqc is performed and that the second half is used to code the actual events of "geometric now".

2. In accordance with the vision about the hierarchy of Planck constants defining a hierarchy of time scales of long term memories and of planned action, the scaled down variants of memories would be obtained by down-wards scaling of Planck constant for the dark space-time sheet

representing the original memory. In principle a scaling by any factor $1/n$ (actually by any rational) is possible and would imply the scaling down of the geometric time span of tqc and of light-like braids. One would have tqc's inside tqc's and braids within braids (flux quanta within flux quanta). The coding of the memories to braidings would be an automatic process as almost so also the formation of their zoomed down variants.

3. A mapping of the time evolution defining memory to a linear array of neurons would take place. This can be understood if the scaled down variant (scaled down value of $\hbar$) of the space-time sheet representing original memory is parallel to the linear neuron array and contains at scaled down time value t_n a stimulus forcing n^{th} neuron to fire. The 4-D character of the expression of the outcome of tqc allows to achieve this automatically without complex program structure.

To sum up, it seems that the scaling of Planck constant of time like braids provides a further fundamental mechanism not present in standard tqc allowing to build fractally scaled down variants of not only memories but tqc's in general. The ability to simulate in shorter time scale is a certainly very important prerequisite of intelligent and planned behavior. This ability has also a space-like counterpart: it will be found that the scaling of Planck constant associated with space-like braids connecting bio-molecules might play a fundamental role in DNA replication, control of transcription by proteins, and translation of mRNA to proteins. A further suggestive conclusion is that the period T associated with a given EEG rhythm defines a sequence of tqc's having geometric span $T/2$ each: the rest of the period would be used to perceive the environment of the geometric now. The fractal hierarchy of EEGs would mean that there are tqc's within tqc's in a very wide range of time scales.

3.4 Codes and tqc

TGD suggests the existence of several (genetic) codes besides 3-codon code [L1, N4]. The experience from ordinary computers and the fact that genes in general do not correspond to $3n$ nucleotides encourages to take this idea more seriously. The use of different codes would allow to tell what kind of information a given piece of DNA strand represents. DNA strand would be like a drawing of building containing figures (3-code) and various kinds of text (other codes). A simple drawing for the building would become a complex manual containing mostly text as the evolution proceeds: for humans 96 per cent of code would corresponds to introns perhaps obeying some other code.

The hierarchy of genetic codes is obtained by starting from n basic statements and going to the meta level by forming all possible statements about them (higher order logics) and throwing away one which is not physically realizable (it would correspond to empty set in the set theoretic realization). This allows $2^n - 1$ statements and one can select 2^{n-1} mutually consistent statements (half of the full set of statements) and say that these are true and give kind of axiomatics about world. The remaining statements are false. DNA would realize only the true statements.

The hierarchy of Mersenne primes $M_n = 2^n - 1$ with $M_{n(next)} = M_{M_n}$ starting from $n = 2$ with $M_2 = 3$ gives rise to 1-code with 4 codons, 3-code with 64 codons, and $3 \times 21 = 63$-code with 2^{126} codons [L1] realized as sequences of 63 nucleotides (the length of 63-codon is about $2L(151)$, roughly twice the cell membrane thickness. It is not known whether this Combinatorial Hierarchy continues ad infinitum. Hilbert conjectured that this is the case.

In the model of pre-biotic evolution also 2-codons appear and 3-code is formed as the fusion of 1- and 2-codes. The problem is that 2-code is not predicted by the basic Combinatorial Hierarchy associated with $n = 2$.

There are however also other Mersenne hierarchies and the next hierarchy allows the realization of the 2-code. This Combinatorial Hierarchy begins from Fermat prime $n = 2^k + 1 = 5$ with $M_5 = 2^5 - 1 = 31$ gives rise to a code with 16 codons realized as 2-codons (2 nucleotides). Second level corresponds to Mersenne prime $M_{31} = 2^{31} - 1$ and a code with $2^{30=15\times 2}$ codons realized by sequences of 15 3-codons containing 45 nucleotides. This corresponds to DNA length of 15 nm, or length scale $3L(149)$, where $L(149) = 5$ nm defines the thickness of the lipid layer of cell membrane. $L(151) = 10$ nm corresponds to 3 full 2π twists for DNA double strand. The model for 3-code as fusion of 1- and 2-codes suggests that also this hierarchy - which probably does not continue further - is realized.

There are also further short Combinatorial hierarchies corresponding to Mersenne primes [16].

1. $n = 13$ defines Mersenne prime M_{13}. The code would have $2^{12=6\times 2}$ codons representable as sequences of 6 nucleotides or 2 3-codons. This code might be associated with microtubuli.

2. The Fermat prime $17 = 2^4 + 1$ defines Mersenne prime M_{17} and the code would have $2^{16=8\times 2}$ codons representable as sequences of 8 nucleotides.

3. $n = 19$ defines Mersenne prime M_{19} and code would have $2^{18=9\times 2}$ codons representable as sequences of 9 nucleotides or three DNA codons.

4. The next Mersennes are M_{31} belonging to $n = 5$ hierarchy, M_{61} with $2^{60=30\times 2}$ codons represented by 30-codons. This corresponds to DNA length $L(151) = 10$ nm (cell membrane thickness). M_{89} (44-codons), M_{107} (53-codons) and M_{127} (belonging to the basic hierarchy) are the next Mersennes. Next Mersenne corresponds to M_{521} (260-codon) and to completely super-astrophysical p-adic length scale and might not be present in the hierarchy.

   This hierarchy is realized at the level of elementary particle physics and might appear also at the level of DNA. The 1-, 2-, 3-, 6-, 8-, and 9-codons would define lowest Combinatorial Hierarchies.

4 How to realize the basic gates?

In order to have a more concrete view about realization of tqc, one must understand how quantum computation can be reduced to a construction of braidings from fundamental unitary operations. The article "Braiding Operators are Universal Quantum Gates" by Kaufmann and Lomonaco [25] contains a very lucid summary of how braids can be used in topological quantum computation.

1. The identification of the braiding operator R - a unitary solution of Yang-Baxter equation - as a universal 2-gate is discussed. In the following I sum up only those points which are most relevant for the recent discussion.

2. One can assign to braids both knots and links and the assignment is not unique without additional conditions. The so called braid closure assigns a unique knot to a given braid by connecting n^{th} incoming strand to n^{th} outgoing strand without generating additional knotting. All braids related by so called Markov moves yield the same knot. The Markov trace (q-trace actually) of the unitary braiding S-matrix U is a knot invariant characterizing the braid closure.

3. Braid closure can be mimicked by a topological quantum computation for the original n-braid plus trivial n-braid and this leads to a quantum computation of the modulus of the Markov trace of U. The probability for the diagonal transition for one particular element of Bell basis (whose states are maximally entangled) gives the modulus squared of the trace. The closure can be mimicked quantum computationally.

4.1 Universality of tqc

Quantum computer is universal if all unitary transformations of n^{th} tensor power of a finite-dimensional state space V can be realized. Universality is achieved by using only two kinds of gates. The gates of first type are single particle gates realizing arbitrary unitary transformation of $U(2)$ in the case of qubits. Only single 2-particle gate is necessary and universality is guaranteed if the corresponding unitary transformation is entangling for some state pair. The standard choice for the 2-gate is CNOT acting on bit pair (t, c). The value of the control bit c remains of course unchanged and the value of the target bit changes for $c = 1$ and remains unchanged for $c = 0$.

4.2 The fundamental braiding operation as a universal 2-gate

The realization of CNOT or gate equivalent to it is the key problem in topological quantum computation. For instance, the slow de-coherence of photons makes quantum optics a promising approach but the realization of CNOT requires strongly nonlinear optics. The interaction of control and target photon should be such that for second polarization of the control photon target photon changes its direction but keeps it for the second polarization direction.

For braids CNOT can be be expressed in terms of the fundamental braiding operation e_n representing the exchange of the strands n and $n+1$ of the braid represented as a unitary matrix R acting on $V_n \otimes V_{n+1}$.

The basic condition on R is Yang-Baxter equation expressing the defining condition $e_n e_{n+1} e_n = e_{n+1} e_n e_{n+1}$ for braid group generators. The solutions of Yang-Baxter equation for spinors are well-known and CNOT can be expressed in the general case as a transformation of form $A_1 \otimes A_2 R A_3 \otimes A_4$ in which single particle operators A_i act on incoming and outgoing lines. 3-braid is the simplest possible braid able to perform interesting tqc, which suggests that genetic codons are associated with 3-braids.

The dance of lipids on chessboard defined by the lipid layer would reduce R to an exchange of neighboring lipids. For instance, the matrix $R = DS$, $D = diag(1, 1, 1, -1)$ and $S = e_{11} + e_{23} + e_{32} + e_{44}$ the swap matrix permuting the neighboring spins satisfies Yang-Baxter equation and is entangling.

4.3 What the replacement of linear braid with planar braid could mean?

Standard braids are essentially linear objects in plane. The possibility to perform the basic braiding operation for the nearest neighbors in two different directions must affect the situation somehow.

1. Classically it would seem that the tensor product defined by a linear array must be replaced by a tensor product defined by the lattice defined by lipids. Braid strands would be labelled by two indices and the relations for braid group would be affected in an obvious manner.

2. The fact that DNA is a linear structure would suggests that the situation is actually effectively one-dimensional, and that the points of the lipid layer inherit the linear ordering of nucleotides of DNA strand. One can however ask whether the genuine 2-dimensionality could provide a mathematical realization for possible long range correlations between distant nucleotides n and $n + N$ for some N. p-Adic effective topology for DNA might become manifest via this kind of correlations and would predict that N is power of some prime p which might depend on organism's evolutionary level.

3. Quantum conformal invariance would suggest effective one-dimensionality in the sense that only the observables associated with a suitably chosen linear braid commute. One might also speak about topological quantum computation in a direction transversal to the braid strands giving a slicing of the cell membrane to parallel braid strands. This might mean an additional computational power.

4. Partonic picture would suggest a generalization of the linear braid to a structure consisting of curves defining the decomposition of membrane surface regions such that conformal invariance applies separately in each region: this would mean breaking of conformal invariance and 2-dimensionality in discrete sense. Each region would define a one parameter set of topological quantum computations. These regions might corresponds to genes. If each lipid defines its own conformal patch one would have a planar braid.

4.4 Single particle gates

The realization of single particle gates as $U(2)$ transformations leads naturally to the extension of the braid group by assigning to the strands sequences of group elements satisfying the group multiplication rules. The group elements associated with a n^{th} strand commute with the generators of braid group which do not act on n^{th} strand. G would be naturally subgroup of the covering group of rotation group acting in spin degrees of spin 1/2 object. Since $U(1)$ transformations generate only an overall phase to the state, the presence of this factor might not be necessary. A possible candidate for $U(1)$ factor is as a rotation induced by a time-like parallel translation defined by the electromagnetic scalar potential $\Phi = A_t$.

One of the challenges is the realization of single particle gates representing $U(2)$ rotation of the qubit. The first thing to come mind was that $U(2)$ corresponds to $U(2)$ rotation induced by magnetic field and electric fields. A more elegant realization is in terms of $SU(3)$ rotation, where $SU(3)$ is color group associated with strong interactions. This looks rather weird but there is direct evidence for the prediction that color $SU(3)$ is associated with tqc and thus cognition: something that does not come first in mind! I have myself written text about the strange finding of topologist Barbara Shipman suggesting that quarks are in some mysterious manner involved with honeybee dance and proposed an interpretation.

4.4.1 The realization of qubit as ordinary spin

A possible realization for single particle gate $s \subset SU(2)$ would be as $SU(2)$ rotation induced by a magnetic pulse. This transformation is fixed by the rotation axis and rotation angle around this axes. This kind of transformation would result by applying to the strand a magnetic pulse with magnetic field in the direction of rotation axes. The duration of the pulse determines the rotation angle. Pulse could be created by bringing a magnetic flux tube to the system, letting it act for the required time, and moving it away. $U(1)$ phase factor could result from the electromagnetic gauge potential as a non-integrable phase factor $exp(ie \int A_t dt/\hbar)$ coming from the presence of scale potential $\Phi = A_t$ in the Hamiltonian.

4.4.2 Conrete model for realization of 1-gates in terms of ordinary rotations

What could be the simplest realization of the $U(2)$ transformation in the case of cell membrane assuming that it corresponds to ordinary rotation?

1. There should be a dark spin 1/2 particle associated with each lipid, electron or proton most plausibly. TGD based model for high T_c superconductivity [J1] predicts that Cooper pairs correspond to pairs of cylindrical space-time sheets with electrons at the two space-time sheets. The size scale of the entire Cooper corresponds to p-adic length scale $L(151)$ defining the thickness of the cell membrane and cylindrical structure to $L(149)$, the thickness of lipid layer so that electrons are the natural candidates for tqc. The Cooper pair BE condensate would fuse the lipid pairs to form particles of lipid liquid.

2. Starting of tqc requires the splitting of electron Cooper pairs and its halting the formation of Cooper pairs again. The initiation of tqc could involve increase of temperature or an introduction of magnetic field destroying the Cooper pairs. Tqc could be also controlled by supra currents flowing along cylindrical flux tubes connecting 5- and/or aromatic cycles of conjugate DNA nucleotides to the cell membrane. The cutting of the current flow would make it possible for braid strand to split and tqc to begin.

3. By shifting a magnetic flux tube or sheet parallel to the cell membrane to the position of the portion of membrane participating to tqc is the simplest manner to achieve this. Halting could be achieved by removing the flux tube. The unitary rotation induced by the constant background magnetic field would not represent gate and it should be possible to eliminate its effect from tqc proper.

4. The gate would mean the application of a magnetic pulse much stronger than background magnetic field on the braid strands ending at the lipid layer. The model for the communication of sensory data to the magnetic body requires that magnetic flux tubes go through the cell membrane. This would suggest that the direction of the magnetic flux tube is temporarily altered and that the flux tube then covers part of the lipid for the required period of time.

   The realization of the single particle gates requires electromagnetic interactions. That single particle gates are not purely topological transformations could bring in the problems caused by a de-coherence due to electromagnetic perturbations. The large values of Planck constant playing a key role in the TGD based model of living matter could save the situation. The large value of $\hbar$ would be also required by the anyonic character of the system necessary to obtain R-matrix defining a universal 2-gate.

   The minimum time needed to inducing full 2π rotation around the magnetic axes would be essentially the inverse of cyclotron frequency for the particle in question in the magnetic field considered$T = 1/f_c = 2\pi m/ZeB$. For electrons in the dark magnetic field of $B = .2$ Gauss assigned to living matter in the quantum model of EEG this frequency would be about $f_c = .6$ MHz. For protons one would have $f_c = 300$ Hz. For a magnetic field of Tesla the time scales would be reduced by a factor 2×10^{-5}.

4.4.3 The realization of 1-gate in terms of color rotations

One can criticize the model of 1-gates based on ordinary spin. The introduction of magnetic pulses does not look an attractive idea and seems to require additional structures besides magnetic flux tubes

(MEs?). It would be much nicer to assign the magnetic field with the flux tubes defining the braid strands. The rotation of magnetic field would however require changing the direction of braid strands. This does not look natural. Could one do without this rotation by identifying spin like degree of freedom in some other manner? This is indeed possible.

TGD predicts a hierarchy of copies of scaled up variants of both weak and color interactions and these play a key role in TGD inspired model of living matter. Both weak isospin and color isospin could be considered as alternatives for the ordinary spin as a realization of qubit in TGD framework. Below color isospin is discussed but one could consider also a realization in terms of nuclei and their exotic counterparts [F9] differing only by the replacement of neutral color bond between nuclei of nuclear string with a charged one. Charge entanglement between nuclei would guarantee overall charge conservation.

1. Each space-time sheet of braid strands contains quark and antiquark at its ends. Color isospin and hypercharge label their states. Two of the quarks of the color triplet form doublet with respect to color isospin and the third is singlet and has different hyper charge Y. Hence qubit could be realized in terms of color isospin I_3 instead of ordinary spin but third quark would be inert in the Boolean sense. Qubit could be also replaced with qutrit and isospin singlet could be identified as a statement with ill-defined truth value. Trits are used also in ordinary computers. In TGD framework finite measurement resolution implies fuzzy qubits and the third state might relate to this fuzziness. Also Gödelian interpretation can be consideredthe quark state with vanishing isospin would be associated with counterparts of undecidable propositions to which one cannot assign truth value (consider sensory input which is so ambiguous that one cannot tell what is there or a situation in which one cannot decide whether to do something or not). Note that hyper-charge would induce naturally the U(1) factor affecting the over all phase of qubit but affecting differently to the third quark.

2. Magnetic flux tubes are also color magnetic flux tubes carrying non-vanishing classical color gauge field in the case that they are non-vacuum extremals. The holonomy group of classical color field is an Abelian subgroup of the $U(1) \times U(1)$ Cartan subgroup of color group. Classical color magnetic field defines the choice of quantization axes for color quantum numbers. For instance, magnetic moment is replaced with color magnetic moment and this replacement is in key role in simple model for color magnetic spin spin splittings between spin 0 and 1 mesons as well as spin 1/2 and 3/2 baryons.

3. There is a symmetry breaking of color symmetry to subgroup $U(1)_{I_3} \times U(1)_Y$ and color singletness is in TGD framework replaced by a weaker condition stating that physical states have vanishing net color quantum numbers. This makes possible the measurement of color quantum numbers in the manner similar to that for spin. For instance, color singlet formed by quark and antiquark with opposite color quantum numbers can in the measurement of color quantum numbers of quark reduce to a state in which quark has definite color quantum numbers. This state is a superposition of states with vanishing Y and I_3 in color singlet and color octet representations. Strong form of color confinement would not allow this kind of measurement.

4. Color rotation in general changes the directions of quantization axis of I_3 and Y and generates a new state basis. Since $U(1) \times U(1)$ leaves the state basis invariant, the space defined by the choices of quantization axes is 6-dimensional flag manifold $F = SU(3)/U(1) \times U(1)$. In contrast to standard model, color rotations in general do not leave classical electromagnetic field invariant since classical em field is a superposition of color invariant induced Kähler from and color non-invariant part proportional classical Z^0 field. Hence, although the magnetic flux tube retains its direction and shape in M^4 degrees of freedom, its electromagnetic properties are affected and this is visible at the level of classical electromagnetic interactions.

5. If color isospin defines the qubit or qutrit in topological quantum computation, color quantum numbers and the flag manifold F should have direct relevance for cognition. Amazingly, there is a direct experimental support for this! Years ago topologist Barbara Shipman made the intriguing observation that honeybee dance can be understood in terms of a model involving the flag manifold F [18]. This led her to propose that quarks are in some mysterious manner involved with the honeybee dance. My proposal [K3] was that color rotations of the space-time

sheets associated with neurons represent geometric information: sensory input would be coded to color rotations defining the directions of quantization axes for I_3 and Y. Subsequent state function reduction would provide conscious representations in terms of trits characterizing for instance sensory input symbolically.

In [K3] I introduced the notions of geometric and sensory qualia corresponding to two choices involved with the quantum measurement: the choice of quantization axes performed by the measurer and the "choice" of final state quantum numbers in state function reduction. In the case of honeybee dance geometric qualia could code information about the position of the food source. The changes of color quantum numbers in quantum jump were identified as visual colors. In state function reduction one cannot speak about change of quantum numbers but about their emergence. Therefore one must distinguish between color qualia and the conscious experience defined by the emergence of color quantum numbers: the latter would have interpretation as qutrit.

Summarizing, this picture suggests that 1-gates of DNA tqc (understood as "dance of lipids") are defined by color rotations of the ends of space-like braid strands and at lipids. The color rotations would be induced by sensory and other inputs to the system. Topological quantum computation would be directly related to conscious experience and sensory and other inputs would fix the directions of the color magnetic fields.

5 About realization of braiding

The most plausible identification of braid strands is as magnetic or wormhole magnetic flux tubes. Flux tubes can contain charged particles such as protons, electrons, and biologically important ions as dark matter with large Planck constant and the model for nerve pulse and EEG indeed relies on this assumption [M2].

5.1 Could braid strands be split and reconnect all the time?

As far as braiding alone is considered, braid strands could be split all the time. In other words, there would be no continuation of strands through the cell membrane. Computation would halt when lipids lose their unsaturated cis bonds so that they cannot follow the liquid flow. The conservation of strand color would be trivially true but would not have any implications. Supra currents would not be needed to control tqc and there would be no connection with generalized EEG. It is not obvious how the gene expression for the outcome of tqc could take place since the strands would not connect genome to genome. For these reasons this option does not look attractive.

The models for prebiotic evolution [N4] and protein folding [L7] lead to a conclusion that braids can connect all kind of bio-molecules to each other and also water molecules and bio-molecules Thus DNA tqc would represent only one example of tqc like activities performed by the living matter. The conclusion is that braidings are dynamical with reconnection of flux tubes representing a fundamental transformation changing the braiding and thus also tqc programs.

5.2 What do braid strands look like?

In the following the anatomy of braid strands is discussed at general level and then identification in terms of flux tubes of magnetic body is proposed.

5.2.1 Braid strands as nearly vacuum extremals

The braid strands should be nearly quantum critical sub-manifolds of $M^4 \times CP_2$ so that phase transitions changing Planck constant and thus their length can take place easily (DNA replication, binding of mRNA molecules to DNA during transcription, binding of transcription factors to promoters, binding of tRNA-amino-acid complexes to mRNA...).

Depending on whether phase transition takes place in M^4 or CP_2 degrees of freedom, either their M^4 projection belongs to $M^2 \subset M^4$ or their CP_2 projection to the homological trivial geodesic sphere $S^2 \subset CP_2$. In the latter case a vacuum extremal is in question. Maximal quantum criticality means

$X^4 \subset M^2 \times S^2$ so that one has straight string with a vanishing string tension. The almost vacuum extremal property guarantees the braid strands can be easily generated from vacuum.

An additional requirement is that the gravitational mass is small. For objects of type $M^2 \times X^2_g$, $X^2_g \subset E^2 \times CP_2$, the gravitational mass vanishes for $g = 1$ (genus) and is of order CP_2 mass otherwise and negative for $g > 1$. Torus topology is the unique choice. A simple model for the braid strand is as a small non-vacuum deformation of $X^4 = M^2 \times X^2_g \subset M^2 \subset E^2 \times S^2$, $g = 1$. As a special case one has $X^4 = M^2 \times S^1 \times S^1 \subset M^2 \subset E^2 \times S^1$, for which M^4 projection is a hollow cylinder, which could connect the aromatic 5- or 6-cycle of sugar backbone to another DNA strand, lipid, or amino-acid.

5.2.2 Braid strands as flux tubes of color magnetic body

One can make this model more detailed by feeding in simple physical inputs. The flux tubes carry magnetic field when the supra current is on. In TGD Universe all classical fields are expressible in terms of the four CP_2 coordinates and their gradients so that em, weak, color and gravitational fields are not independent as in standard model framework. In particular, the ordinary classical em field is necessarily accompanied by a classical color field in the case of non-vacuum extremals. This predicts color and ew fields in arbitrary long scales and quantum classical correspondence forces to conclude that there exists fractal hierarchy of electro-weak and color interactions.

Since the classical color gauge field is proportional to Kähler form, its holonomy group is Abelian so that effectively $U(1) \times U(1) \subset SU(3)$ gauge field is in question. The generation of color flux requires colored particles at the ends of color flux tube so that the presence of pairs of quark and antiquark assignable to the pairs of wormhole throats at the ends of the tube is unavoidable if one accepts quantum classical correspondence.

In the case of cell, a highly idealized model for color magnetic flux tubes is as flux tubes of a dipole field. The preferred axis could be determined by the position of the centrosomes forming a T shaped structure. DNA strands would define the idealized dipole creating this field: DNA is indeed negatively charged and electronic currents along DNA could create the magnetic field. The flux tubes of this field would go through nuclear and cell membrane and return back unless they end up to another cell. This is indeed required by the proposed model of tqc.

It has been assumed that the initiation of tqc means that the supra current ceases and induces the splitting of braid strands. The magnetic flux need not however disappear completely. As a matter fact, its presence forced by the conservation of magnetic flux seems to be crucial for the conservation of braiding. Indeed, during tqc magnetic and color magnetic flux could return from lipid to DNA along another space-time sheet at a distance of order CP_2 radius from it. For long time ago I proposed that this kind of structures -which I christened "wormhole magnetic fields" - might play key role in living matter [J5]. The wormhole contacts having quark and antiquark at their opposite throats and coding for A,T,C,G would define the places where the current flows to the "lower" space-time sheet to return back to DNA. Quarks would also generate the remaining magnetic field and supra current could indeed cease.

The fact that classical em fields and thus classical color fields are always present for non-vacuum extremals means that also the motion of any kind of particles (space-time sheets), say water flow, induces a braiding of magnetic flux tubes associated with molecules in water if the temporary splitting of flux tubes is possible. Hence the prerequisites for tqc are met in extremely general situation and tqc involving DNA could have developed from a much simpler form of tqc performed by water giving perhaps rise to what is known as water memory [127, 128, 129, 130]. This would also suggest that the braiding operation is induced by the a controlled flow of cellular water.

5.3 How to induce the basic braiding operation?

The basic braiding operation requires the exchange of two neighboring lipids. After some basic facts about phospholipids the simplest model found hitherto is discussed.

5.3.1 Some facts about phospholipids

Phospholipids [91] - which form about 30 per cent of the lipid content of the monolayer - contain phosphate group. The dance of lipids requires metabolic energy and the hydrophilic ends of the

phospholipid could provide it. They could also couple the lipids to the flow of water in the vicinity of the lipid monolayer possibly inducing the braiding. Of course, the causal arrow could be also opposite.

The hydrophilic part of the phospholipid is a nitrogen containing alcohol such as serine, inositol or ethanolamine, or an organic compound such as choline. Phospholipids are classified into 3 kinds of phosphoglycerides [92] and sphingomyelin.

1. Phosphoglycerides

In cell membranes, phosphoglycerides are the more common of the two phospholipids, which suggest that they are involved with tqc. One speaks of phosphotidyl X, where X= serine, inositol, ethanolamine is the nitrogen containing alcohol and X=Ch the organic compound. The shorthand notion OS, PI, PE, PCh is used.

The structure of the phospholipid is most easily explained using the dancer metaphor. The two fatty chains define the hydrophobic feet of the dancer, glycerol and phosphate group define the body providing the energy to the dance, and serine, inositol, ethanolamine or choline define the hydrophilic head of the dancer (perhaps "deciding" the dancing pattern).

There is a lipid asymmetry in the cell membrane. PS, PE, PI in cytoplasmic monolayer (alcohols). PC (organic) and sphingomyelin in outer monolayer. Also glycolipids are found only in the outer monolayer. The asymmetry is due to the manner that the phospholipids are manufactured.

PS [96] in the inner monolayer is negatively charged and its presence is necessary for the normal functioning of the cell membrane. It activates protein kinase C which is associated with memory function. PS slows down cognitive decline in animals models. This encourages to think that the hydrophilic polar end of at least PS is involved with tqc, perhaps to the generation of braiding via the coupling to the hydrodynamic flow of cytoplasm in the vicinity of the inner monolayer.

2. Fatty acids

The fatty acid chains in phospholipids and glycolipids usually contain an even number of carbon atoms, typically between 14 and 24 making 5 possibilities altogether. The 16- and 18-carbon fatty acids are the most common. Fatty acids [94] may be saturated or unsaturated, with the configuration of the double bonds nearly always cis.

The length and the degree of unsaturation of fatty acids chains have a profound effect on membranes fluidity as unsaturated lipids create a kink, preventing the fatty acids from packing together as tightly, thus decreasing the melting point (increasing the fluidity) of the membrane. The number of unsaturaded cis bonds and their positions besides the number of Carbon atoms characterizes the lipid. Quite generally, there are $3n$ Carbons after each bond. The creation of unsatured bond by removing H atom from the fatty acid could be an initiating step in the basic braiding operation creating room for the dancers. The bond should be created on both neighboring lipids simultaneously.

5.3.2 Could hydrodynamic flow induce braiding operations?

One can imagine several models for what might happen during the braiding operation in the lipid bilayer [95]. One such view is following.

1. The creation of unsaturated bond and involving elimination of H atom from fatty acid would lead to cis configuration and create the room needed by dancers. This operation should be performed for both lipids participating in the braiding operation. After the braiding it might be necessary to add H atom back to stabilize the situation. The energy needed to perform either or both of these operations could be provided by the phosphate group.

2. The hydrophilic ends of lipids couple the lipids to the surrounding hydrodynamic flow in the case that the lipids are able to move. This coupling could induce the braiding. The primary control of tqc would thus be by using the hydrodynamic flow by generating localized vortices. There is considerable evidence for water memory [127] but its mechanism remains to be poorly understood. If also water memory is realized in terms of the braid strands connecting fluid particles, DNA tqc could have evolved from water memory.

3. Sol-gel phase transition is conjectured to be important for the quantum information processing of cell [97]. In the transition which can occur cyclically actin filaments (also at EEG frequencies) are assembled and lead to a gel phase resembling solid. Sol phase could correspond to tqc and

gel to the phase following the halting of tqc. Actin filaments might be assignable with braid strands or bundles of them and shield the braiding. Also microtubules might shield bundles of braid strands.

4. Only inner braid strands are directly connected to DNA which also supports the view that only the inner monolayer suffers a braiding operation during tqc and that the outer monolayer should be in a "freezed" state during it. There is a net negative charge associated with the inner monolayer possibly relating to its participation to the braiding. The vigorous hydrodynamical flows known to take place below the cell membrane could induce the braiding.

5.4 Some qualitative tests

In life sciences the standard manner to test a model is to look whether the function of the system is affected in the predicted manner if one somehow interferes the system. Now interfering with tqc should affect the gene expression resulting otherwise.

1. Lipid layer hydrodynamics is predicted to allow two fundamental phases. The pairs of lipids should behave like single dynamical unit in super-conducting phase and as independent units in non-super-conducting phase. The application of magnetic field or increase of temperature should induce a transition between these two phases. These phase transitions applied selectively to the regions of cell membrane should affect gene expression. One could prevent halting of tqc by applying an external magnetic field and thus prevent gene expression. One could dream of deducing gene-membrane mapping with endoplasmic reticulum included.

2. The temperature range in which quantum critical high T_c super-conductivity is possible is probably rather narrow and should correspond to the temperature range in which cell membrane is functional. Brain is functional in a very narrow range of temperatures. Selective freezing of cell membrane might provide information about gene map provided by cell membrane.

3. One could do various things to the cell membrane. One could effectively remove part of it, freeze, or heat some part of the lipid liquid and look whether this has effects on gene expression. The known effects of ELF em fields on the behavior and physiology of vertebrates [M3] might relate to the fact that these fields interfere with tqc.

4. Artificially induced braiding by inducing a motion of lipids by some kind of stirring during tqc could induce/affect gene expression.

5. The application of external dark magnetic fields could affect gene expression. Tqc could be initiated artificially in some part of cell membrane by the application of dark magnetic field. Running tqc could be halted by an application of dark magnetic field interfering to zero with the background field. The application of magnetic pulses would affect tqc and thus gene expression. The problem is how to create dark magnetic fields in given length scale (range of magnetic field strength). Perhaps one could generate first ordinary magnetic field and then transform it to dark magnetic field by $\hbar$ changing phase transition. This could be achieved by a variation of some macroscopic parameters such as temperature, magnetic field strength, and analog of doping fraction appearing in standard high T_c super-conductivity.

6. Artificially induced scalings of $\hbar$ by varying temperature and parameters such as pH should induce or stop DNA replication, DNA-mRNA transcription and the translation of mRNA to proteins.

6 A model for flux tubes

Biochemistry represents extremely complex and refined choreography. It is hard to believe that this reduces to a mere unconscious and actually apparent fight for chemical survival. In TGD Universe consciousness would be involved even at the molecular level and magnetic body would be the choreographer whose dance would induce the molecular activities. This picture combined with the idea of standard plugs and terminals at which flux tubes end, leads to a to a picture allowing to get rather concrete picture about DNA as topological quantum computer. It becomes also possible to formulate

a model for protein folding in which DNA codons can be said to code for both amino-acid sequences and their folding. Hence the information loss thought to occur because of the many-to-one character of the code does not really happen. The model is discussed in [L7].

6.1 Flux tubes as a correlate for directed attention

Molecular survival is the standard candidate for the fundamental variational principle motivating the molecular intentional actions. There is entire hierarchy of selves and the survival at the higher level of hierarchy would force co-operation and altruistic behavior at the lower levels. One might hope that this hypothesis reduces to Negentropy Maximization Principle [H2], which states that the information contents of conscious experience is maximized. If this picture is accepted, the evolution of molecular system becomes analogous to the evolution of a society.

Directed attention is the basic aspect of consciousness and the natural guess would be that directed attention corresponds to the formation of magnetic flux tubes between subject and target. The directedness property requires some manner to order the subject and target.

1. The ordering by the values of Planck constant is what first comes in mind. The larger space-time sheet characterized by a larger value of Planck constant and thus at a higher level of evolutionary hierarchy would direct its attention to the smaller one.

2. Also the ordering by the value of p-adic prime characterizing the size scale of the space-time sheet could be considered but in this case directedness could be questioned.

3. Attention can be directed also to thoughts. Could this mean that attention is directed from real space-time sheets to p-adic space-time sheets for various values of primes but not vice versa? Or could the direction be just the opposite at least in the intentional action transforming p-adic space-time sheet to real space-time sheet? Perhaps directions are opposite for cognition and intention.

The generation of wormhole magnetic flux tubes could be the correlate for the directed attention, not only at molecular level, but quite generally. Metaphorically, the strands of braid would be the light rays from the eyes of the perceiver to the target and their braiding would code the motions of the target to a topological quantum computation like activity and form a memory representation at least. The additional aspect of directed attention would be the coloring of the braid strands, kind of coloring for the virtual light rays emerging from the eyes of the molecular observer. In the case of DNA this can induce a coloring of braid strands emerging from amino-acids and other molecules so that it would indeed become possible to assign to amino-acid the conjugate of the middle nucleotide of the codon XYZ coding for it.

Attention can be also redirected. For this process there is a very nice topological description as a reconnection of flux tubes. What happens is that flux tubes $A \to B$ and $C \to D$ fuse for a moment and become flux tubes $A \to D$ and $C \to B$. This process is possible only if the strands have the same color so that the values of the quark charges associated with A and B are the same.

This kind of process can modify tqc programs. For instance, in the case of the flux tubes coming from nucleotides X and X_c and ending to the lipid layer this process means that X and X_c and corresponding lipids become connected and genome builds memory representation about this process via similar link. If proteins are connected with mRNA connected to DNA in this manner, this process would allow the formation of flux tubes between amino-acids of two proteins in such a manner that protein would inherit from DNA codon the color of the middle nucleotide and its interactions effectively reduce to base pairing.

DNA would have memory representation about molecular processes via these changing braiding topologies, and one could say that these molecular processes reflect the bodily motions of the magnetic body. Entire molecular dynamics of the organism could represent an enormous tqc induced by the motor activities of the magnetic body. At the level of sensory experience similar idea has been discussed earlier [H11]: out of body experiences (OBEs) and illusions such as train illusion could be understood in terms of motor action of magnetic body inducing virtual sensory percepts.

Attention can be also switched on and off. Here the structure of the lipid ends containing two nearby situated $= O$:s suggests the mechanism: the short flux tube connecting $= O$:s disappears. The minimization of Coulomb interaction energy at each end implies that re-appearance of the flux tubes

creates a short flux tube with the original strand color. Note that the conservation of magnetic flux allows this option only for wormhole magnetic flux tubes.

6.2 Does directed attention generate memory representations and tqc like processes?

Directed attention induces braiding if the target is moving and changing its shape. This gives rise to a memory representation of the behavior of the object of attention and also to a tqc like process. A considerable generalization of tqc paradigm suggests itself.

Tqc could be induced by the braiding between DNA and lipids, DNA and proteins via folding processes, DNA RNA braiding and braiding between DNA and its conjugate, DNA and protein braiding. The outcome of tqc would be represented as the temporal patterns of biochemical concentrations and rates and there would be hierarchy of p-adic time scales and those associated with the dark matter hierarchy.

For instance, the protein content of lipid membranes is about 50 per cent and varies between 25-75 per cent so that protein folding and lipid flow could define tqc programs as self-organization patterns. The folding of protein is dynamical process: alpha helices are created and disappear in time scale of 10^{-7} seconds and the side chains of protein can rotate.

The details of the tqc like process depend on what one assumes. The minimal scenario is deduced from the transcription and translation processes and from the condition that magnetic body keeps control or at least keeps book about what happens using genome as a tool. The picture would be essentially what one might obtain by applying a rough model for web in terms of nodes and links. The reader is encouraged to use paper and pencil to make the following description more illustrative.

1. Assume that mRNA and DNA remain connected by flux tubes after transcription and that only reconnection process can cut this connection so that mRNA inherits the conjugate colors of DNA. Assume same for mRNA and tRNA. Assume that amino-acid associated with tRNA has similar flux tube connections with the nucleotides of tRNA. Under these assumptions amino-acid inherits the conjugate colors of DNA nucleotides via the connection line DNA-mRNA-tRNA-amino-acid faith-fully if all links are correspond to quark pairs rather than their superpositions. Wobble pairing for Z nucleotide could actually correspond to this kind of superposition.

2. One can consider several options for the amino-acid-acid DNA correspondence but trial-and-error work showed that a realistic folding code is obtained only if X, Y, and Z correspond to $O-H$, $O=$, and NH_2 in the constant part of free amino-acid. During translation the formation of the peptide bond between amino-acids dehydration leads to a loss of $O-H$ and one H from NH_2. The flux tube from tRNA to $O-H$ becomes a flux tube to water molecule inheriting the color of X so that $O=-NH_2$ of the amino-acid inside protein represents the conjugate of YZ.

3. Hydrogen bonding between NH and $O=$ in alpha helices and beta sheets reduces effectively to base pairing taking place only if the condition $Y_1 = Z_2$ (briefly $Y = Z$ in the sequel) is satisfied. This is extremely restrictive condition on the gene coding the amino-acid unless one assumes quantum counterpart of wobble base pairing for mRNA or tRNA-amino-acid pairing in the case of Z nucleotide (as one indeed must do). Note that the $O=$ atom of the amino-acid is in a special role in that it can have hydrogen bond flux tubes to donors and flux tube connections with $O=$:s of other amino-acids, the residues of amino-acids containing acceptors (say $O=$ or aromatic ring), and with the aromatic rings of say ATP.

4. The recombination process for two conjugate DNA-mRNA-tRNA-amino-acid links can transform the flux tubes in such manner that one obtains link between the $=O$:s of amino-acids A_1 and A_2 characterized by Y and Y_c. Besides hydrogen bonding this mechanism could be central in the enzyme substrate interaction. The process would pair tRNAs corresponding to Y and Y_c together to give DNA-mRNA-tRNA-tRNA-mRNA-DNA link providing a memory representation about amino-acid pairing $A_1 - A_2$. One could say that magnetic body creates with the mediation of the genome dynamical tqc programs to which much of the bio-molecular activity reduces. Not all however, since two amino-acid pairs $A_1 - A_2$ and $A_3 - A_4$ can recombine to $A_1 - A_4$ and $A_3 - A_2$ without DNA knowing anything about it. Magnetic body would however know.

5. The constant part of non-hydrogen bonded amino-acid inside protein would behave like Y_cZ_c if amino-acid is coded by XYZ. The $COOH$ end of protein would behave like $X_cY_cZ_c$. Also flux tubes connecting the residue groups become possible and protein does not behave like single nucleotide anymore. By color inheritance everything resulting in the reconnection process between $O=$ and NH_2 and residues reduces in a well-defined sense to the genetic code.

6.3 Realization of flux tubes

The basic questions about flux are following. Where do they begin, where do they end, and do they have intermediate plugs which allow temporary cutting of the flux tube.

6.3.1 Where do flux tubes begin from?

The view about magnetic body as a controller of biological body using genome as a control tool suggests that DNA is to a high degree responsible for directed attention and other molecules as targets so that flux tubes emanate from DNA nucleotides. The reason would be that the aromatic cycles of DNA correspond to larger value of Planck constant. Some chemical or geometric property of DNA nucleotides or of DNA nucleotides of DNA strand could raise them to the role of subject. Aromatic cycle property correlates with the symmetries associated with large value of Planck constant and is the best candidate for this property.

If this picture is accepted then also some amino-acid residues might act as subjects/objects depending on the option. Phe, His, Trp, Tyr contain aromatic cycle. The derivatives of Trp and Tyr act as neurotransmitters and His is extremely effective nucleophilic catalyst. This would make possible more specific catalytic mechanisms through the pairing of Phe, His, Trp, and Tyr with residues having flux tube terminals.

This raises the question about the physical interaction determining the color of the strand emerging from the aromatic cycle. The interaction energy of quark at the end of flux tube with the classical electromagnetic fields of nuclei and electrons of the ring should determine this. The wormhole contact containing quark/antiquark at the throat at space-time sheet containing nuclei and electrons could also delocalize inside the ring. One of the earliest hypothesis of TGD inspired model for living matter was that wormhole Bose-Einstein condensates could be crucial for understanding of the behavior of biomolecules [J5]. Wormhole throats with quark and antiquark at their throats appear also in the model of high T_c superconductivity [J1]. As far as couplings are considered, these wormhole contacts are in many respects analogous to the so called axions predicted by some theories of elementary particle physics. The wormhole contact like property is by no means exceptional: all gauge bosons correspond to wormhole contacts in TGD Universe.

The only manner for the electronic space-time sheet to feed its electromagnetic gauge flux to larger space-time sheets using exactly two wormhole contacts is to use wormhole contacts with $\overline{u}$ and d at their "upper" throat (T,G). For proton one would have $\overline{d}$ and u at their "upper" throat (A,C). The presence of electron or proton at nucleotide space-time sheet near the end of flux tube might allow to understand the correlation. The transfer of electrons and protons between space-time sheets with different p-adic length scale is basic element of TGD based model of metabolism so that there might be some relation.

6.3.2 Acceptors as plugs and donors as terminals of flux tubes?

Standardization constraint suggests that flux tubes are attached to standard plugs and terminals. The explicit study of various biological molecules and the role of water in biology gives some hints.

1. An attractive idea is that $=O$ serves as a plug to which flux arrives and from which it can also continue. For the minimal option suggested by hydrogen bonding $O=$ could be connected to two donors and $O=$ could not be connected to $O=$. The assumption that the flux tube can connect also two $O=$:s represents a hypothesis going outside the framework of standard physics. A stronger assumption is that all acceptors can act as plugs. For instance, the aromatic rings of DNA nucleotides could act as acceptors and be connected to a sequence of $O=$ plugs eventually terminating to a hydrogen bond.

2. Donors such as $O-H$ would in turn correspond to a terminal at which flux tube can end. One might be very naive and say that conscious bio-molecules have learned the fundamental role of oxygen and water in the metabolism and become very attentive to the presence of $=O$ and $O-H$. $=O$ appears in $COOH$ part of each amino-acid so that this part defines the standard plug. $=O$ appears also in the residues of Asp, Glu, Asn, Gln. $O-H$ groups appear inside the residues of Asp,Glu and Ser, Thr.

3. Hydrogen bonds $X-H--Y$ have the basic defining property associated with directed attention, namely the asymmetry between donor X and acceptor Y. Hence there is a great temptation consider the possibility that hydrogen bonds correspond to short flux tubes, that flux tubes could be seen as generalized hydrogen bonds. Quite generally, Y could be seen as the object of directed attention of X characterized by larger value of Planck constant. The assumption that two $O=$:s, or even two acceptors of a hydrogen bond, can be connected by a flux tube means more than a generalization of hydrogen bond the connection with a donor would correspond only to the final step in the sequence of flux tubes and plugs giving rise to a directed attention.

4. This hypothesis makes the model rather predictive. For instance, $N-H$, NH_2, $O-H$ and much less often $C-H$ and $S-H$ are the basic donors in the case of proteins whereas $O=$, $-O-$, $-N=S-S$, $-S^-$ and aromatic rings are the basic acceptors. Reconnection process should be involved with the dynamics of ordinary hydrogen bonding. Reconnection process implies inheritance of the flux tube color and means a realization of the symbol based dynamics. It turns out that this hypothesis leads to a model explaining basic qualitative facts about protein folding.

What about ions like Ca^{++} and Mg_{++}: can flux tubes attach also to these? Could n flux tubes terminate to an n-valent ion? This assumption leads to a model of the gel phase in which Ca^{++} ions serve as cross links between proteins in the sense that Ca^{++} ion is connected by flux tubes to two proteins whereas monovalent ions such as Na^+ cannot perform such a function. Gel-sol phase transition would be induced by a flow of Na^+ ions to the interior of cell inducing a reconnection process so that in the sol phase proteins would be connected to Na^+ ions.

6.4 Flux tubes and DNA

The model of DNA as topological quantum computer gives useful guide lines in the attempt to form a vision about flux tubes. It was assumed that braid strands defined by "wormhole magnetic" flux tubes join nucleotides to lipids and can continue through the nuclear or cell membrane but are split during tqc. The hydrophilic ends of lipids attach to water molecules and self-organization patterns for the water flow in gel phase induce a 2-D flow in the lipid layer which is liquid crystal defining tqc programs at the classical level as braidings. The flow indeed induces braiding if one assumes that during topological computation the connection through the cell membrane is split and reconnected after the halting of tqc.

The challenge is to understand microscopically how the flux tube joins DNA nucleotide to the phospholipid [91]. Certainly the points at which the flux tubes attach should be completely standard plugs and the formation of polypeptide bonds is an excellent guide line here. Recall that phospholipid, the tqc dancer, has two hydrophobic legs and head. Each leg has at the hydrophilic end O=C-O-C part joining it to glyceride connected to monophosphate group in turn connected to a hydrophilic residue R. The most often appearing residues are serine, inositol, ethanolamine, and choline. Only three of these appear in large quantities and there is asymmetry between cell exterior and interior.

Let us denote by $=O_1$ and $=O_2$ the two oxygens (maybe analogs of right and left hemispheres!) in question. The proposal is that DNA nucleotide and $=O_1$ are connected by a flux tube: the asymmetry between right and left lipid legs should determine which of the legs is "left leg" and which $O=$ is the "left brain hemisphere". $=O_2$, the "holistic right brain hemisphere", connects in turn to the flux tube coming from the other symmetrically situated $=O_2$ at the outer surface of the second lipid layer. Besides this $=O_1$ and $=O_2$ are connected by a flux tube serving as switch on both sides of the membrane.

During tqc the short $O=-O=$ flux tube would experience reconnection with a flux tube acting as hydrogen bond between water molecules so that the connection is split and $O=$:s form hydrogen bonds. The reversal of this reconnection creates the connection again and halts the computation. The

lipid residue R couples with the flow of the liquid in gel phase. Since $=O$ is in question the quark or antiquark at the end can correspond to the DNA nucleotide in question. The necessary complete correlation between quark and antiquark charges at the ends of flux tubes associated with $=O_1$ and $=O_2$ can be understood as being due to the minimization of Coulomb interaction energy.

If one is ready to accept magnetic flux tubes between all acceptors then the aromatic rings of nucleotides known to be acceptors could be connected by a flux tube to the $O=$ atom of the lipid or to some intermediate $O=$ atom. The phosphate groups associated with nucleotides of DNA strand contain also $=O$, which could act as a plug to which the flux tube from the nucleotide is attached. The detailed charge structure of the aromatic ring(s) should determine the quark-nucleotide correspondence. The connection line to the lipid could involve several intermediate $O=$ plugs and the first plug in the series would be the $O=$ atom of the monophosphate of the nucleotide.

There is a strong temptation to assume that subset of XYP molecules, $X = A, G, T, C$, $Y = M, D, T$ act as standard plugs with X and phosphates connected by flux tubes to a string. This would make it possible to engineer braid strands from standard pieces connected by standard plugs. DNA nucleotide XMP would have flux tube connection to the aromatic ring of X and the $O=$ of last P would be connected to next plug of the communication line. If so, a close connection with metabolism and topological quantum computation would emerge.

1. Phosphorylation [93] would be an absolutely essential for both metabolism and buildup of connection lines acting as braid strands. Phosphorylation is indeed known to be the basic step activating enzymes. In eukaryotes the phosphorylation takes plane amino-acids most often for ser but also thr, and trp with aromatic rings are phosphorylated. Mitochondrions have specialized to produce ATP in oxidative phosphorylation from ADP and photosynthesis produces ATP. All these activities could be seen as a production of standard plugs for braid strands making possible directed attention and quantum information processing at molecular level.

2. As already noticed, $O = -O =$ flux tubes could also act as switches inducing a shortcut of the flux tube connection by reconnecting with a hydrogen bond connecting two water molecules. This is an essential step in the model for how DNA acts as topological quantum computer. De-phosphorylation might be standard manner to realized this process.

3. This picture would fit with the fact that XYP molecules, in particular AMP, ADP, and ATP, appear in bio-molecules involved with varying functions such as signalling, control, and metabolism. $=O$ might act as a universal plug to which flux tubes from electronegative atoms of information molecules can attach their flux tubes. This would also provide a concrete realization of the idea that information molecules (neurotransmitters, hormones) are analogous to links in Internet [M2]: they would not represent the information but establish a communication channel. The magnetic flux tube associated with the information molecule would connect it to another cell and by the join to $=O$ plug having flux tube to another cell, say to its nucleus, would create a communication or control channel.

7 Some predictions related to the representation of braid color

Even in the rudimentary form discussed above the model makes predictions. In particular, the hypothesis that neutral quark pairs represent braid color is easily testable.

7.1 Anomalous em charge of DNA as a basic prediction

The basic prediction is anomalous charge of DNA. Also integer valued anomalous charge for the structural units of genome is highly suggestive.

The selection of the working option - if any such exists - is indeed experimentally possible. The anomalous charge coupling to the *difference* of the gauge potentials at the two space-time sheets defines the signature of the wormhole contact at the DNA end of braid strand. The effective (or anomalous) em charge is given as sum of quark charges associated with DNA space-time sheet:

$$Q_a = [n(A) - n(T)]Q(q_A) + [n(G) - n(C)]Q(q_G) \tag{7.1}$$

is predicted. The four possible options for charge are given explicitly in the table below

$$\begin{array}{l} Q_a = [n(A)-n(T)]\frac{2}{3} - [n(G)-n(C)]\frac{1}{3} \ , \\ Q_a = -[n(A)-n(T)]\frac{1}{3} + [n(G)-n(C)]\frac{2}{3} \ , \\ Q_a = -[n(A)-n(T)]\frac{2}{3} + [n(G)-n(C)]\frac{1}{3} \ , \\ Q_a = [n(A)-n(T)]\frac{1}{3} - [n(G)-n(C)]\frac{2}{3} \ . \end{array} \tag{7.2}$$

Second option is obtained from the first option $(A,T,G,C) \to (u,\overline{u},d,\overline{d})$ by permuting u and d quark in the correspondence and the last two options by performing charge conjugation for quarks in the first two options.

The anomalous charge is experimentally visible only if the external electromagnetic fields at the two sheets are different. The negative charge of DNA due to the presence of phosphate groups implies that the first sheet carries different em field so that this is indeed the case.

The presence effective em charge depending on the details of DNA sequence means that electromagnetism differentiates between different DNA:s strands and some strands might be more favored dynamically than others. It is interesting to look basic features of DNA from this view point. Vertebral mitochondrial code has full $A \leftrightarrow G$ and $C \leftrightarrow T$ symmetries with respect to the third nucleotide of the codon and for the nuclear code the symmetry is almost exact. In the above scenario A and C *resp.* G and T would have different signs and magnitudes of em charge but they would correspond to different weak isospin states for the third quark so that this symmetry would be mathematically equivalent to the isospin symmetry of strong interactions.

The average gauge potential due to the anomalous charge per length at space-time sheet containing ordinary em field of a straight portion of DNA strand is predicted to be proportional to

$$\frac{dQ_a}{dl} = [p(A)-p(T)]Q(q_A) + [p(G)-p(C)]Q(q_G)\frac{1}{\Delta L} \ ,$$

where ΔL corresponds to the length increment corresponding to single nucleotide and $p(X)$ represents the frequency for nucleotide X to appear in the sequence. Hence the strength of the anomalous scalar potential would depend on DNA and vanish for DNA for which A and T *resp.* G and C appear with the same frequency.

7.2 Chargaff's second parity rule and the vanishing of net anomalous charge

Chargaff's second parity rule states that the frequencies of nucleotides for single DNA strand satisfy the conditions $p(A) \simeq p(T)$ and $p(C) \simeq p(G)$ (I am grateful for Faramarz Faghihi for mentioning this rule and the related article [78] to me). This rule holds true in a good approximation. In the recent context the interpretation would be as the vanishing of the net anomalous charge of the DNA strand and thus charge conjugation invariance. Stability of DNA might explain the rule and the poly-A tail in the untranslated mRNA could relate stabilization of DNA and mRNA strands.

Together with $p(A)+p(T)+p(G)+p(C) = 1$ Chargaff's rule implies the conditions

$$\begin{array}{llll} p(A)+p(C) \simeq 1/2 \ , & p(A)+p(G) \simeq 1/2 \ , \\ p(T)+p(C) \simeq 1/2 \ , & p(T)+p(G) \simeq 1/2 \ . \end{array} \tag{7.3}$$

An interesting empirical finding [78] is that only some points at the line $p(A)+p(C) \simeq 1/2$ are realized in the case of human genome and that these points are in a good accuracy expressible in terms of Fibonacci numbers resulting as a prediction of optimization problem in which Fibonacci numbers are however put in by hand. $p(A) = p(G) = p(C) = p(T) = 1/4$ results as a limiting case. The poly-A tail of mRNA (not coded by DNA) could reflect to the compensation of this asymmetry for translated mRNA.

The physical interpretation would be as a breaking of isospin symmetry in the sense that isospin up and down states for quarks (A and G *resp.* T and C) do not appear with identical probabilities. This need not have any effect on protein distributions if the asymmetry corresponds to asymmetry for the third nucleotide of the codon having $A \leftrightarrow G$ and $T \leftrightarrow C$ symmetries as almost exact symmetries. This of course if protein distribution is invariant under this symmetry for the first two codons.

The challenge would be to understand the probabilities $p_3(X)$ for the third codon from a physical model for the breaking of isospin symmetry for the third codon in the sense that u and $\overline{u}$ at DNA space-time sheet are more favored than d and $\overline{d}$ or vice versa. There is an obvious analogy with spontaneous breaking of vacuum symmetry.

7.3 Are genes and other genetic sub-structures singlets with respect to QCD color?

Genes are defined usually as transcribed portions of DNA. Genes are however accompanied by promoter regions and other regions affecting the transcription so that the definition of what one really means with gene is far from clear. In the recent case gene would be naturally tqc program module and gene in standard sense would only correspond to its sub-module responsible for the translated mRNA output of tqc.

Whatever the definition of gene is, genes as tqc program modules could be dynamical units with respect to color interaction and thus QCD color singlets (QCD color should not be confused with braid color) or equivalently - possess integer valued anomalous em charge.

One can consider two alternative working hypothesis - in a well-defined sense diametrical opposites of each other.

1. The division of the gene into structural sub-units correlates with the separation into color singlets. Thus various structural sub-units of gene (say transcribed part, translated part, intronic portions, etc...) would be color singlets.

2. Also different genetic codes that I have discussed in [N4] could distinguish between different structural sub-units. For this option only gene - understood as tqc unit with un-transcribed regions included - would be color singlet.

Color singletness condition is unavoidable for mRNA and leads to a testable prediction about the length of poly-A tail added to the transcribed mRNA after translation.

7.3.1 The condition of integer valued anomalous charge for coding regions

In the case of coding region of gene the condition for integer charge is replaced by the conditions

$$n(A) + n(G) \ \ mod \ \ 3 = 0 \ , \qquad n(C) + n(T) \ \ mod \ \ 3 = 0 \ . \tag{7.4}$$

These conditions are not independent and it suffices to check whether either of them is satisfied. The conditions are consistent with $A \leftrightarrow G$ and $T \leftrightarrow C$ symmetries of the third nucleotide. Note that the contribution of the stop codon (TAA, TGA or TAG) and initiating codon ATG to the A+G count is one unit.

7.3.2 General condition for integer valued anomalous charge

The anomalous charge of gene or even that of an appropriate sub-unit of gene is integer valued implies in the general case

$$n(A) - n(T) + n(G) - n(C) \ \ mod \ \ 3 = 0 \ . \tag{7.5}$$

Note that this condition does not assume that gene corresponds to $3n$ nucleotides (as I had accustomed to think). The surprising (to me) finding was that gene and also mRNA coding region of the gene in general fails to satisfy $3n$ rule. This rule is of course by no means requiredonly the regions coding for proteins can be thought of as consisting of DNA triplets.

A possible interpretation is in terms of TGD based model for pre-biotic evolution [N4] according to which genetic code (or 3-code) was formed as a fusion of 2-code and 1-code. 2-code and 1-code could still be present in genome and be associated with non-translated regions of mRNA preceding and following the translated region. The genes of 2-code and coding for RNA would have $2n$ nucleotides and the genes of 1-code could also consist of odd number of nucleotides.

There might be analogy with drawings for a building. These contain both figures providing information about building and text giving meta-level information about how to interpret figures. Figures could correspond to 3-code coding for proteins and text could be written with other codes and give instructions for the transcription and translation processes. Prokaryotic code would contain mostly figures (CDS). In eukaryotic code intronic portions could carry rich amounts of this kind of metalevel information. In the case of mRNA untranslated region preceding $5'$ end could provide similar information.

1. Repeating sequences consisting of n copies of same repeating unit could obey 1-code or 2-code. The simplest building blocks of repeating sequences are AT and CG having vanishing anomalous em charge. TATATA.... and CGCGCG... indeed appear often. Also combinations of CG and AT could repeat: so called mini-satellites are CG rich repeating sequences. Interpretation in terms of 2-code suggests itself.

2. Triplet of the unit ATTCG with integer charge repeats also often: in this case 3-code suggests itself. Telomeres of vertebrates consist of a repeating unit TTAGGG which does not have integer charge: this unit appears also as 8-nucleotide variant which suggests 2-code. Color singletness would require that this unit appears $3n$ times.

3. I have also proposed that intronic regions could obey memetic code [11] predicting that intronic codon can be represented as a sequence of 21 3-codons (implying 2^{63} 63-codons!). Individual intronic segments need not satisfy this rule, only their union if even that. Direct experimentation with gene bank data show that neither introns nor their union correspond to integer multiples of 63 nor 3 or 2 in general.

7.3.3 Color singletness conditions for gene

Gene is usually defined as the sequence of DNA coding for mRNA. mRNA involves also two untranslated regions (UTRs) [77].

1. The $5'$ end of mRNA contains $5'$ cap (methylated G) and $5'$ untranslated region (UTR). The latter can be several kb long for eukaryotes. Methylated G is not coded by DNA but added so that it does not contribute to A+G-T-C count at DNA level.

2. mRNA continues after the stop codon as $3'$ UTR. Translation assigns to UTR also a poly-A tail (up to several hundreds A:s) not coded by DNA and not contributing to A+G-T-C count in the case of DNA. This region contains also AAUAAA which does not contribute to A+G-T-C count of mRNA.

   One could argue that any amino-acid sequence must allow coding and that one function of UTRs is to guarantee integer valued charge for the part of gene beginning from the initiating codon. Of course, also the non-transcribed regions of DNA not included in the standard definition of gene could take care of this.

7.3.4 Color singletness conditions for mRNA

Both poly-A tail and G gap are known to relate to the stabilization of mRNA. The mechanism could be addition of an anomalous charge compensating for the anomalous charge of mRNA to guarantee that second Chargaff's rule is satisfied in a good approximation: this hypothesis is testable.

Second function would be to guarantee color-singletness property. Color singletness would mean that transcribed mRNA + cap G + poly-A tail as a separate unit must be QCD color singlet at DNA space-time sheet. mRNA stability requires the condition

$$n(A) - n(T) + n(G) - n(C) + n_{tail}(A) + 1 \ \ mod \ \ 3 = 0 \tag{7.6}$$

to be satisfied. The knowledge of gene would thus predict $n_{tail}(A) \ \ mod \ \ 3$. This hypothesis is testable.

7.3.5 Chargaff's rule for mRNA

If Chargaff's rule applies also to mRNA strands one obtains one of the following predictions

$$\begin{aligned} 2\left[n(A)+n_{tail}(A)-n(T)\right]-\left[n(G)+1-n(C)\right] &\simeq 0 \ , \\ -\left[n(A)+n_{tail}(A)-n(T)\right]+2\left[n(G)+1-n(C)\right] &\simeq 0 \ , \\ -2\left[n(A)+n_{tail}(A)-n(T)\right]+\left[n(G)+1-n(C)\right] &\simeq 0 \ , \\ \left[n(A)+n_{tail}(A)-n(T)\right]-2\left[n(G)+1-n(C)\right] &\simeq 0 \ . \end{aligned} \tag{7.7}$$

Here $n_{tail}(A)$ includes also AAUAA contributing 3 units to it plus possible other structures appearing in the tail added to the translated mRNA. The presence of poly-A tail which could also compensate for the ordinary negative charge of translated part of mRNA would suggest that A corresponds to u or $\overline{d}$ corresponding to options 1 and 4.

7.3.6 Moving genes and repeating elements

Transposons [109, 110] are moving or self-copying genes. Moving genes cut from initial position and past to another position of double strand. Copying genes copy themselves first to RNA and them to a full DNA sequence which is then glued to the double strand by cut and paste procedure. They were earlier regarded as mere parasites but now it is known that their transcription is activated under stress situations so that they help DNA to evolve. In tqc picture their function would be to modify tqc hardware. For copying transposons the cutting of DNA strand occurs usually at different points for DNA and cDNA so that "sticky ends" result ("overhang" and its complement) [111]. Often the overhang has four nucleotides. The copied transposon have ends which are reversed conjugates of each other so that transposons are palindromes as are also DNA hairpins. This is suggestive of the origin of transposons.

In order to avoid boring repetitions let us denote by "satisfy P" for having having integer valued (or even vanishing) Q_a. The predictions are following:

1) The double strand parts associated with the segments of DNA produced by cutting should satisfy P.

2) The cutting of DNA should take place only at positions separated by segments satisfying P.

3) The overhangs should satisfy P.

4) Transposons should satisfy P: their reverse ends certainly satisfy P.

In the example mentioned in [112] the overhang is $CTAG$ and has vanishing Q_a. The cut site $CCTAGG$ has also vanishing Q_a. It is known [110] that transposons - repeating regions themselves - tend to attach to the repeating regions of DNA [113].

1. There are several kinds of repeating regions. 6-10 base pair long sequences can be repeated in untranslated regions up to 10^5 times and whole genes can repeat themselves $50-10^4$ times.

2. Repeats are classified into tandems (say TTAGGG associated with telomeres), interspersed repetitive DNA (nuclear elements), and transposable repeat elements. Interspersed nuclear elements (INEs) are classified LINEs (long), SINEs (short), TLTRs (Transposable elements with Long Terminal Repeats), and DNA transposons themselves.

3. LINEs contain AT rich regions. SINEs known as alus (about 280 bps) contain GC rich regions whereas mariner elements (about 80 bps) are flanked by TA pairs. LTRs have length 300-1000 bps. DNA transposons are flanked with two short inverted repeat sequences flanking the reading frame: "inverted" refers to the palindrome property already mentioned.

AT and CG have vanishing Q_a so that their presence in LINEs and SINEs would make the cutting and pasting easy allowing to understand why transposons favor these regions. Viruses are known to contain long repeating terminal sequences (LTR). One could also check whether DNA decomposes to regions satisfying P and surrounded by repeating sequences which satisfy P separately or as whole as in the case DNA transposons.

7.3.7 Tests

Some checks of the color singletness hypothesis were made for human genome [76].

1. For the coding sequences (CDSs) the strong prediction in general fails as expected (condition would pose restrictions on possible amino-acid contents).

2. Color singletness condition fails for genes defined in terms of translated part of mRNA (with gap and poly-A tail excluded). The un-transcribed regions of DNA involved with the gene expression (promoter region, etc...) could guarantee the color singletness. They could also stabilize DNA by bringing in compensating anomalous charge to guarantee second Chargaff's rule. Different genetic codes could distinguish between the subunits of gene.

3. To test color singletness conditions for mRNA one should know the length of poly-A tail. Unfortunately, I do not have access to this information.

4. The computation of total anomalous charges for a handful of genes, introns, and repeat units for some gene bank examples in the case of human genome indicates that both of them tend to carry net em charge which is largest for $(a, g) \leftrightarrow (\overline{d}, \overline{u})$ correspondence. The charge is in the range 5-10 per cent from the charge associated with the phosphates (-2 units per nucleotide). For second option giving negative charge (permute u and d) the anomalous charge is few per cent smaller.

   By Chargaff's law the regions outside genes responsible for the control of gene expression must contain a compensating charge of opposite sign. Kind of spontaneous symmetry breaking of charge conjugation symmetry $A \leftrightarrow T, G \leftrightarrow C$ and analogous to matter antimatter symmetry seems to take place. That control regions and translated regions have opposite densities of anomalous charge might also help in the control gene expression.

5. The poly-A tail of mRNA would carry compensating positive anomalous charge: the RNA-quark assignment could be conjugate to the DNA-quark assignment as suggested by what takes place in transcription. For instance, for the option $A \to \overline{d}$, the prediction for the length of polytail for $A \to \overline{d}$ option would be about $n_{tail}/n_{mRNA} \simeq 3p_a(mRNA)$ where $N(mRNa)$ is the number of nucleotides in transcribed mRNA and $p_a(mRNA)$ is the per cent of anomalous charge which is typically 5-10 per cent. For $p_a(mRNA) = 10$ per cent this gives as much as 30 per cent. For $A \to \overline{u}$ option one has $n_{tail}/n_{mRNA} \simeq 3p_a(mRNA)/2$. In this case also p_a is considerably smaller, typically by a factor of of order 2-3 per cent and even below per cent in some cases. Hence the relative length of tail would around 3-5 per cent. This option is perhaps more since it minimizes anomalous charge and maximizes the effectiveness of charge compensation by poly-A tail.

6. The predictions for transposons and their cut and past process should be easily testable.

7.4 Summary of possible symmetries of DNA

The following gives a list of possible symmetries of DNA inspired by the identification of braid color.

7.4.1 Color confinement in strong form

The states of quarks and anti-quarks associated with DNA both wormhole wormhole throats of braided (living) DNA strand can be color singlets and have thus integer valued anomalous em charge. The resulting prediction depends on the assignment of quarks and antiquarks to A,T,C,G which in principle should be determined by the minimization of em interaction energy between quark and nucleotide. For instance $2(A-T)-(G-C) \ \ mod \ \ 3 = 0$ for a piece of living DNA which could make possible color singletness. As a matter fact, color singletness conditions are equivalent for all possible for braid color assignments. This hypothesis might be weakened. For instance, it could hold true only for braided parts of DNA and this braiding are dynamical. It could also hold for entire braid with both ends included only: in this case it does not pose any conditions on DNA.

Questions: Do all living DNA strands satisfy this rule? Are only the double stranded parts of DNA braided and satisfy the rule. What about loops of hairpins?

7.4.2 Matter antimatter asymmetry at quark level

$A \leftrightarrow T$ and $G \leftrightarrow C$ corresponds to charge conjugation at the level of quarks (quark $\leftrightarrow$ antiquark). Chargaff's rules states $A \simeq T$ and $C \simeq G$ for long DNA strands and mean matter-antimatter symmetry in the scale of DNA strand. Double strand as a whole is matter anti-matter symmetric.

Matter-antimatter asymmetry is realized functionally at the level of DNA double strand in the sense that only DNA strand is transcribed. The study of some examples shows that genes defined as transcribed parts of DNA do not satisfy Chargaff's rule. This inspires the hypothesis about the breaking of matter antimatter symmetry. Genes have non-vanishing net $A-T$ and $C-G$ and therefore also net Q_a with sign opposite to that in control regions. Just as the Universe is matter-antimatter asymmetric, also genes would be matter-antimatter asymmetric.

7.4.3 Isospin symmetry at quark level

$A \leftrightarrow G$ and $T \leftrightarrow A$ correspond change of anomalous em charge by 1 unit and these operations respect color confinement condition. Local modifications of DNA inducing these changes should be preferred. The identification for the symmetries $A \leftrightarrow G$ and $T \leftrightarrow A$ for the third nucleotide of code is as isospin symmetries. For the vertebrate mitochondrial code the symmetry exact and for nuclear code slightly broken.

7.4.4 Matter antimatter asymmetry and isospin symmetries for the first two nucleotides

The first two nucleotides of the codon dictate to a high degree which amino-acid is coded. This inspires the idea that 3-code has emerged as fusion of 1- and 2-codes in some sense. There are two kinds of 2-codons. The codons of type A have fractional em charge and net quark number (consisting of either matter or antimatter at quark level) and are not able to form color singlets. The codons of type B have integer em charge and vanishing quark number (consisting of matter and antimatter) and are able to form color singlets. The 2-codons of type A (resp. B) are related by isospin rotations and there should be some property distinguishing between types A and B. There indeed is: if 2-codon is matter-antimatter symmetric, 1-codon is not and vice versa.

1. For almost all type A codons the amino-acid coded by the codon does not depend on the last nucleotide. There are two exceptions in the case of the nuclear code: (leu,leu,phe,phe) and (ile,ile,ile,met). For human mitochondrial code one has (ile,ile,ile,ile) and thus only one exception to the rule. The breaking of matter-antimatter symmetry for the third nucleotide is thus very small.

2. For codons of type B the 4-columns code always for two doublets in the case of vertebrate mitochondrial code so that for codons with vanishing net quark number the breaking of matter-antimatter symmetry for the third nucleotide is always present.

7.4.5 Em stability

Anomalous em charge Q_a vanishes for DNA and perhaps also mRNA strand containing also the G cap and poly-A tail which could compensate for the Q_a of the transcribed region so that

$$2(A-T)-(G-C) \simeq 0$$

or some variant of it holds true. Chargaff's rules for long DNA strands imply the smallness of Q_a.

7.4.6 Summary of testable working hypothesis

Following gives a summary of testable working hypothesis related to the isospin symmetry and color singletness. The property of having integer valued/vanishing Q_a is referred to as property P.

1. Gene plus control region and also DNA repeats should have property P. Transcribed and control regions of gene have Q_a with opposite signs.

2. Transposons, repeating regions, the overhangs associated with the cut and paste of transposon, and the DNA strands resulting in cutting should have property P. This could explain why transposons can paste themselves to AT and GC ($Q_a = 0$) rich repeating regions of DNA. The points at which DNA can be cut should differ by a DNA section having property P. This gives precise predictions for the points at which transposons and pieces of viral DNA can join and could have implications for genetic engineering.

3. If also mRNA is braided, it has property P. This can be only true if the poly-A tail compensates for the non-vanishing Q_a associated with the translated region.

4. Living hairpins should have property P. If only double helix parts of hairpins are braided, the prediction is trivially true by the palindrome property. tRNA or at least parts of it could be braided. Braids could end to the nuclear membrane or mRNA or to the amino-acid attachable to tRNA. For stem regions Q_a is integer valued. The fact that the nucleotide of the anticodon corresponding to the third nucleotide of codon can base pair with several nucleotides of mRNA suggests that $I(nositol)$ can have Q_a opposite to that of A, T, C and U opposite to that of A, G. For 2-anticodon the pairing would be unique. This would give a lot of freedom to achieve property P in weak sense for tRNA. Braid structure for tRNA + amino-acid could be different that for tRNA alone and also in the translation the braid structure could change.

5. Telomeres [114] are of special interests as far as anomalous em charge is considered. Chromosomes are not copied completely in cell replication, and one function of telomeres is to guarantee that the translated part of genome replicates completely for sufficiently many cell divisions. Telomeres consists of 3-20 kilobases long repetitions of TTAGGG, and there is a 100-300 kilobases long repeating sequence between telomere and the rest of the chromosome. Telomeres can form can also 4-stranded structures. Telomere end contains a hair-pin loop as a single stranded part, which prevents the action of DNA repair enzymes on the chromosome end. Telomerase is a reverse transcriptase enzyme involved with the synthesis of telomeres using RNA strand as a template but since its expression is repressed in many types of human cells, telomere length shortens in each cell replication. In the case of germ cells, stem cells and white blood cells telomerase is expressed and telomere length preserved. Telomere shortening is known to relate to ageing related diseases. On the other hand, overactive telomere expression seems to correlate with cancer.

   If telomeres possess braid strands, the compensation of Q_a might provide an additional reason for their presence. If this the case and if telomeres are strict multiples of TTAGGG, the shortening of telomeres generates a non-vanishing Q_a unless something happens for the active part of DNA too. Color singletness condition should however remain true: the disappearance of $3n$ multiples of TTAGGG in each replication is the simplest guess for what might happen. In any case, DNA strands would become unstable in cell replication. Q_a could be reduced by a partial death of DNA in the sense that some portions of braiding disappear. Also this would induce ill functioning of tqc harware perhaps related to ageing related diseases. Perhaps evolution has purposefully developed this ageing mechanism since eternal life would stop evolution.

6. Also aminoacids could be braided. Q_a could vary and correspond to Q_a for one of the codons coding for it. The aminoacid sequences of catalysts attaching to DNA strand should have opposite Q_a for each codon-aminoacid pair so that aminoacid would attach only to the codons coding for it. The TGD based model for nerve pulse [M2] inspires the proposal that magnetic flux tubes connecting microtubules to the axonal membrane allow tqc during nerve pulse propagation when axonal membrane makes transition from gel like phase to liquid crystal phase. Aminoacids of tubulin dimers would be connected by 3-braids, smallest interesting braid, to groups of 3-lipids in axonal membrane and tubulin dimers would define fundamental tqc modules.

7.5 Empirical rules about DNA and mRNA supporting the symmetry breaking picture

Somewhat surprisingly, basic facts which can be found from Wikipedia, support the proposed vision about symmetry breaking although, the mechanism of matter antimatter symmetry breaking is more

complex than the first guess. I am grateful for Dale Trenary for references which made possible to realize this. Before continuing some comments about the physical picture are in order.

1. The vanishing of the induced Kähler field means that the space-time sheet of DNA is a highly unstable vacuum extremal. The non-vanishing of the induced Kähler electric field is thus a natural correlate for both the stability and the non-vanishing quark number density (matter antimatter asymmetry). The generation of matter antimatter asymmetry induces a net density of anomalous em charge, isospin, and quark number in the portion of DNA considered. This in turn generates not only longitudinal electric field but also a longitudinal Kähler electric field along DNA.

2. Weak electric fields play a key role in living matter. There are electric fields associated with embryos, central nervous system, individual neurons, and microtubules and their direction determines the direction of a process involved (head-to-tail direction, direction of propagation of nerve pulse, ...).

3. Same mechanism is expected to be at work also in the case of DNA and RNA. In the case of gene the direction of transcription could be determined by the direction of the electric field created by gene and telomeres at the ends of chromosomes carrying a net anomalous quark number could be partially responsible for the generation of this field. In the case of mRNA the direction of translation would be determined in the similar manner. The net anomalous em charges of poly-A tail and the transcribed part of mRNA would have opposite signs so that a longitudinal electric field would result.

It will be found that this picture is consistent with empirical findings about properties of DNA.

7.5.1 Breaking of matter antimatter symmetry and isospin symmetry for entire genome

Chargaff's rules are not exact and the breaking gives important information about small breakings of isospin and matter-antimatter symmetries at the level of entire genome. The basic parameters are em charge per nucleotide, isospin per nucleotide, the amount of quark number per nucleotide, and the ratio of u and d type matters coded by $(G+C)/(A+T)$ ratio. Recall that there are four options for the map of A,T,C,G to quarks and antiquarks and for option 3) *resp.* 4) the anomalous em charge is opposite to that for 1) *resp.* 2).

The following table gives A,T,C,G contents (these data are from Wikipedia [118]), the amount of quark charge per nucleotide for the options 1) *resp.* 2) given by $dq_1/dn = p[2(A-T)-G-C)]/3$ *resp.* $dq_2/dn = p[A-T-2(G-C)]/3$, the amount $dI_3/dn = p(A-G+C-T]/2$ of isospin per nucleotide, the amount $d(q-\overline{q})/dn = p(A-T+G-C)$ of quark number per nucleotide, and $(A+T)/(C+G)$ ratio for *entire genomes* in some cases. It will be found that so called Szybalski's rules state that for coding regions there is breaking of the approximate matter antimatter asymmetry.

Note that matter antimatter asymmetry in the scale of entire genome has largest positive value for human genome and negative value only for yeast genome: this case the magnitude of the asymmetry is largest.

	$Human$	$Chicken$	$Grass-$ $hopper$	Sea $Urchin$	$Wheat$	$Yeast$	$E.Coli$
$p(A)$	0.3090	0.2880	0.2930	0.3280	0.2730	0.3130	0.2470
$p(T)$	0.2940	0.2920	0.2930	0.3210	0.2710	0.3290	0.2360
$p(C)$	0.1990	0.2050	0.2050	0.1770	0.2270	0.1870	0.2600
$p(G)$	0.1980	0.2170	0.2070	0.1730	0.2280	0.1710	0.2570
$\frac{dq_1}{dn}$	0.0103	−0.0067	−0.0007	0.0060	0.0010	−0.0053	0.0083
$\frac{dq_2}{dn}$	0.0057	−0.0093	−0.0013	0.0050	−0.0000	0.0053	0.0057
$\frac{dI_3}{dn}$	0.0080	−0.0080	−0.0010	0.0055	0.0005	0.0000	0.0070
$\frac{d(q-\overline{q})}{dn}$	0.0140	0.0080	0.0020	0.0030	0.0030	−0.0320	0.0080
$\frac{p(A+T)}{p(G+C)}$	1.5189	1.3744	1.4223	1.8543	1.1956	1.7933	0.9342

(7.8)

For option 2) the amount of anomalous charge is about .0057e per nucleotide and thus about $3\times 10^7 e$ for entire human DNA having length of about 1.8 meters. The inspection of tables of [114] shows that the anomalous em charge for the repeating sequence defining the telomere is always non-vanishing and has always the same sign. Telomeres for human chromosomes consist of TTAGGG repetitions with anomalous em charge with magnitude $5e/3$ for all options and have a length measured in few kbases. Human genome as has 24 chromosomes so that the total anomalous em charge of telomeres is roughly $24 \times (5/18) \times x10^3 e \sim .8 \times 10^3 xe$, $1 < x < 10$. The anomalous em charge of telomeres is three orders of magnitude smaller than that of entire DNA but if DNA is quantum critical system the change the total anomalous em charge and quark number due to the shortening of telomeres could induce instabilities of DNA (due to the approach to vacuum extremal) contributing to ageing. Note that the small net value of quark number in all the cases considered might be necessary for overall stability of DNA. Telomeres are also known to prevent the ends of chromosomes to stick to each other. This could be partially due to the Coulomb repulsion due to the anomalous em charge.

According to [118] Chargaff's rules do not apply to viral organellar genomes (mitochondria [115], plastids) or single stranded viral DNA and RNA genomes. Thus approximate matter antimatter symmetry fails for DNA:s of organelles involved with metabolism. This might relate to the fact that the coding portion of DNA is very high and repeats are absent. Chargaff's rule applies not only to nucleotides but also for oligonucleotides which corresponds to DNA or RNA sequences with not more than 20 bases. This means that for single strand oligonucleotides and their conjugates appear in pairs. Matter antimatter asymmetry would be realized as presence of matter blobs and their conjugates. This might relate to the mechanism how the sequences of oligonucleotides are generated from DNA and its conjugate.

7.5.2 Breaking of matter antimatter symmetry for coding regions

As noticed, one can consider three type of symmetry breaking parameters for DNA in DNA as tqc model. There are indeed three empirical parameters of this kind. Chargaff' rules have been already discussed and correspond to approximate matter antimatter symmetry. The second asymmetry parameter would measure the asymmetry between $u\overline{u}$ and $d\overline{d}$ type matter. $p(G+C)$ corresponds to the fraction of $d\overline{d}$ type quark matter for option 1) and $u\overline{u}$ matter for option 2). It is known that G+C fraction $p(G+C)$ characterizes genes [117] and the value of $p(G+C)$ is proportional to the length of the coding sequence [117, 116].

Besides Chargaff' rules holding true for entire genome also Szybalski's rules [118] hold true but only for coding coding regions. The biological basis of neither rules is not understood. The interpretation of Chargaff's rules would be in terms of approximate matter antimatter symmetry and the vanishing of net isospin at the level of quarks whereas Szybalski's rule would state the breaking of these symmetries non-coding regions. Hence all the three basic empirical rules would have a nice interpretation in DNA as tqc picture.

Consider now Szybalski's rules in more detail.

1. In most bacterial genomes (which are generally 80-90 % coding) genes are arranged in such a fashion that approximately 50 % of the coding sequence lies on either strand. Note that either strand can act as a template (this came as a surprise for me). Szybalski, in the 1960s, showed that in bacteriophage coding sequences purines (A and G) exceed pyrimidines (C and T). This rule has since been confirmed in other organisms and known as Szybalski's rule [118, 119]. While Szybalski's rule generally holds, exceptions are known to exist.

   Interpretation. A breaking of matter antimatter symmetry occurs in coding regions such that the net breakings are opposite for regions using different templates and thus different directions of transcription (promoter to the right/left of coding region).

2. One can actually characterize Szybalski's rules more precisely. By Chargaff's rules one has $p(A+T) \simeq 1 - p(G+C))$. In coding regions with low value of $p(G+C)$ $p(A)$ is known to be higher than on the average whereas for high value of $p(G+C)$ $p(G)$ tends to higher than on the average.

   Interpretation. These data do not fix completely the pattern of breaking of the approximate matter antimatter symmetry.

i) It could take place for both kinds of quark matter ($u\overline{u}$ and $d\overline{d}$): both $p(A)$ and $p(G)$ would increase from its value for entire genome but the dominance of A over G or vice versa would explain the observation.

ii) The breaking could also occur only for the dominating type of quark matter ($u\overline{u}$ or $d\overline{d}$) in which case only $p(A)$ or $p(G)$ would increase from the value for entire genome.

Also a net isospin is generated which is of opposite sign for short and long coding sequences so that there must be some critical length of the coding sequences for which isospin per nucleotide vanishes. This length should have biological meaning.

3. For mRNA $A+G$ content is always high. This is possible only because the template part of the DNA which need not be always the same strand varies so that if it is strand it has higher $A+G$ content and if it is conjugate strand it has higher $T+C$ content.

Interpretation. mRNA breaks always matter antimatter symmetry and the sign of matter antimatter asymmetry is always the same. Thus mRNA is analogous to matter in observed universe. The poly-A tail added to the end of mRNA after transcription to stabilize it would reduce the too large values of isospin and anomalous em charge per nucleon due to the fact that mRNA does not contain regions satisfying Chargaff's rules. It would also generate the needed longitudinal electric field determining the direction of translation. In the case of DNA the breaking of matter antimatter symmetry is realized at the functional level by a varying direction of transcription and variation of template strand so that matter antimatter symmetry for the entire DNA is only slightly broken. Direction of transcription would be determined by the direction of the electric field. The stability of long DNA sequences might require approximate matter antimatter symmetry for single DNA strand if it is long. In the case of simple genomes (mitochondrial, plastid, and viral) the small size of the genome, the high fraction of coding regions, and the absence of repeating sequences might make approximate matter antimatter symmetry un-necessary. An interesting working hypothesis is that the direction of transcription is always the same for these genomes.

One can try to use this information to fix the most probable option for nucleotide quark correspondence.

1. In nuclear physics the neutron to proton ratio of nucleus increases as nucleus becomes heavier so that the nuclear isospin becomes negative: $I_3 < 0$. The increase of the nuclear mass corresponds to the increase for the length of the coding region. Since G/A fraction increases with the length of coding region, G should correspond to either d quark ($(Q_a < 0, I_3 = -1/2)$) or its charge conjugate d_c ($Q_a < 0$). Hence option 1) or its charge conjugate would be favored.

2. If one takes very seriously the analogy with cosmic matter antimatter asymmetry then matter should dominate and only $(A, G, T, C) \to (u, d, \overline{u}, \overline{d})$ option would remain.

Szybalski's findings leave open the question whether non-coding regions obey the Chargaff' rules in good approximation or whether also they appear as pairs with opposite matter antimatter asymmetry. Introns are belong to coding regions in the sense that they are transcribed to mRNA. Splicing however cuts them off from mRNA. It is not clear whether introns break the approximate matter antimatter symmetry or not. If breaking takes place it might mean that introns code for something but not chemically. On the other hand, the absence of asymmetry might serve at least partially as a signal telling that introns must be cut off before translation. Many interesting questions represent itself. For instance, how the symmetry breaking parameters, in particular matter antimatter asymmetry parameter, depend on genes. The correlation with gene length is the most plausible guess.

7.6 Genetic codes and tqc

TGD suggests the existence of several genetic codes besides 3-codon code [L1, N4]. The experience from ordinary computers and the fact that genes in general do not correspond to $3n$ nucleotides encourages to take this idea more seriously. The use of different codes would allow to tell what kind of information a given piece of DNA strand represents. DNA strand would be like a drawing of building containing figures (3-code) and various kinds of text (other codes). A simple drawing for the building would become a complex manual containing mostly text as the evolution proceeds: for humans 96 per cent of code would corresponds to introns perhaps obeying some other code.

The hierarchy of genetic codes is obtained by starting from n basic statements and going to the meta level by forming all possible statements about them (higher order logics) and throwing away one which is not physically realizable (it would correspond to empty set in the set theoretic realization). This allows $2^n - 1$ statements and one can select 2^{n-1} mutually consistent statements (half of the full set of statements) and say that these are true and give kind of axiomatics about world. The remaining statements are false. DNA would realize only the true statements.

The hierarchy of Mersenne primes $M_n = 2^n - 1$ with $M_{n(next)} = M_{M_n}$ starting from $n = 2$ with $M_2 = 3$ gives rise to 1-code with 4 codons, 3-code with 64 codons, and $3 \times 21 = 63$-code with 2^{126} codons [L1] realized as sequences of 63 nucleotides (the length of 63-codon is about $2L(151)$, roughly twice the cell membrane thickness. It is not known whether this Combinatorial Hierarchy continues ad infinitum. Hilbert conjectured that this is the case.

In the model of pre-biotic evolution also 2-codons appear and 3-code is formed as the fusion of 1- and 2-codes. The problem is that 2-code is not predicted by the basic Combinatorial Hierarchy associated with $n = 2$.

There are however also other Mersenne hierarchies and the next hierarchy allows the realization of the 2-code. This Combinatorial Hierarchy begins from Fermat prime $n = 2^k + 1 = 5$ with $M_5 = 2^5 - 1 = 31$ gives rise to a code with 16 codons realized as 2-codons (2 nucleotides). Second level corresponds to Mersenne prime $M_{31} = 2^{31} - 1$ and a code with $2^{30=15\times 2}$ codons realized by sequences of 15 3-codons containing 45 nucleotides. This corresponds to DNA length of 15 nm, or length scale $3L(149)$, where $L(149) = 5$ nm defines the thickness of the lipid layer of cell membrane. $L(151) = 10$ nm corresponds to 3 full 2π twists for DNA double strand. The model for 3-code as fusion of 1- and 2-codes suggests that also this hierarchy - which probably does not continue further - is realized.

There are also further short Combinatorial hierarchies corresponding to Mersenne primes [16].

1. $n = 13$ defines Mersenne prime M_{13}. The code would have $2^{12=6\times 2}$ codons representable as sequences of 6 nucleotides or 2 3-codons. This code might be associated with microtubuli.

2. The Fermat prime $17 = 2^4 + 1$ defines Mersenne prime M_{17} and the code would have $2^{16=8\times 2}$ codons representable as sequences of 8 nucleotides.

3. $n = 19$ defines Mersenne prime M_{19} and code would have $2^{18=9\times 2}$ codons representable as sequences of 9 nucleotides or three DNA codons.

4. The next Mersennes are M_{31} belonging to $n = 5$ hierarchy, M_{61} with $2^{60=30\times 2}$ codons represented by 30-codons. This corresponds to DNA length $L(151) = 10$ nm (cell membrane thickness). M_{89} (44-codons), M_{107} (53-codons) and M_{127} (belonging to the basic hierarchy) are the next Mersennes. Next Mersenne corresponds to M_{521} (260-codon) and to completely super-astrophysical p-adic length scale and might not be present in the hierarchy.

   This hierarchy is realized at the level of elementary particle physics and might appear also at the level of DNA. The 1-, 2-, 3-, 6-, 8-, and 9-codons would define lowest Combinatorial Hierarchies.

8 Cell replication and tqc

DNA as tqc model leads to quite detailed ideas about the evolution of the genetic code and the mechanisms of bio-catalysis and of protein folding [N4]. These applications in turn leads to a considerable generalization of DNA as tqc concept [N4]. The presence of braiding leads also to a revision of the model of nerve pulse and EEG [M2, M3]. Here the discussion is restricted to one particular example. One can look what happens in the cell replication in the hope of developing more concrete ideas about tqc in multicellular system. This process must mean a replication of the braid's strand system and a model for this process gives concrete ideas about how multicellular system performs tqc.

8.1 Mitosis and tqc

Mitosis is the form of cell replication yielding soma cells and it is interesting what constraints this process gives on tqc and whether the special features of this process could be understood from computational point of view.

1. During mitosis chromosomes [71] are replicated. During this process the strands connecting chromosomes become visible: the pattern brings in mind flux tubes of magnetic field. For prokaryotes the replication of chromosomes is followed by the fission of the cell membrane. Also plant nuclei separated by cellulose walls suffer fission after the replication of chromosomes. For animals nuclear membranes break down before the replication suggesting that nuclear tqc programs are reset and newly formed nuclei start tqc from a clean table. For eukaryotes cell division is controlled by centrosomes [82]. The presence of centrosomes is not necessary for the survival of the cell or its replication but is necessary for the survival of multicellular. This conforms with the proposed picture.

2. If the conjugate strands are specialized in tqc, the formation of new double strands does not involve braids in an essential manner. The formation of conjugate strand should lead to also to a generation of braid strands unless they already exist as strands connecting DNA and its conjugate and are responsible for "printing". These strands need not be short. The braiding associated with printing would be hardware program which could be genetically determined or at least inherited as such so that the strands should be restricted inside the inner cell membrane or at most traverse the inner nuclear membrane and turn back in the volume between inner membrane and endoplasmic reticulum.

   The return would be most naturally from the opposite side of nuclear membrane which suggest a breaking of rotational symmetry to axial symmetry. The presence of centriole implies this kind of symmetry breaking: in neurons this breaking becomes especially obvious. The outgoing braid strands would be analogous to axon and returning braid strands to dendrites. Inner nuclear membrane would decompose the braiding to three parts: one for strand, second for conjugate strand, and a part in the empty space inside nuclear envelope.

3. The formation of new DNA strands requires recognition relying on "strand color" telling which nucleotide can condense at it. The process would conserve the braidings connecting DNA to the external world. The braidings associated with the daughter nuclei would be generated from the braiding between DNA and its conjugate. As printing software they should be identical so that the braiding connecting DNA double strands should be a product of a braiding and its inverse. This would however mean that the braiding is trivial. The division of the braid to three parts hinders the transformation to a trivial braid if the braids combine to form longer braids only during the "printing" activity.

4. The new conjugate strands are formed from the old strands associated with printing. In the case of plants the nuclear envelope does not disintegrate and splits only after the replication of chromosomes. This would suggest that plant cells separated by cell walls perform only intracellular tqc. Hermits do not need social skills. In the case of animals nuclear envelope disintegrates. This is as it must be since the process splits the braids connecting strand and conjugate strands so that they can connect to the cell membrane. The printing braids are inherited as such which conforms with the interpretation as a fixed software.

5. The braids connecting mother and daughter cells to extranuclear world would be different and tqc braidings would give to the cell a memory about its life-cycle. The age ordering of cells would have the architecture of a tree defined by the sequence of cell replications and the life history of the organism. The 4-D body would contain kind of log file about tqc performed during life time: kind of fundamental body memory.

6. Quite generally, the evolution of tqc programs means giving up the dogma of genetic determinism. The evolution of tqc programs during life cycle and the fact that half of them is inherited means kind of quantum Lamarckism [69]. This inherited wisdom at DNA level might partly explain why we differ so dramatically from our cousins.

8.2 Sexual reproduction and tqc

Meiosis [72] produces gametes in which the pair of chromosomes from parents is replaced with single chromosome obtained as chimera of the chromosomes of parents. Meiosis is the basic step of sexual reproduction and it is interesting to study it from tqc point of view.

1. Sexual reproduction of eukaryotes relies on haploid cells differing from diploid cells in that chromatids do not possess sister chromatids. Whereas mitosis produces from single diploid [70] cell two diploid cells, meiosis gives rise to 4 haploid [70] cells. The first stage is very much like mitosis. DNA and chromosomes duplicate but cell remains a diploid in the sense that there is only single centrosome: in mitosis also centrosome duplicates. After this the cell membrane divides into two. At the next step the chromosomes in daughter cells split into two sister chromosomes each going into its own cell. The outcome is four haploid cells.

2. The presence of only single chromatid [73] in haploids means that germ cells would perform only one half of the "social" tqc performed by soma cells [74] who must spend their life cycle as a member of cell community. In some cells the tqc would be performed by chromatids of both father and mother making perhaps possible kind of stereo view about world and a model for couple - the simplest possible social structure.

3. This brings in mind the sensory rivalry between left and right brain: could it be that the two tqc's give competing computational views about world and how to act in it? We would have inside us our parents and their experiences as a pair of chromatids representing chemical chimeras of chromatid pairs possessed by the parents: as a hardware - one might say. Our parents would have the same mixture in software via sharing and fusion of chromatid mental images or via quantum computational rivalry. What is in software becomes hardware in the next generation.¡/p¿¡p¿

4. The ability of sexual reproduction to generate something new relates to meiosis. During meiosis genetic recombination [75] occurs via chromosomal crossover which in string model picture would mean splitting of chromatids and the recombination of pieces in a new manner $(A_1+B_1)+(A_2+B_2) \to (A_1+B_2)+(A_2+B_1)$ takes place in crossover and $(A_1+B_1+C_1)+(A_2+B_2+C_2) \to (A_1+B_2+C_1)+(A_2+B_1+C_2)$ in double crossover. New hardware for tqc would result by combining pieces of existing hardware. What this means in terms of braids should be clarified.

5. Fertilization is in well-define sense the inverse of meiosis. In fertilization the chromatids of spermatozoa and ova combine to form the chromatids of diploid cell. The recombination of genetic programs during meiosis becomes visible in the resulting tqc programs.

8.3 What is the role of centrosomes and basal bodies?

Centrosomes [82] and basal bodies [83] form the main part of Microtubule Organizing Center [84]. They are somewhat mysterious objects and at first do not seem to fit to the proposed picture in an obvious manner.

1. Centrosomes consist two centrioles [85] forming a T shaped antenna like structure in the center of cell. Also basal bodies consist of two centrioles but are associated with the cell membrane. Centrioles and basal bodies have cylindrical geometry consisting of nine triplets of microtubules along the wall of cylinder. Centrosome is associated with nuclear membrane during mitosis.

2. The function of basal bodies which have evolved from centrosomes seems to be the motor control (both cilia [80] and flagella [81]) and sensory perception (cilia). Cell uses flagella and cilia to move and perceive. Flagella and cilia are cylindrical structures associated with the basal bodies. The core of both structures is axoneme having $9 \times 2 + 2$ microtubular structure. So called primary cilia do not posses the central doublet and the possible interpretation is that the inner doublet is involved with the motor control of cilia. Microtubules [86] of the pairs are partially fused together.

3. Centrosomes are involved with the control of mitosis [71]. Mitosis can take place also without them but the organism consisting of this kind of cells does not survive. Hence the presence of centrosomes might control the proper formation of tqc programs. The polymerization of microtubules [86] is nucleated at microtubule self-organizing center which can be centriole or basal body. One can say that microtubules which are highly dynamical structures whose length is changing all the time have their second end anchored to the self-organizing center. Since this function is essential during mitosis it is natural that centrosome controls it.

4. The key to the understanding of the role of centrosomes and basal bodies comes from a paradox. DNA and corresponding tqc programs cannot be active during mitosis. What does then control mitosis?

   i) Perhaps centrosome and corresponding tqc program represents the analog of the minimum seed program in computer allowing to generate an operating system [64] like Windows 2000 (the files from CD containing operating system must be read!). The braid strands going through the microtubules of centrosome might define the corresponding tqc program. The isolation from environment by the microtubular surface might be essential for keeping the braidings defining these programs strictly unchanged.

   ii) The RNA defining the genome of centrosome (yes: centrosome has its own genome defined by RNA rather than DNA [82]!) would define the hardware for this tqc. The basal bodies could be interpreted as a minimal sensory-motor system needed during mitosis.

   iii) As a matter fact, centrosome and basal bodies could be seen as very important remnants of RNA era believed by many biologists to have preceded DNA era. This assumption is also made in TGD inspired model of prebiotic evolution [N4].

   iv) Also other cellular organelles possessing own DNA and own tqc could remain partly functional during mitosis. In particular, mitochondria are necessary for satisfying energy needs during the period when DNA is unable to control the situation so that they must have some minimum amount of own genome.

5. Neurons [90] do not possess centrosome which explains why they cannot replicate. The centrioles are replaced with long microtubules associated with axons and dendrites. The system consisting of microtubules corresponds to a sensory-motor system controlled by the tqc programs having as a hardware the RNA of centrosomes and basal bodies. Also this system would have a multicellular part.

6. Intermediate filaments [87], actin filaments [88], and microtubules [86] are the basic building elements of the eukaryotic cytoskeleton [89]. Microtubules, which are hollow cylinders with outer radius of 24 nm, are especially attractive candidates for structures carrying bundles of braid strands inside them. The microtubular outer-surfaces could be involved with signalling besides other well-established functions. It would seem that microtubules cannot be assigned with tqc associated with nuclear DNA but with RNA of centrosomes and could contain corresponding braid strand bundles. It is easy to make a rough estimate for the number of strands and this would give an estimate for the amount of RNA associated with centrosomes. Also intermediate filaments and actin filaments might relate to cellular organelles having their own DNA.

9 Appendix: A generalization of the notion of imbedding space

In the following the recent view about structure of imbedding space forced by the quantization of Planck constant is described. This view has developed much before the original version of this chapter was written.

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.

9.1 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. Zero energy ontology forces to modify this picture somewhat. In zero energy ontology causal diamonds (CDs) defined as the intersections of future and past directed light-cones are loci for zero energy states containing positive and negative energy parts of state at the two light-cone boundaries. The location of CD in M^4 is arbitrary but p-adic length scale hypothesis suggests that the temporal distances between tips of CD come as powers of 2 using CP_2 size as unit. Thus M^4 is replaces by CD and $\hat{M}^4$ is replaced with $\hat{CD}$ defined in obvious manner.

3. H_4 represents a straight cosmic string inside CD. 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 $\hat{CD} \times \hat{CP}_2$ implying that surfaces in $CD \times S^2$ and $(M^2 \cap CD) \times CP_2$ 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.

4. The covering spaces in question would correspond to the Cartesian products $\hat{CD}_{n_a} \times \hat{CP}_{2n_b}$ of the covering spaces of $\hat{CD}$ and $\hat{CP}_2$ 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 $M^2 \cap CD$ and S^2 with its orbit under G_a (say tedrahedral, octahedral, or icosahedral group). The resulting space will be denoted by $\hat{CD}\hat{\times}G_a$ *resp.* $\hat{CP}_2\hat{\times}G_b$.

5. 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 $M^2 \cap CD$ 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 $M^2 \cap CD$ 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.

6. Also the orbifolds $\hat{CD}/G_a \times \hat{CP}_2/G_b$ can be allowed as also the spaces $\hat{CD}/G_a \times (\hat{CP}_2\hat{\times}G_b)$ and $(\hat{CD}\hat{\times}G_a) \times \hat{CP}_2/G_b$. 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 $(M^2 \cap CD) \times CP_2$ 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 CD degrees of freedom. This is not the case. Light-likeness in $(M^2 \cap CD) \times S^2$ makes sense only for surfaces $X^1 \times D^2 \subset (M^2 \cap CD) \times S^2$, 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 $(M^2 \cap CD) \times S^2$ irrespective of the value of Planck constant requires that X^2 has single point of $(M^2 \cap CD)$ 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 tunneling. 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.

9.2 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 $\hat{CD}\hat{\times}G_a$ 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 labelled 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.

The question how do the Planck constants associated with factors and coverings relate is far from trivial and I have considered several options.

1. If one assumes that $\hbar^2(X)$, $X = M^4$, CP_2 corresponds to the scaling of the covariant metric tensor g_{ij} and performs an over-all scaling of metric allowed by Weyl invariance of Kähler action by dividing metric with $\hbar^2(CP_2)$, one obtains $r^2 \equiv \hbar^2/\hbar_0^2\hbar^2(M^4)/\hbar^2(CP_2)$. This puts M^4 and CP_2 in a very symmetric role and allows much more flexibility in the identification of symmetries associated with large Planck constant phases.

2. Algebraist would argue that Planck constant must define a homomorphism respecting multiplication and division (when possible) by G_i. This requires $r(X) = \hbar(X)\hbar_0 = n$ for covering and $r(X) = 1/n$ for factor space or vice versa. This gives two options.

3. Option I: $r(X) = n$ for covering and $r(X) = 1/n$ for factor space gives $r \equiv \hbar/\hbar_0 = r(M^4)/r(CP_2)$. This gives $r = n_a/n_b$ for $\hat{H}/G_a \times G_b$ option and $r = n_b/n_a$ for $\hat{H}\hat{times}(G_a \times G_b)$ option with obvious formulas for hybrid cases.

4. Option II: $r(X) = 1/n$ for covering and $r(X) = n$ for factor space gives $r = r(CP_2)/r(M^4)$. This gives $r = n_b/n_a$ for $\hat{H}/G_a \times G_b$ option and $r = n_a/n_b$ for $\hat{H}\hat{times}(G_a \times G_b)$ option with obvious formulas for the hybrid cases.

5. At quantum level the fractionization would come from the modification of fermionic anti-commutation (bosonic commutation) relations involving $\hbar$ at the right hand side so that particle number becomes a multiple of $1/n$ or n. If one postulates that the total number states is invariant in the transition, the increase in the number of sheets is compensated by the increase of the fundamental phase space volume proportional to $\hbar$. This would give $r(X) \to r(X)/n$ for factor space and $r(X) \to nr(X)$ for the covering space to compensate the n-fold reduction/increase of states. This would favor Option II.

6. The second manner to distinguish between these two options is to apply the theory to concrete physical situations. Since G_a and G_b act as symmetries in CD and CP_2 degrees of freedom, one might of being able to distinguish between the two options if it is possible to distinguish between the action of G as symmetry of quantum states associated with covering and factor space. Also the quantization of the orbital spin quantum number at single particle level as multiples of n can be distinguished from that in multiples of $1/n$.

9.3 A simple model of fractional quantum Hall effect

The generalization of the imbedding space suggests that it could possible to understand fractional quantum Hall effect [34] at the level of basic quantum TGD. This section represents the first rough model of QHE constructed for a couple of years ago is discussed. Needless to emphasize, the model represents only the basic idea and involves ad hoc assumption about charge fractionization.

Recall that the formula for the quantized Hall conductance is given by

$$\begin{aligned} \sigma &= \nu \times \frac{e^2}{h} \ , \\ \nu &= \frac{n}{m} \ . \end{aligned} \tag{9.1}$$

Series of fractions in $\nu = 1/3, 2/5, 3/7, 4/9, 5/11, 6/13, 7/15...$, $2/3, 3/5, 4/7, 5/9, 6/11, 7/13...$, $5/3, 8/5, 11/7, 14/9...$ $1/5, 2/9, 3/13...$, $2/7, 3/11...$, $1/7....$ with odd denominator have been observed as are also $\nu = 1/2$ and $\nu = 5/2$ states with even denominator [34].

The model of Laughlin [32] cannot explain all aspects of FQHE. The best existing model proposed originally by Jain is based on composite fermions resulting as bound states of electron and even number of magnetic flux quanta [35]. Electrons remain integer charged but due to the effective magnetic field electrons appear to have fractional charges. Composite fermion picture predicts all the observed fractions and also their relative intensities and the order in which they appear as the quality of sample improves.

The generalization of the notion of imbedding space suggests the possibility to interpret these states in terms of fractionized charge, spin, and electron number. There are four combinations of covering and factors spaces of CP_2 and three of them can lead to the increase of Planck constant. Besides this there are two options for the formula of Planck constant so that which the very meager theoretical background one can make only guesses. On the following just for fun consideration option I is considered although the conservation of number of states in the phase transition changing $\hbar$ favors option II.

1. The easiest manner to understand the observed fractions is by assuming that both M^4 and CP_2 correspond to covering spaces so that both spin and electric charge and fermion number are fractionized. This means that e in electronic charge density is replaced with fractional charge. Quantized magnetic flux is proportional to e and the question is whether also here fractional charge appears. Assume that this does not occur.

2. With this assumption the expression for the Planck constant becomes for Option II as $r = \hbar/\hbar_0 = n_a/n_b$ and charge and spin units are equal to $1/n_b$ and $1/n_a$ respectively. This gives $\nu = nn_a/n_b$. The values $m = 2, 3, 5, 7, ..$ are observed. Planck constant can have arbitrarily large values. There are general arguments stating that also spin is fractionized in FQHE.

3. The appearance of $\nu = 5/2$ has been observed [36]. The fractionized charge is $e/4$ in this case. Since $n_i > 3$ holds true if coverings are correlates for Jones inclusions, this requires to $n_b = 4$ and $n_a = 10$. n_b predicting a correct fractionization of charge. The alternative option would be $n_b = 2$ that also Z_2 would appear as the fundamental group of the covering space. Filling fraction $1/2$ corresponds in the composite fermion model and also experimentally to the limit of zero magnetic field [35]. $n_b = 2$ is however inconsistent with the observed fractionization of electric charge and with the vision inspired by Jones inclusions.

4. A possible problematic aspect of the TGD based model is the experimental absence of even values of n_b except $n_b = 2$ (Laughlin's model predicts only odd values of n). A possible explanation is that by some symmetry condition possibly related to fermionic statistics (as in Laughlin model) n_a/n_b must reduce to a rational with an odd denominator for $n_b > 2$. In other words, one has $n_a \propto 2^r$, where 2^r the largest power of 2 divisor of n_b.

5. Large values of n_a emerge as B increases. This can be understood from flux quantization. One has $e \int BdS = n\hbar(M^4) = nn_a\hbar_0$. By using actual fractional charge $e_F = e/n_b$ in the flux factor would give $e_F \int BdS = n(n_a/n_b)\hbar_0 = n\hbar$. The interpretation is that each of the n_a sheets contributes one unit to the flux for e. Note that the value of magnetic field in given sheet is not affected so that the build-up of multiple covering seems to keep magnetic field strength below critical value.

6. The understanding of the thermal stability is not trivial. The original FQHE was observed in 80 mK temperature corresponding roughly to a thermal energy of $T \sim 10^{-5}$ eV. For graphene the effect is observed at room temperature. Cyclotron energy for electron is (from $f_e = 6 \times 10^5$ Hz at $B = .2$ Gauss) of order thermal energy at room temperature in a magnetic field varying in the range 1-10 Tesla. This raises the question why the original FQHE requires so low temperature. The magnetic energy of a flux tube of length L is by flux quantization roughly $e^2B^2S \sim E_c(e)m_eL$ ($\hbar_0 = c = 1$) and exceeds cyclotron roughly by a factor L/L_e, L_e electron Compton length so that thermal stability of magnetic flux quanta is not the explanation. A possible explanation is that since FQHE involves several values of Planck constant, it is quantum critical phenomenon and is characterized by a critical temperature. The differences of

the energies associated with the phase with ordinary Planck constant and phases with different Planck constant would characterize the transition temperature.

As already noticed, it is possible to imagine several other options and the identification of charge unit is rather ad hoc. Therefore this model can be taken only as a warm-up exercise.

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