flute

Quantum biological teleportation using multiple 6-qubits

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Abstract

The recent discovery of N-photon states emitted and absorbed as a single quantum coherent unit is in conflict with the standard physics wisdom. TGD predicts the realization of genes and also other basic biomolecules as dark $3N$-nucleon sequences such tht the codon is represented by a dark nucleon triplet. Also a representation in terms of dark $3N$-photons states is possible and makes communications based on $3N$-resonance.

It is possible to loosen the earlier assumption that ordinary genes and dark genes are permanently in 1-1 correspondence. This allows dynamical dark genes and biological quantum computation based on N dark 6-bit sequences and their superpositions. This picture generalizes to ordinary quantum computations.

Contents

1 Introduction

It is amazing how fast experimental discoveries, which look mysterious in the standard physics framework but are readily explainable in the TGD framework, are emerging recently.

Now University of Chicago physicists have invented a "quantum flute" that, like the Pied Piper, can coerce photons to move together in a way that's never been seen before. The discovery is described in Physical Review Letters and Nature Physics [D1, D2].

1.1 Quantum flute

The system, devised in the lab of Assoc. Prof. Schuster, consists of a long cavity made in a single block of metal, designed to trap photons at microwave frequencies. The cavity is made by drilling offset holes—like holes in a flute. One can send one or more wavelengths to the "flute" and each wavelength creates a note coding for quantum information. The interactions of notes are then controlled by a superconducting electrical circuit.

The real surprise was the interaction of photons. In quantum electrodynamics (QED) the interaction of photons is extremely weak. When photons achieve critical total energy, the situation changes dramatically. One can say that photons interact, not pairwise as usually, but all at the same time. Photon state behaves somewhat like a Bose-Einstein condensate or a bound state.

1.2 TGD view of quantum flute

Galois confinement as a universal mechanism for the formation of bound states would explain the findings elegantly. TGD involves $M^8 - H$ duality in an essential manner. $M^8 - H$ duality relates differential geometric and number theoretic descriptions of quantum physics and is analogous to Langlands duality. Number theoretical vision, involving classical number fields, extensions of rationals, and extensions of p-adic number fields induced by them, is essential for understanding the physical correlates of cognition [L2, L3] but has led to a breakthrough in the understanding of also ordinary physics [L4, L5].

1. The number theoretic side of the $M^8 - H$ duality predicts Galois confinement as a universal mechanism for the formation of bound states from the dark variants of ordinary particles characterized by effective Planck constant $h_eff = nh_0 > h$: integer n has interpretation as the dimension of extension of rationals induced by a polynomial and serves as a measure of algebraic complexity defining evolutionary level and a kind of IQ for the system.

2. Galois confinement states that physical bound states are Galois singlets transforming trivially under the Galois group of a polynomial P determining space-time region if $M^8 - H$ duality holds true. There is (more than) an analogy with hadrons, which are color singlets. Galois confinement is central in TGD inspired quantum biology and also allows us to understand various nanoscopic and macroscopic quantum phenomena of condensed matter physics.

   For instance, Cooper pairs would represent on a lowest level in a hierarchy and there is evidence for 4-fermion analogs of Cooper pairs [L9].

3. Galois confinement is central in TGD inspired quantum biology and also allows us to understand various nanoscopic and macroscopic quantum phenomena of condensed matter physics [L15].

   In particular, N photons can form bound states in which they behave like a single particle. This bound state is a more general state than Bose-Einstein condensate since photons need not have identical quantum numbers. These many-photon states described in the article could be states of this kind.

   These $N-$photon states are very similar to the dark $3N-$ photon states proposed to represent genes consisting of N codons in which a codo is represented as a dark photon triplet.

4. Another representation of the genetic code paired with ordinary DNA would would be in terms of dark $3N-$proton states, or more generally, $3N-$nucleon states and realized at magnetic flux tubes parallel to DNA [L15, L7]. In both cases, Galois confinement would bind the particles to form quantum coherent states behaving like a single particle, which is also emitted and absorbed as a single entity. This behavior is just what was observed in the experiments.

The biological communications based on dark $3N$ resonances makes possible quantum teleportation in bunches consisting of N dark 6-qubits without Alice and Bob. This would allow the manipulation of quantum memories which would not be reduced to that for single qubits.

In the sequel this picture is considered in more detail on the basis of TGD inspired quantum biology. It is possible to loosen the earlier assumption ordinary genes and dark genes are all the

time in 1-1 correspondence. This allows dynamical dark genes and biological quantum computation based on N dark 6-bit sequences and even their superpositions. This picture generalizes to ordinary quantum computations.

2 Dark $3N$-resonances and quantum teleportation

Could the communication by $3N$-resonances relate to quantum teleportation? This is possible but requires loosening the previous assumption that the states of dark proton sequences are fixed and correspond to those of ordinary genes with which they are in energy resonance when communicating.

2.1 Loosening the view about connection between ordinary and dark genes

The assumption that ordinary and dark genes are in 1-1 correspondence all the time is unnecessarily tight and does not allow any dynamics for dark DNA.

1. Give up the assumption that cyclotron states of the dark $3N$-proton are always the same and correspond to a gene. Assume that in some time scale, perhaps of order cyclotron time, dark proton sequences representing genes decay to the ground state configuration defining an analog of ferromagnet.

2. Assume that some excited dark $3N$-photon states, dark geme states, can be in energy resonance with ordinary genes, most naturally the nearest one if dark DNA strands are parallel to an ordinary DNA strand. Even this assumption might be unnecessarily strong. Dark $3N$-proton would interact with its ordinary counterpart by energy resonance only when it corresponds to the dark variant of the gene.

   Same applies to dark genes in general. Only identical dark genes can have resonance interaction. This applies also to the level of other fundamental biomolecules RNA,tRNA and amino acids.

3. What is this interaction in its simplest form? Suppose dark $3N$- proton is in an excited state and thus defines a dark gene. Suppose that it decays by SFR to the ground state (magnetization) by emitting dark $3N$-photon. If this $3N$ photon is absorbed in SFR by a dark proton sequence originally in ferromagnetic state, it excites by resonance the same gene. The transfer of entanglement takes place.

   This is nothing but quantum teleportation but without Alice, doing Bell measurements and sending the resulting bit sequences to Bob , performing the reversals of Bell measurements to rebuild the entanglement.

2.2 Chemical bonds as flux tube links and a realization of dark codons using only dark protons

In the proposed model of dark DNA, one must assume that the dark codon is formed by a triplet of dark nucleons (proton and neutron). In the TGD framework one could justify the presence of neutrons by the large value of Planck constant increasing the weak scale to at least atomic length scale so that weak bosons would behave like massless particles in atomic scales at the MB. Therefore the dark protons could transform to dark neutrons easily. Neutron would be connected to either neighbor by a meson-like flux tube bond which is positively charged so that each codon would have a charge of 3 units neutralized by an opposite charge of 3 phosphates.

2.2.1 The sign of the magnetic flux as bit?

The introduction of neutrons brings in an additional bit. Therefore one could use only dark protons, if one could bring in this additional bit in some way. An obvious candidate would be the direction of a monopole magnetic flux assignable to the letter of the codon as a closed flux tube with respect

to reference direction defined by the DNA sequence. If the letters of codon are closed linked flux tubes containing dark protons forming dark DNA as a chain, this kind of option might work.

Consider first the topology of the monopole flux tubes.

1. Magnetic monopole flux tubes correspond to closed 3-surfaces in the TGD framework. They are closed because the boundary conditions do not allow boundaries with a monopole charge nor boundaries at all. In dimension 3, these flux tubes can become knotted and closed flux tubes can get linked.

2. If one has a braiding of N flux tubes, one can connect the ends of the N flux tubes. There are many manners to connect the ends, and one obtains at most N linked closed flux tubes, which are knots. The simplest option is that the ends of each braid strand are connected so that one has N linked flux tubes. This corresponds to the "upper" ends as a trivial permutation of the "lower" ends.

3. Any permutation in the permutation group S_N is possible. A given permutation can be expressed as a product of permutations such that each permutation leaves invariant a subset. Permutations are therefore characterized by a partition of N objects to subsets such that the given set consist of N_i objects with $\sum N_i = N$ and that these sets do not decompose to smaller subsets. The allowed permutations for N_i objects correspond to elements of the cyclic group Z_{N_i}. These cyclic permutations give rise to a single closed tube when the ends of the braid ends and permuted braid ends are connected. The number of closed flux tubes is therefore the number of summands in $\sum N_i = N$.

   These permutations are obtained by reconnections from the permutation corresponding to N closed loops so that there are two levels: the level of braiding and the level of reconnections behind the stages not visible in the properties of the braiding.

Linking is a metaphor for bonding. One speaks of the chain of generations, of a weak link in the chain, etc.

1. Chemical bonds are classified into ionic bonds, valence bonds involving delocalization of electrons, and hydrogen bonds involving delocalization of protons. Chemical bonds are not well-understood in the framework of standard chemistry. TGD suggests that they involve space-time topology: monopole flux tube pairs would be associated with the bonds and the splitting of the bond would correspond to a reconnection splitting the pair to two U-shaped flux tubes. Flux tubes and connecting molecules as nodes are proposed to form a network.

2. I have not considered in detail how the U-shaped flux tubes are associated with the nodes. Bonding=linking metaphor encourages a crazy question. The members of the flux tube pairs, which are proposed to connect molecules, which serve as nodes of a network . These flux tubes must close and could be linked with shorter closed flux tubes assignable to molecules.

3. Could this linking bind the molecules and atoms to a single topological structure. If so, both chemistry and topological quantum computation (TQC) in the TGD framework would involve linking, braiding, and reconnections as new topological elements. Biomatter at molecular level would consist of chains of closed flux tubes which can be also stretched and give rise to braids.

   Note that 2 U-shaped flux tubes can reconnect and this transition can lead to a pair of flux tubes or to a linked pair of U-shaped flux tubes so that 3 different states are possible.

4. I have proposed that the pairing of molecules by a pair of monopole flux tubes serves as a correlate for entanglement. If dark protons are associated with closed flux tubes, they must entangle. Could also the linking of the U-shaped flux tubes give rise to entanglement? Stable linking correlates the positions of the flux tubes but this need not mean entanglement since wave function can be a product of wave functions in cm coordinates and relative coordinates.

Linking as an additional topological element inspires some quantum chemical and -biological speculations.

1. Could the presence of valence-/hydrogen bonds involve a closed flux tube at which the electron (pair)/proton is delocalized and that this flux tube is linked with another such flux tube. This picture is consistent with the proposed role of quantum gravitation in metabolism [L10] and generation of the predecessor of the nervous system [L11] based on very long variants of hydrogen bonds characterized by gravitational Planck constant. In this view, living matter would be an extremely highly organized structure whereas in the standard chemistry organism would be a soup of biomolecules.

2. What comes to mind as an example, is the secondary structure of proteins (`https://cutt.ly/sZ5rRiQ`) involving α- helices, β-strands and β-sheets. Tertiary structure refers to 3-D structure created by a single protein molecule. It can have several domains. There are also quaternary structures formed by several polypeptide chains. Proteins consist of relatively few substructures known as domains, motives and folds. Could these structures involve braided and linked flux tube structures with dynamical reconnections?

2.2.2 Dark codons as triplets of dark protons at linked closed flux tubes?

Consider now a possible model of dark DNA involving only dark protons.

1. One can imagine that dark protons are associated with closed flux tubes acting as hydrogen bonds, such that 3 closed flux tubes as letters are linked to form a dark codon. The dark codons could in turn be linked to form genes as sequences of codons. The direction of the magnetic flux can be opposite or parallel to that of the chain so that each closed flux tube represents a bit of topological information. The chains of links would define sequences of bits and even qubits. Could this define the predecessor of the genetic code for which letter represents a single bit?

2. If one has only dark protons, one obtains only 32 dark codons. An additional bit is required to get 64 codons. Could the direction of the closed flux tube in the chain provide the missing bit and thus represent strong isospin distinguishing between p and n?

What implications could this identification have?

1. It is known that the genetic code has a slightly broken symmetry with respect to the last letter of the codon. For almost all RNA codons U and C resp. A and G define code for the same amino-acid. A possible interpretation of the symmetry is that this symmetry is that U-C pair and A-G pair correspond to the bit defined by magnetic flux so that the sign of magnetic flux would not matter much at the level of proteins. For this interpretation, the additional bit would not mean much at the level of proteins.

   Dark DNA and presumably also RNA codons are linked chains of 3 closed flux tubes serving as bits. Could this chain in the case of dark amino acids be replaced with a single closed flux tube obtained by two reconnections so that amino-acid becomes a basic unit?

2. Could the breaking of A-G symmetry (stop-trp pair and ile-met pair) have a topological meaning? Could the direction of the magnetic flux for the third flux tube of the dark codon coding for these pairs matter (this is not the only possibility that one can imagine)? Note that the 4 tetrahedral dark codons in the bioharmony model [L15, L6] contain at least one of these pairs.

3. What could topologically distinguish met as a starting codon and stop codons from the other codons? Could it be that met is not linked to the codons preceding it so that transcription would naturally start at it.

   Could stop codons be unlinked to the codons following them so that the transcription would naturally stop at them? Or could the stop codons correspond to a single closed flux tube so that no RNA codon could be assigned to them?

4. Genes contain intronic parts and the splicing of RNA eliminates these parts after the transcription. Could the topology of DNA and RNA isolate intronic portions from those to be translated. Could the intronic portions correspond to a single flux tube linked to the rest of

the gene both at the level of DNA and RNA. If so, the information about the decomposition of intron to RNA codons would be missing and the assignment of tRNA codons to the intronic portion would not be possible.

2.3 Could dark genes be dynamical?

It was found that the earlier 1-1 correspondence between dark codons and ordinary genetic codons is unnecessarily strict and a modification of the earlier picture of the relation between dark and chemical genetic code and of the function of dark genetic code was considered.

1. Dark DNA (DDNA) strand is dynamical and has the ordinary DNA strand associated with it and dark gene state can be in resonant interaction with ordinary gene only when it corresponds to the ordinary gene. This applies also to DRNA, DtRNA and DAA (AA is for amino acids).

   This would allow DDNA, DRNA, DtRNA and DAA to perform all kinds of information processing such as TQC by applying dark-dark resonance in quantum communications. The control of fundamental biomolecules by their dark counterparts by energy resonance would be only one particular function.

2. Most importantly, flux tubes magnetization direction could define qubit. If the additional qubit corresponds to nucleon isospin, it is not clear whether this is the case. One can also allow superpositions of the dark genes representing 6-qubit units. A generalization of quantum computation so that it would use 6-qubits units instead of a single qubit as a unit, is highly suggestive.

3. Genetic code code could be also interpreted as an error code in which dark proteins correspond to logical 6-qubits and the DNA codons coding for the protein correspond to the physical qubits associated with the logical qubit.

4. The teleportation mechanism could make possible remote replication and remote transcription of DNA by sending the information about the ordinary DNA strand to the corresponding dark DNA strand by energy resonance. After that, the information would be teleported to a DNA strand in a ferromagnetic ground state at the receiver. After this, ordinary replication or transcription, which would also use the resonance mechanism, would take place.

2.4 How does this relate to the bioharmony model of genetic code?

Could there be a connection with bioharmony as a model of harmony providing also a model of genetic code [L1, L6, L8]?

1. In the icosa-tetrahedral model, the orbit of the face of icosahedron under the group Z_6, Z_4, $Z_{2,rot}$ or $Z_{2,refl}$ would correspond to single physical 6-qubit represented as dark protein.

   This representation of the logical qubit would be geometric: orbit rather than sub-space of a state space. One could however assign to this kind of orbit a state space as wave functions defined at the orbit. This representation of Z_6, Z_4, $Z_{2,rot}$ or $Z_{2,refl}$ would correspond to a set of 6-qubits, which replaces a single 6-qubit.

2. The TGD proposal for TQC [L13, L14] is that the irreps of Galois groups could replace qubits as analogs of anyons. Could these orbits correspond to irreps of Galois groups or their subgroups, say isotropy groups of roots?

   Another option is the finite subgroups G of quaternionic automorphisms, whose MacKay graphs, characterizing the tensor products of irreps of G with the canonical 2-D irrep, give rise to extended Dynkin diagrams [L12]. What puts bells ringing is that Z_6, Z_4, $Z_{2,rot}$ or $Z_{2,refl}$ are subgroups of the icosahedral group, which corresponds to the Dynkin diagram of E_8.

   These alternatives need not be mutually exclusive. I have proposed that Galois groups could act as the Weyl groups of extended ADE Dynkin diagrams given by McKay graphs of finite subgroups of $SU(2)$ interpreted as the covering group for the automorphism group of

octonions. The Galois group and its subgroup would define a cognitive representation for the subgroup of the covering group of quaternion automorphisms.

2.5 Communications based on the modulation of dark $3N$-Josephson frequencies

The communications by the modulation of frequency scale $3N$-Josephson frequency scale are still possible.

1. The $3N$-resonance occurs when the receiver $3N$-proton is in ferromagnetic ground state and the $3N$-Josephson frequency corresponds to $3N$-cyclotron frequency. If the time scale for the return to the ferromagnetic state is considerably shorter than the time scale of modulations, a sequence of resonance pulses results and codes for the frequency modulation as an analog of nerve pulse pattern. This communication can lead to communication if the ordinary gene accompanying the excited dark gene is in energy resonance with it.

2. It must be noticed that the communications by dark $3N$-resonances are not possible in standard physics and are made possible only by Galois confinement and h_{eff} hierarchy. In standard physics only single photon fermion interactions would be present and would be relatively weak. In quantum computation, this suggests the possibility of quantum coherent manipulation of N-qubit states by dark N-photons instead of qubit-wise manipulations prone to errors and destroying the coherence. There is evidence for N-photon states with these properties [D1, D1]: for the TGD inspired comments see [L9].

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