The Chern-Simons Current in Time Series of Knots and Links in Proteins

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A superspace model of knots and links for DNA time series data is proposed to take into account the feedback loop from docking to undocking state of protein-protein interactions. In particular, the direction of interactions between the 8 hidden states of DNA is considered. It is an $E_8 \times E_8$ unified spin model where the genotype, from active and inactive side of DNA time data series, can be considered for any living organism. The mathematical model is borrowed from loop-quantum gravity and adapted to biology. It is used to derive equations for gene expression describing transitions from ground to excited states, and for the 8 coupling states between geneon and anti-geneon transposon and retrotransposon in trash DNA. Specifically, we adopt a modified Grothendieck cohomology and a modified Khovanov cohomology for biology. The result is a Chern-Simons current in $(8 + 3)$ extradimensions of a given unoriented supermanifold with ghost fields of protein structures. The 8 dimensions come from the 8 hidden states of spinor field of genetic code. The extradimensions come from the 3 types of principle fiber bundle in the secondary protein.

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I. INTRODUCTION

The attempt to explain living organisms by mathematical model is a long story that dates back to Turing [1]. It is well known that all living organisms have their own character deriving from the gene expression of their genome. Up to now, there is no general mathematical expression for the coordinate changes in gene expression of genetic code for active and inactive areas of DNA, for RNA and for proteins. Recent discoveries in biology are the knotted DNA, the knotted protein [2], and the unknotted RNA folding with the role of knotted protein in codon correction of RNA in methyl transfer [3]. Knots are four dimensional topological objects, embedded in 3 dimensions, used for long time in loop-quantum gravity and superconductor theory. One can also set up a theoretical route [4] searching for the general equation to solve knotted protein folding [5] by using the Wilson loop operator [6] in loop-quantum gravity [7, 8] for gene expression with a boundary phase [9, 10] condition. The theory should support the problem of adaptive changing of docking curvature of knotted protein folding. The definition of curvature from parallel transport of gauge field of genetic code along fiber of protein while docking to each other is still have no precise definition. One of the most suitable equation to explain this phenomenon is the Seiberg-Witten equation that can be adapted to biology. Here, we use a new approach, based on algebraic topology, to define biological structures: specifically the Grothendieck topology is the mathematical structure that we are going to adopt this work.

A sheaf cohomology of retrotransposon replication cycle is defined as an exact short sequence in loop space of underlying moduli state of genetic code. This sequence is missing of knotted property [11] and folding behavior of protein and RNA [12]. We use the category approach for a modified algebraic construction coming from loop-quantum gravity where Khovanov cohomology [13] and Grothendick topology are used in order to describe biological properties of knots and links into time series of protein, DNA and RNA. The key of protein folding behavior are the curvature and volume of hyperbolic knot of underlying time series of link in protein. We modify the Khovanov cohomology [14] to define a new mathematical object in the framework of modified Grothendieck cohomology [15] for the definition of time series of knots and links in proteins. The source of folding diversity from the primary structure of protein

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is considered to be a source of knot hidden super state of link \[18\] between interaction of all species. This happens in the space of superstates over principal fiber bundle of secondary protein with curvature of docking. The process occurs in the modified Wilson loop of gauge field over the invariant property of spinor field in genetic code of a living organism. It can be defined as a Witten invariant \[35\] for biology. Knots and links in protein folding might be the resulting structures of optimized free energy over the partition function of co-states between 2 pairs of geneon and anti-geneon states with transposon and retrotransposon in the wave function of genotype. The result of secondary protein optimized complex surface is given by the transition of hidden states among adaptive feedback loops that change the curvature of protein docking state in viruses and host cells in replication cycle represented as hyperbolic knots. The time series model of knotted protein can be defined by a modified Khovanov sheaf cohomology for living organisms. It can be useful to understand the behavior of hidden states in the parasitism of viral attach to host cell with co-cycle elements defined by the curvature of protein docking state in spin space as transitions between partition function in the cell structure \[19\]. The underlying context is the algebraic topology of knots and links.

A new approach for solving knotted protein folding problem is based on the quantum loop invariant of the link number with homotopic path in ribbon graph of time series of knotted protein folding. Results are expressed in hyperbolic volume and hyperbola graph as relations between the parameters gene sequence evolution. With this model of Chern-Simons current in biology \[20\], we can give a new definition of Ramanujan-Jones-Laurent polynomials \[21-23\]. We use the homotopy class of hyperbolic knotted fundamental group \[24\] to define the obstruction curvature components of viral glycoprotein as transposon and retrotransposon \[26,29\]. The Chern-Simons supercurrent \[30\] is a potential field of life free energy in the canonical form of genotype. It is a new definition of gene partition function \[31\] \( Z_c \) in the form of modified Wilson loop of the gene behavior field. We derive curvature by the normalized curvature of unit circle. The blend radius is centered at the cell nucleus. The curve of equivalent class of current, the single strand nucleotide homotopy path of protein primary structure, before folding into modified Grothendieck cohomology class of equivalent curvature, is a moduli state space with Hopf fibration as principle fiber for the classification of secondary protein folding parameters.

The biological functions of proteins depend on the intramolecular docking processes that can transmit the free energy as Chern-Simons supercurrent between the substrate binding sides with a sum of curvature which is zero at equilibrium state. It is an adjoint left and right group action over the Hopf fibration of gene expression. With this new definition, we can explain the inactive area of trash DNA by using the feedback loop in extra-dimensions. The process gives rise to a change of protein docking state from non-equilibrium to equilibrium. The successful docking state of drug with receptor protein is represented as an icosahedral viral glycoprotein induced from knotted DNA with underlying 8 hidden states in octomer of histone complex \[32\]. An example is the chromatin structure of human nucleosomes inside the chromosome. The extra \((8 + 3)\) supersymmetry dimensions of human genome come from the so called Reidemeister moves in histone modification with knots and links structure. The move represent the docking mechanism between feedback loop of underlying central dogma between coupling state of DNA, RNA, and protein structure.

The superpace of data time series in DNA and their hidden states of genetic code can be model with a loop space plus extra-properties of adjoint representation as category of sieve in extend central dogma of Grothendieck topology. The observation of gene expression can appear only on one side of supersymmetry of chiral molecule in living organism. The other side is the inactive part of hidden state in trash DNA which can be explain by the Laurent polynomial with negative degree as hidden state in left and right hand chiral molecular supersymmetry space of DNA, RNA and protein.

Another problem in biology is how the genome of viral DNA is knotted and why TrmD bacterial knot protein \[33\] is involved with RNA methyl transfer and genetic code error correction. In other words, the problem consists in how we can set up a general equation with initial conditions for knotted DNA, RNA and proteins in living organism. The coupling states between 2 biological systems can be modeled by a distribution over a statistical theory with 2 Laurent polynomials of knotted states. It implies an underlying vortex operator with the convolution of 2 quantum wave functions of 2 geneotype. Jones \[34\] defines relations of hyperbolic 4i knot invariants by statistical mechanics and von Neumann algebras. Witten \[35\] was the first who explained the meaning of Jones polynomials as Chern-Simons currents and in relation to Khovanov cohomology \[13\]. The description is achieved in loop-quantum gravity appearing in a system of partial differential equation over connection, a Seiberg-Witten equation for instantons and monopoles.

We can also interpret Jones polynomials, Laurent polynomials and Khovanov cohomology as coordinates of Grothendieck topology in the categories of living organisms with the geneotype which is the Yang-Mill field acting in replication cycles over the principle bundle of protein structure. The interaction between their adaptation behavior in ecosystem are coordinates changing under their morphisms with co-adjoint co-continuous functors as parasitism state or mutual state between viral replication cycle coupling with host cell or mother cell fertilized by father cell. We solve these complicated self-dual supersymmetry problem, based on the genotype of capsid protein in icosahedral virus and knotted protein in methyl transfer of inactive gene, resetting methylation state in DNA, RNA and in histone modification.
It is an effective supersymmetry of spinor field hidden states of time series data of knotted protein which represents a 8 hyperbolic knotted loop gravity. Specifically, the atomic units of gene can be defined in term of Jones polynomial over the Seiberg-Witten equation. The duality of unoriented supermanifold over living organism with extradimensions can break a chiral supersymmetry over central dogma adopting the dynamics of string and d-brane theory.

The paper is organized as follows. In Section II we summarize the basic definitions of modified Grothendieck topology for biology. Modified Khovanov cohomology for time series of knotted protein is discussed in Section III. The Seiberg-Witten invariant for knots and links in proteins is considered in Section IV. In Section V, a computation in synthetic time series of knots and links in proteins is presented. Another computation of Chern-Simons current in viral capsid glycoprotein is reported in Section VI. Results of data analysis are in Section VII. Discussion and conclusions are in Section VIII.

II. GROTHENDIECK TOPOLOGY FOR BIOLOGY

We use existence axioms of Grothendieck topology as a main tool to define a general coordinate frame for every protein in metabolism of living organisms by the open set of space of secondary protein folding structure. In the new approach of Grothendieck topology, we define sheaves on a category of protein structure and their modified Khovanov cohomology for biology.

The open set, as the coordinates of transmission signal intracell superspace and intercellular superspace, is the co-adjoint co-continuous functor of the Grothendieck open set with more analytic extra properties of the Laurent polynomial of knot and complex surface of protein with curvature.

We need to modify the Atiyah axioms for Topological Quantum Field Theory for all parameterized components, i.e. organelles, proteins, DNA, RNA and cell membrane. The choice of solutions of higher algebraic topology and differential geometrical object is a sheaf cohomology theory intuitively derived from the axioms of Grothendieck topology with some extra property of Atiyah and Hitchin systems. Let $D$ be the space of DNA, $R$ be the space of RNA, $P$ be the space of protein. They have a mirror symmetry with their partner superspace, mitDNA $D^*$, mitRNA, $R^*$, $P^*$, structural (i.e. histone protein) inactive enzyme state of protein. A free Abelian group over sheaf sequence of coordinates defines a genetic code as a link or knotted quantum observable states. For these 4 particle-like in genotype, the shift and drift are transition hidden states in inactive area of tissue DNA. This analogy works also for DNA, RNA methylation and histone modification, for open and closed gene states, for active gene states to anti-gene states, for inactive gene state transition to exit state by methyl transfer life energy group. It is worth noticing that methyle group consists of a tetrahedral geometry with the shape of water molecule with high energy in respiration without oxygen, i.e. fermentation in Krebs cycle. The methyl transfer is in analogy with some property of the transfer of proton, $H^+$ and electron in Krebs cycle, where it is known that stem cells have a resetting of all methyl states. The methyl transfer states hold some memory in form of entanglement states from mother and father genes for their methyl transfer purpose.

In this section, we discuss the role of RNA as an enzyme to control protein docking state in reversed direction of central dogma $\cdots \rightarrow \mathcal{O}_R \rightarrow \mathcal{O}_R \rightarrow \cdots$ compared with enzyme property of induced passive and active structure of protein in $\cdots \rightarrow \mathcal{O}_P \rightarrow \mathcal{O}_P \rightarrow \cdots$. The example of Reidemeister move in knot theory is a gene splicing of pre-mRNAs with the consensus sequence at the exon-intron junction of euakreotic cell. The phenomenon of the so called self-splicing of Tetrahymena group I intron is in analogy with the new definition of knot differential operator and of link operator to generate closed loops of cyclized intron and spliced exons. It is a well known result that some groups of knotted RNA form by introns giving the so called tetraloops. The closed loop is formed by knotted RNA and generate a new type of RNA called group I ribozymes. In this section, we give an example of time series of knotted RNA, called exon-intron self-dual-splicing time series of knotted RNA. The existence of hidden states of proteins in nature is induced from hidden states as a genotype: it is the so called lac operon state and trp operon state in noncoding area of trash DNA. The active state of protein interaction, as starting and ending unknotted state in proteins in nature is induced from hidden states as a genotype: it is the so called lac operon state and trp operon state.

Another example of application of Khovanov cohomology in biology is a methyl transfer control in transcription encoding mechanism. The process is well known as DNA methylation. It is an interaction of protein to DNA directly called DNA metyltransferase (DNA MTase). This mechanism can turn on and off gene. It is involved with gene imprinting and process of life energy production in mitochondria and in some bacteria. Some recent experiments revealed that without metylation, all cells die. The theory to explain this process is based on a quantum field approach for biology. This gene expression process consumes life energy and is related to the Krebs cycle. The enzymes in Krebs cycle in all living organism share 8 common states of Grothendieck topology in a common equation to produce the life energy for controlling the gene expression. Recently, some experiment revealed that stem cells...
induce, from the resetting state of DNA-Methylation, a mechanism to clean all methyl-transfer group from mother and father genome. The result of reset state cells can be a differentiation to other types of cells and also to nerve cell. This happens also when a retrotransposon gene in trash DNA is contaminated by the methyl transfer group. There will be an exception for reset states in trash DNA of methyl group in retrotransposon. Researchers still cannot explain this phenomena and the biophysical mechanism by which the cell can reset methyl group only in active area but not in inactive area.

Here, we use supersymmetry with knotted time series data in RNA to explain this situation by adopting the Khovanov cohomology for knotted RNA. The methylation can appear in both RNA, DNA and histone protein to switch the 8 hidden states in underlying genotype to a transition to each other among the 64 hidden states. The approach is based on the experimental fact that protein structure comes from 3 layers in transcription process with 3 types of connection. According to this fact, the active protein states, $P$ have their partner in passive protein $P^*$ in the docking process (see Fig. 1 for a detailed explanation). This 3 types of sequence are involved with structure of protein as 1-1 maps of intrinsic homogenous coordinates from the 8 hidden spinor states in DNA molecule. We classify the biopolymer molecules involved with the protein folding structure with co-continuous co-adjoint Grothendieck topology as an open set for measuring the degree of protein folding in the higher dimensions space of loop space of cell. We identify by their own symmetry and chemical property by using invariant properties of curvature in closed surface of protein pair docking state.

Let $O_D, O_R$ and $O_P$ be active objects in a categories of DNA, RNA, active state of protein. Let $O_D^-, O_R^-$ and $O_P^-$ be passive states of DNA, RNA and protein in hidden transition state over inactive area of trash DNA. Let the open set of Grothendieck topology be a continuous adjoint and co-adjoint function over 2 categories of active objects and inactive objects with an extend sheaf sequence of short exact sequences of central dogma. The continuous functor between these 4 objects from different 4 categories play a role of open set in the topology of cell. Let an adjoint continuous functor be $C^*: 0 \rightarrow O_D \rightarrow O_R \rightarrow O_P \rightarrow 0$ and co-adjoint co-continuous functor be $C^*: 0 \leftarrow O_D \leftarrow O_R \leftarrow O_P \leftarrow 0$. If these co-adjoint continuous functor over 2 superspace exists in 2 layers of dbrane and anti-dbrane of living organism $X$ and $Y$, then the chain and the co-chain complex of short exact sequences of extended central dogma are co-adjoint and co-continuous as replication cycle, that is $C_*(X) \circ C_*(Y) = C_*(X) \circ C_*(Y) = 0$. We can define a genotype as a grade over genetic shift and drift operator from their evolution of their own species with analogy with differential and co-differential operator in a chain sequence $C_*$.

The genotype is represented as 4 hidden directions of gene expression represented as 4 wave function of a particle-like in a quantum field theory for biology. They are the geneon, anti-geneon, transposon and retrotransposon. The knots and links in inactive area of trash DNA (the unknotted DNA also classified as a special case of knotted DNA with unknotted state). The particle-like are the geneon, anti-geneon, transposon and retrotransposon. The knots and links in protein are represented by time series over transition coupling states of these 4 particles in genotype. We have enzyme properties of some protein with active and inactive states which imply that geneons have their partner passive states, the anti-geneon states of genotype. The transposon is defined as a cut and glue protein complex hypersurface into 2 parts. The Atiyah-Segal and Hitchin-system axioms define the sheaf sequence of transposon, retrotransposon, geneon and anti-geneon states in protein complex manifold. This approach opens the possibility to link under the same standard quantum field theory and biophysics.

**Definition 1.** Let $G$ be the gauge group of genotype. Let $[s_1] = [e^{i\beta}]$, $[s_i^*] = [e^{i\beta}]^* = [e^{-i\beta}]$ be a spinor field of genotype over DNA. Let $\Phi^\pm : (A, s) \mapsto \{1, -1\}$ be ghost and anti-ghost field in protein secondary structure with supersymmetry in genetic code. Let $A$ be a supermanifold of living organism and $s$ be the Hamiltonian system of gene expression mechanism in living organism DNA, RNA and protein over underlying gauge group of genotype as lie group, $G$. Let $U \subset K$ be an open set in a manifold of protein secondary structure with smooth embedded homotopy path of genetic code lift a fix alphabet as base point to equivalent class of fiber with parallel transport in covering space by $[\gamma(t)] \in [K, E]$. It contain a starting point at $\gamma(t_1) = a \in U$ and an ending point of gene expression at $\gamma(t_2) = b \in U$. Let $[A_\mu] = [\Gamma_{\mu}^\gamma]$ be an equivalent class of representation of genetic code independent of the chosen alphabet. Let $\gamma(t)$ be a connection over principle fiber of underlying protein encoding, $P_\gamma$ (for more detail of definition see [20]). The connection used for parallel transport from path of state in the genetic code of DNA 

\[ [A_\mu] = \{(s_1(\gamma(t_1)), s_2(\gamma(t_2)), s_3(\gamma(t_3)), s_4(\gamma(t_4)), s_5(\gamma(t_5)), s_6(\gamma(t_6)), s_7(\gamma(t_7)), s_8(\gamma(t_8))\} \]

starts at the position $\gamma(t_1) = a$ to $\gamma(t_2) = b$ in fiber (with the Hopf fibration) of $U \times F \rightarrow E = P_\gamma$ with $F_\gamma \equiv F_\gamma^+ = \pi^{-1}(a)$ and $F_\gamma \equiv F_\gamma^- = \pi^{-1}(b)$ with the size of gene defined by $\text{rank} F_\gamma = n = \text{rank} F_\gamma^+$, a ghost field of gauge field over genetic code in fiber of protein secondary structure. The connection $[A_\mu] \gamma$ represents the gauge field of genetic code as the parallel transport with gauge group operation as translation and reversed translation in gene expression from protein fiber $F_a$ to $F_b$ in the tangent of manifold of proteins for their genotype. We have that the spinor field of genetic code spans in fiber $F_a$ and transports to $F_b$ by $A_\mu \Phi^+ = \Phi^+ (A_\mu)$, where $A_\mu = \Gamma_{\mu}^\gamma (\Phi^+) = \Phi^+ (A_\mu), \Phi^+ \Phi^- = << [s_1], [s_2], \cdots, [s_n] >>$ and $\Phi^- = \Phi^-$ is the anti-ghost field. It comes from translation in reversed direction as reversed
FIG. 1: On the left, a diagram for the interaction of 2 proteins with 3 gauge fields is represented as the connection $A_1$, $A_2$ and $A_3$. The docking state is induced from opposite direction of spinor field in $A_1$ and $A_2$ and is canceled to each other to produce an equilibrium state embedded into the connection $A_3$. For undocking state, the coupling between $A_1$ and $A_2$ does not cancel each other. In the picture shown in the middle, a Chern-Simons current, represented as a knot 3 with 3 types of connections over 3 types of principle fiber bundle of secondary protein structure is reported. The picture shown on the right is a 8 knot of short exact sequence of extended central dogma. We glue the starting point of a short exact sequence $0_{\text{brane}} \simeq 0_{\text{anti-brane}}$ like a hyperbolic 4 when $0_{\text{brane}} \rightarrow O_D \xrightarrow{\phi^4} O_R \xrightarrow{\phi^3} O_{P} \xrightarrow{\phi^2} O_{P^*} \xrightarrow{\phi^1} O_D \rightarrow 0_{\text{anti-brane}}$. The trajectory in 4 indus an infinite modified Khovanov cohomology sequence in higher dimensions in categories of biological systems. We label 4 knot with 2 different color from coupling between 2 cycles, i.e. host cell and viral particle. This 4 knot can also be used to understand parasitism states of a virus attack to the host cell as hyperbolic manifold with hyperbolic volume.

transcription with hidden state in dual fiber $\Phi^{-}\in F^{*}_{a}, \Phi^{-} = << [s^*_n], [s^*_{n-1}], \ldots, [s^*_1] >>$.

The definition of connection in biology is used for two reasons: firstly, it is a source of gauge potential field over genetic code where the original transmission comes from our ancestors in the past in which we do not know yet where DNA come from. Secondly, it defines coordinates over the fiber of secondary protein in knots and links of time series data of proteins where the protein structure wave function, the geneon denoted by $\Phi_{\pm}(A_\mu)$ of underlying genotype, is defined independent of the chosen coordinate representation but it is intrinsically defined by $[A_\mu]$ over a principal fiber bundle of protein $P_K$ which satisfy 7 of Atiyah axioms for biological quantum field.

There exists several ways to define connections $A_\mu$ with different purposes of applications in both differential geometry and quantum field theory. The reasons is related to the connection to be used to define the parallel transport of principal fiber along the tangent of a Riemannian manifold as vertical differentiation perpendicular to the horizontal axis.

**Definition 2 (Parallel transport along gene sequence).** Let a path of sequence of alphabet in genetic code of underlying genotype be parametrized by underlying smooth curve $\gamma(t)$ with path ordering. We can define an equilibrium state of genotype without evolution in specific species where different species can be obtained by the parallel transport along the curve of expression of secondary structure protein. Let $X$ be a space of protein structure. Let $E$ be a covering space of underlying secondary protein. We have a connection of path in genetic code of underlying genotype with start from position $a$ and stop translation in position $b$ defined by $\Gamma(\gamma)^b_a$,

$$\Gamma(\gamma)^b_a : E_{\gamma_a} \rightarrow E_{\gamma_b}$$

(1)

such that

- $\Gamma(\gamma)^a_a = \text{Id}$ the identity transformation of fiber of secondary protein $E_{\gamma(a)}$.
- $\Gamma(\gamma)^b_a \circ \Gamma(\gamma)^a_c = \Gamma(\gamma)^b_c$.
- $\Gamma$ is smooth transport curve with preserved direction of gauge field and connecting all fibers together along $\gamma_a, \gamma_a$ and $\gamma_c$. 

The gauge field of genetic code $A_\mu = \Gamma^b_{a\mu}$ is a parallel transport along geodesic curve of protein (the minimum distance along protein folding) $\gamma : I \to X$ and $\beta = \frac{\partial \gamma}{\partial t}$ be tangent smooth curve embedded in underlying protein surface if and only if
\[
\nabla_\beta(t) \beta(t) = 0.
\]

**Definition 3.** Let $D^+_\Phi$ be an active docking operator of 2 proteins in cell membrane. We use the same notation of Dirac operator for transition state in gene, $D^+$ and attach operator for docking process in protein $D^+_{\Phi}$ in different category of biological object. The first operator acts over category of DNA cat($D, D^+$), the second operator acts over category of protein $\text{Cat}(P, P^*)$, we can define also with attachment of protein to DNA in cat($P^*, D$), also process of miRNA to RNA in cat($R, R^*$) with the similar definitions of Grothendieck topology as coordinate of co-adjoint functor between them. It is a modified Dirac operator which brings the attachment of spinor field to the ghost field of viral glycopolypeptide $\Phi^+(A_\mu)$: It translates, by the parallel transport of spinor field of genetic code to dock with host cell receptor protein $\Phi^-(A_\mu)$ as anti-ghost field with fixes the site embedded in host cell membrane. The definition is analogue to the covariant derivative of differential geometry with some extra-properties of genetic code gauge field over connection. We have a docking between active protein and inactive (passive) protein by docking operator defined as
\[
D^+_{\Phi^+(A_\mu)}|\Phi^-(A_\mu) > = \lim_{t_a \to t_b} \frac{\Gamma^\mu_a \Phi^+(\gamma(t_b)) - \Phi^-(\gamma(t_a))}{t_b - t_a}.
\]

Let $D^+_{\Phi^-}$ be a passive docking operator of 2 proteins in cell membrane. It is a docking of antibody to viral glycoprotein in anti-parallel spin, that is in reversed direction of docking. We have
\[
D^-_{\Phi^+(A_\mu)}|\Phi^+(A_\mu) > = \lim_{t_a \to t_b} \frac{\Gamma^\mu_a \Phi^+(\gamma(t_a)) - \Phi^+(\gamma(t_b))}{t_b - t_a}.
\]

**Definition 4.** (Principle fiber bundle of secondary protein structure) Let $X_t = S^3$ be a Kolmogorov space $[39]$ in spinor field of time data series. Let $\rho$ be the representation of gauge group $G = SU(2)$. Let $G$ be a Lie group of spinor field of geneon-anti-geneon pair (analogue with gene in chromosome pairs between dominant and recessive genotype) in supermanifold of living organism $\mathcal{M}$ with fundamental group of complement in hyperbolic knot $\kappa \in K$ representation; $\pi_1(S^3 - K) = <x, y, z>, x, y$ are alphabets for geneon pairs in hidden state of DNA sequence of genotype and $z$ is the alphabet for a supersymmetry of transposon and retrotransposon hidden in trash DNA. We choose $\kappa$ be a hyperbolic knot $4_{11}$, a figure 8 with $x, y, z$. Let $\rho$ be a representation of knotted group over genetic 3-alphabet of supercodon. It is a group action to finite vector space $G \times X_t \to X_t$, with dimension $\dim V = n$. Let $\beta$ be the co-cycle of genotype $, \beta(x_0) : X_t \to X_t / G$. Let the projection $\pi : P_{X_t} \to X_t$ be the canonical projection with $p \in \pi^{-1}(x_0), P_{X_t}$, a principal bundle. Let $A_\mu$ be a connection with underlying class of gauge field in genetic code $[A_\mu]$ (see $[20]$ for definition of genetic code as connection in detail) on covering space $P_{X_t}$, then the parallel transport along co-cycle $\gamma A_\mu$ maps the fiber bundle $\pi^{-1}(x_0) \to \pi^{-1}(x_0)$. Because group action $G$ is a trivialization on principal fiber bundle, so there exists $g_{A_\mu} \in G$ such that co-cycle of particle-like wave function of quantum biological observable over gauge field (connection or gauge potential of genetic code $[A_\mu]$) is the holonomy of connection $A_{\beta_\mu}$ and $A_{\beta_{\mu, \kappa}}$, represented, for folding type of fibers, in beta sheet, alpha helix and loop region of secondary structure of protein folding according to the Axioms of Atiyah for biology.

We have a group action as folding types of translation of adjoint co-continuous functor in context of Grothendieck topology for biology, at $p$, i.e. $\beta A_\mu(p) = p g A_\mu \in X_t / G$. Let $\Phi$ be a quantum observable of coupling state between geneon and anti-geneon pairs and transposon-retrotransposon pair. Let $W_{\rho, \beta, \kappa}$ be the modified Wilson loop over a link states between retrotransposon (RNA) to geneon and retrotransposon and folding fiber type as parallel transport of geneon along connection $A_{\mu}$ (gauge potential); then, we have to define a quantum biological observable of protein structure as a ghost field by
\[
\Phi(A_\mu) := W_{\rho, \beta}(A_\mu) = Tr[p(g A_\mu)], \quad \forall A_\mu \in A_{X_t}
\]

We call $W_{\rho, \beta, \kappa}(A_\mu)$ the modified Wilson loop associated with the representation $\rho$ and co-cyclic $\beta$. A special case is realized when $\rho = Ad$, the adjoint representation of $G$ and $\kappa$ is a knot and link of underlying DNA, RNA and protein structure.

**Definition 5.** Let $\kappa$ will be a hidden knotted state in the trajectory of metabolism of protein in underlying genotype of gene expression. Let $\beta$ will be cocycle of genotype in living cell (e.g. viral replication cycle or cell circle). A modified Wilson loop with Wick rotation of path ordering gene by gauge group operation for transcription process over moduli state space of real line, $\mathbb{R}/\sigma([s]) \in \mathbb{R}/G, \sigma([s]) \in G$ real line with extra properties of spin permutation operator
attach as extradimension to each continuous point in line) for gene expression for real path ordering with genotype in form of connection $[A_\mu]$ is defined by

$$W_{\beta,\rho,\kappa}(A_\mu) = Tr_P e^{\frac{1}{c^2}ds} Tr_P e^{\frac{1}{c^2}ds} = 0.$$ \hspace{1cm} (6)

where $Tr$ means the trace of gauge group representation. $P$ is a solution path ordering of genetic code with solutions ordered by permutations with wedge product property of spinor fields that satisfy the Pauli exclusion principle for all solution states and $p$ is the disjoint representation of underlying gauge group operation for gene translation in gene expression.

If we use the Wigner ray $W(z) = \frac{1}{2}$ projection to project state $[s_1], [s_2]$ with path ordering (i.e. $[s_1], [s_2] \neq [s_2], [s_1]$) of solution of gene expression state in unit cycle of fiber with parallel transport along connection $A_\mu = \Gamma_i^\mu$, the equation for gene expression for one single state of gene is

$$W_{\beta,\rho,\kappa}(A_\mu) = Tr_P e^{\frac{1}{c^2}ds} Tr_P e^{\frac{1}{c^2}ds} = 0.$$ \hspace{1cm} (7)

so, we have the result of gene expression along direct transcription process along space of DNA, i.e. $X = D, G = P^*$, $G \times X \rightarrow X, \phi x_t = x_{t+1}$ with character $Tr_P(G) = 1$. We have solution of gene expression by integrating over circle in fiber of genetic code. We get

$$|s - [s_1]| |s - [s_2]| = 0,$$ \hspace{1cm} (8)

$$s = \pm [s_1], \pm [s_2].$$ \hspace{1cm} (9)

The solution states with path ordering mean that we cannot change an order of solutions. The solution have their mirror supersymmetry in hidden state for transition. We will later call $+[s_i]$ a geneon state and a mirror state in which inactive state in trash DNA is the anti-geneon state of repeated inactive gene and denoted by $-[s_i]$ (the state in genotype here is a sequence of alphabet in biology i.e. $[s_i], i = 1, 2, 3, \cdots 8 = \{ATCGTTTTAAA\}$).

For every genotypes, it contains 8 hidden states. We will extend this solution to a Laurent polynomial and a Jones polynomial by using the Seiberg-Witten invariant. The first 4 states are geneon, anti-geneon, transposon and retrotransposon in dsDNA and the other 4 states are in hidden DNA or passive state of DNA (it might be some form of moving gene in mitDNA, mitochondrial DNA analogy with miRNA), $D^*$. We have $< [s_i]| [s_i^+] >= 0, < [s_i]| [s_i^-] >= 1, D^*|s_i >= [s_i^+], D^-|s_i^- >= |s_i >=$ for all $i$ for a stable pair of orbital of geneon and anti-geneon with modified Dirac operator with transition energy of ground state sets to be zeros as closed shell of spinor field for genotype. This pair is analogy of pair of gene in pair of chromosome in which biologists use for phenotype gene expression with dominant state and recessive state of genotype. Later, we will use the link operator to map this sequence to Khovanov cohomology for time series of knots and links in protein, $\mathcal{F}(0 \rightarrow \mathcal{O}_D \xrightarrow{\phi_d^1} \mathcal{O}_R \xrightarrow{\phi_d^2} \mathcal{O}_{R^*} \rightarrow \mathcal{O}_P \xrightarrow{\phi^3} \mathcal{O}_{P^*} \xrightarrow{\phi_d^4} \mathcal{O}_{D^*} \rightarrow 0)$.

This algebraic construction is analogue to a Khovanov cohomology in loop-quantum gravity context but with different meaning. It is a discretized reaction which is the quantization of a differential map in forward and reversed direction of the transcription, $\phi_d^{\pm}$, of the genotype. It can be represented as the covering space of sieve and site over the supermanifold coordinates of living cell with sieve and site assuming the Grothendieck topology. The modified Atiyah axioms for quantum biology are used to define the coordinates in the loop space of cell by a pullback functor from the categories of states in DNA or the 3-types genotype wave function as a morphism between states in these categories to other categories of the fiber of secondary protein folding structure. The observed categories of a protein $Cat(P, P^*)$ are assumed to be isomorphic to a compact oriented smooth n-dimensional manifold. The manifold of adaptive behavior of gene expression in a living organism with geneon states in genotype are assumed to be isomorphic to the categories of $(n+1)$ dimensional complex vector space of hidden states in cell superspace, $\mathcal{M} \in \text{Obj}(Cat(\mathcal{M}))$.

The morphism is a system transmission of a given cohomology sequence of protein docking as cell signal between intercellular transmission state of geneon, retroposon and transposon in form of DNA, enzyme or siRNA, miRNA, tRNA and noncoding RNA in which arise from intron. The histone structural protein contains an octomer with histone modification process capable of changing the transition state of spinor fields in time series of genetic code according to the homogeneous coordinates of 8 states in $E_8 \times E_8$ grand unity theory of cell.

Definition 6 (Atiyah-Segal and Hitchin System axioms for quantum field in biology). Let $\mathcal{H}$ be a modified Khovanov cohomology-Grothendieck open set-co-continuous functor map between the category of $Cat(P, P^*)$ to the category of $Cat(\mathcal{M})$ which satisfy the following axioms:

- Axiom 1. (Orientation) Let $Pro_{q^b}(A_\mu)$ be the co-bordism of superspace of protein folding or the boundary of protein complex surface during the docking process with underlying connection $A_\mu=1,2,3$ for $\beta$ sheep, $\alpha$ helix &
loop region folding in secondary structure. The curvature of the structure is derived by the variation of connection in parallel transport along the surface of the protein. We denote the curvature inside this object as an extra-property of the adaptive behavior. This curvature emerges as a change docking in evolution of the feedback loop in parallel transport along the surface of the protein. We denote the curvature inside this object as an extra-

Let \( \text{Pro} \) be the dual vector space of superstate in cell where \( \mathcal{M} \in \text{Cat}(\mathcal{M}) \). Then \( \mathcal{H}(\text{Pro}^*_{-}(A_\mu)) = (\mathcal{H}(\text{Pro}^*_{+(A_\mu)})^*, \forall \text{Pro}^*_{+(A_\mu)} \in \text{Cat}(P, P^*) \).

- Axiom 2. (Multiplicativity) Let \( \prod \) be a disjoint union then
  \[
  \mathcal{H}(\text{Pro}^*_{+(A_\mu)}) \prod \text{Pro}^*_{+(A_\mu)} = \mathcal{H}(\text{Pro}^*_{+(A_\mu)}) \otimes \mathcal{H}(\text{Pro}^*_{+(A_\mu)}), \quad \forall \text{Pro}^*_{+(A_\mu)} \in \text{Cat}(P, P^*). \tag{10}
  \]

- Axiom 3. (Transitivity) Let \( F_i : \text{Pro}^*_{+(A_\mu)} \rightarrow \text{Pro}^*_{+(A_\mu)} \) be a morphism. Then
  \[
  \mathcal{H}(F_1 F_2) = \mathcal{H}(F_2) \mathcal{H}(F_1) \in \text{Hom}(\mathcal{H}(\text{Pro}^*_{+(A_\mu)}), \mathcal{H}(\text{Pro}^*_{+(A_\mu)})), \tag{11}
  \]
  where \( F_1, F_2 \) denote the co-continuous Grothendieck topology functor as an open set in coordinates of cell metabolism. The docking mechanism of enzyme catalytic interaction is given by joining fusion surface between protein complex surface of principle bundle \( \text{Pro}^*_{+(A_\mu)} \) in the sense of co-bordism, \( F_1 \prod \text{Pro}^*_{+(A_\mu)} F_2 \) in analogy with quantum field theory.

- Axiom 4. (Identity) Let \( \phi_k \) be the empty of \( n- \) dimensional supermanifold of living organism. Then
  \[
  \mathcal{H}(\phi_k) = C. \tag{12}
  \]

- Axiom 5. (Homotopy of protein folding) For each \( \text{Pro}^*_{+(A_\mu)} \in \text{Cat}(P, P^*) \), we have a homotopy path of protein folding in secondary structure given by,
  \[
  \mathcal{H}(\text{Pro}^*_{+(A_\mu)} \times [0, 1]) : \mathcal{H}(\text{Pro}^*_{+(A_\mu)}) \rightarrow \mathcal{H}(\text{Pro}^*_{+(A_\mu)}). \tag{13}
  \]
  It is an identity map. This map induce a moduli-state space model in protein folding. We have

- Axiom 6. (Partition of Primary and Secondary Structure ) Let \( K = C_n(P) \) be a \( n- \) manifold of chain of primary structure of protein with \( \text{dim}P = n \) a number of states represented as a compact oriented vector space in protein primary structure. The differential \( d : \text{Primary}(P) \rightarrow \text{Secondary}(P) \) maps (we use \( C_n(\cdot) \) for primary structure Grothendieck topology and \( C_{n-1}(\cdot) \) for secondary structure) a primary protein structure Grothendieck topology to a secondary protein folding structure defined by the protein folding in the sense of homotopic map (cohomology functor is the homotopic invariant functor of the protein folding by this new definition) of modified Khovanov cohomology decomposed space into kernel and boundary \( d : C_n(P) \rightarrow C_{n-1}(P) \) with \( \partial C_n(P) = \ker(d(C_n(P)) + \text{Boundary}(d(C_{n-1}(P))) \). If morphism is injective then \( \text{Ker}(d(C_n)) = 0 \). We have a modified co-bordism for global surface of protein docking as the only boundary state of amino-acid sequence of secondary structure without the inner structure of amino-acid sequence. We have
  \[
  \partial K = \text{Pro}^*_{+(A_\mu)} \prod \text{Pro}^*_{-(A_\mu)} \tag{14}
  \]
  with a linear transformation as evolution of feedback loop between docking and undocking state of curvature in secondary protein structure,
  \[
  \mathcal{H}(K) : \mathcal{H}(\text{Pro}^*_{+(A_\mu)}) \rightarrow \mathcal{H}(\text{Pro}^*_{+(A_\mu)}), \tag{15}
  \]
  with co-adjoint co-continuous functor.

- Axiom 7. (Hitchin system in protein docking ) In this axiom, we define the self dual morphism of fiber bundle of protein \( P_K \) as \( \text{End}(P_K) \). The notion of tensor product for secondary protein folding is the effect of evolutionary adaptive behavior feedback loop gauge field. It expresses as knots and links in proteins with changing curvature defined in this extension from Atiyah to Hitchin system axioms for biology. Let \( P_K \) be the principle bundle over
manifold of folding structure as covering space. The change of internal curvature by evolutilional path [3] over cocycle of fiber bundle of secondary protein structure is defined by endomorphism of co-adjoint functor map between fiber, [3] ∈ End(PK) = Hom(PK, PK). Let H1(End(PK)) := [End(PK), S1] be the first cohomology group. Let L be the space of links induced by external influence epigenetic factors of environment which can produce a feedback path evolution. The tensor product End(PK) ⊗ L means that the result of mathematical complex structure, induced from the right hand side of multilinear algebras, is End(PK) ⊗ L = Hom(End(PK), L∗), L∗ = Hom(L, Z).

The time series of knots and links in proteins is parameterized by 3 types of link states in quantum loop crossing, as a projection from 3 dimension, the plane defined by the cohomology sequence of links with the involution of a group operation of rank rank(G) = n, where G is the translation group in amino-acide sequence along the peptide chain (i.e. the protein has a length with k = 1, 2, 3 · · · n number of amino-acid) L⊗k, k = 1, 2, 3 · · · n.

We define a more exact sequence of link operators for the folding of secondary protein structure by,

\[ < L >: 0 \rightarrow < L_{\pm, 0} > (t_1) \rightarrow < L_{\pm, 0} > (t_2) \cdots \rightarrow < L_{\pm, 0} > (t_n) \rightarrow 0. \] (16)

where \(< L_{\pm, 0} > \) mean \(< L_0 > \) or \(< L_+ > \) or \(< L_- > \) are link states which satisfy the modified skein relation parametrized as 3nd exact sequence layers in knots and links in proteins folding. All proteins structure exists in pair \((\Phi^+_i (A_{\mu}), P_K)\) independently of changing curvature in protein folding. It is defined by

\[ \text{End}(P_K) \otimes L, \phi^\pm_i (A_{\mu}) \in H^0(\text{End}(P_K) \otimes L) \] (17)

An element of evolutilional gauge field is defined by \(H^0(L^\otimes k)\) where \(k = 1, 2, 3, \cdots \text{rank}(G), G\) is a group operation over fiber of protein. It can be represented as a change of coordinates in genetic code as the effect of genetic variation in principal fiber bundle of protein structure. The Yang-Mill field and the Seiberg-Witten invariant are solutions of the Hitchin pair for biology, that is \((\Phi^+_i (A_{\mu}), A_{\mu}(P_K))\).

Definition 7. Knots and links in proteins κ are a piecewise smooth embedding of primary structure amino acid peptide sequence, homotopic to the circle S1 in 3-space of protein supermanifold. They satisfy the axioms of quantum field for biology. A unknotted protein is a special case with link number zero. A collection of knots and links in proteins is called a link of proteins \([L]\). For a 2-knot link, we define the linking number as the number of times where one the knot wraps around satisfying the skein relation in a Jones polynomial.

This protein folding structure with knots is actually the U(1) Chern-Simons theory. The characteristic class of co-bordism of secondary protein structure can be identified with ghost and anti-ghost fields for link \([L]_i^{[s_i]}\) of knotted protein with connection \(A_{\mu}\) and underlying hidden state in genetic code \([s_i]\) in this modified Khovanov cohomology for biology. This axioms of secondary protein structure is analogue with axiom of quantum field theory. It will be indentified with Jones-Ramanujan-Witten-Laurent polynomial for the ghost field \(\Phi^+_i ([L]_{A_{\mu}}^{[s_i]})\) of link of knotted protein in modified Khovanov cohomology for loop quantum gravity for biology.

III. MODIFIED KOHANOV COHOMOLOGY FOR TIME SERIES OF KNOTTED PROTEIN

In this section, we give a new definition of time series of protein folding (see Fig. 2) as an infinite long exact sequence of modified Khovanov cohomology for biology and axioms of quantum field theories introduced by Michael Atiyah [42]. First we explicitly give a new definition to 3 types of connection over the principal bundle of secondary structure with their underlying 3-co-cycles of geneon, transposon and retrotransposon states in genotype.

Definition 8. Let \([s_i]\) be a spin state in DNA (for more details on the definition of all states of spinor field in time series of genetic code see [20]). Let \([L]_{A_{\mu}}^{[s_i]}\) be the protein link of the underlying spin state \([s_i]\) and gauge field \(A_{\mu}\) for the behavior of underlying genotyope. The source of line is a category of free Abelian group over a short exact sequence of sheaf cohomology of central dogma. The behavior of gene expression link and the behavior gauge field is induced from interaction adaptive behavior of protein docking with capsid protein and host cell receptor in feedback recursive loop space of underlying hyperbolic knot of link. We define the Khovanov cohomology for biology the vector space of states in genetic code discretized by genetic shift and drift operator, \(\phi^d_i = 0 \rightarrow Z \rightarrow 0, i = 1, 2, 3, \) with co-differential map for co-chain sequence, \(d^*_i\). Let an equivalent class of link operator over figure 8 hyperbolic knot κ = 41 in loop quantum gravity for biology be

\[ [L_\pm]_{A_{\mu}}^{[s_i]} = \mathcal{F}\{0 \rightarrow O_D \xrightarrow{\phi^d_1} O_R \xrightarrow{\phi^d_2} O_{R^*} \rightarrow O_P \xrightarrow{\phi^d_3} O_{P^*} \xrightarrow{\phi^d_4} O_{D^*} \rightarrow 0\} \] (18)
Let $\Phi^\pm_i ([L]|_{A_\mu}^{[s]})$ be ghost and anti-ghost field from docking and undocking state of protein of gene $i$ at position of time series of knot $[L|_{A_\mu}^{[s]}]$ in protein. A time series of knotted protein over Wilson loop of gauge field of genotype $W_{\kappa, \rho}(A_\mu)$ is

$$\Phi^\pm_i ([L]|_{A_\mu}^{[s]}) = \sum_{\mu=1}^{n} [L|_{A_\mu}^{[s]}] W_{\kappa, \rho}(A_\mu).$$  

(19)

where $A_\mu$ is a connection over gauge transformation of a right translation group operation over fiber space of genetic code according to the type of fiber space of protein. A type 1 with a connection $A_\mu=1$ is an $\alpha$ helix connection, type 2, with a connection $A_\mu=2$, is a connection over fiber of $\beta$ sheet in secondary protein, type 3, $A_\mu=3$ is a connection over fiber of loop region in secondary protein. When a protein is folding to the secondary structure, the knots of protein are open states obtained by using the skein relation as a modified covariant derivative over parallel transport of connection of genetic code $[A_\mu]$. Let $[L|_{A_\mu}^{[s]}]$ be the link operator of protein over a modified Grothendieck cohomology. Let $H_{n-0}([L]|_{A_\mu}^{[s]}, P_K)$ be a functor of cobordism of secondary protein satisfying the modified Atiyah-Segal-Hitchin axioms for quantum biology. We have a long exact sequence of Grothendieck cohomology induced by short exact sequence of central dogma with value in principle bundle of secondary protein fiber $P_K$, that is

$$H_{n}([L]|_{A_\mu}^{[s]}, P_K) : 0 \rightarrow \cdots \rightarrow H_{n}([L]|_{A_\mu}^{[s]}, P_K) \xrightarrow{\delta^d_1} H_{n}([L]|_{A_\mu}^{[s]}, P_K) \xrightarrow{\delta^d_2} H_{n}([L]|_{A_\mu}^{[s]}, P_K) \xrightarrow{\delta^d_3} H_{n+1}([L]|_{A_\mu}^{[s]}, P_K) \xrightarrow{\delta^d_4} \cdots \rightarrow 0$$

(20)

We call $H^n([L]|_{A_\mu}^{[s]}, P_K) = Hom(H_{n}([L]|_{A_\mu}^{[s]}, P_K)$ a modified Khovanov cohomology for quantum biology. It is possible to give a new definition of differential one-form for knotted protein structure in every connection of gauge field over
genotype by \( \Phi_1^\pm (A_\mu) \mapsto d\Phi_1^\pm (A_\mu) \) defined by the skein relation over link \( [L]^{[\gamma]}_{A\mu} \):

\[
\nabla^{[L+(\pm\gamma)]}_{\Phi_1^+ (A_\mu)} = \frac{[L_+]^{[\gamma]}_{A\mu} W_{\kappa,\rho}(A_\mu) - [L_-]^{[\gamma]}_{A\mu} W_{\kappa,\rho}(A_\mu)}{[L_0]^{[\gamma]}_{A\mu} W_{\kappa,\rho}(A_\mu)} ,
\]

(21)

and

\[
\nabla^{[L-(\pm\gamma)]}_{\Phi_1^- (A_\mu)} = \frac{[L_-]^{[\gamma]}_{A\mu} W_{\kappa,\rho}(A_\mu) - [L_+]^{[\gamma]}_{A\mu} W_{\kappa,\rho}(A_\mu)}{[L_0]^{[\gamma]}_{A\mu} W_{\kappa,\rho}(A_\mu)} ,
\]

(22)

A modified Grothendieck cohomology with \((\alpha, \beta)\) cocycle is given by

\[
\Phi_1^\pm (A_\mu=\pm) = \alpha_\pm + \beta_\pm \kappa + \epsilon_k ,
\]

(23)

for every gene of viral glycoprotein.

From this definition, we can measure \( \alpha \) and \( \beta \) for regression parameters of trend in \( J^\mu (A_\mu) \) in order to calculate the band gap between the transition of adaptive curvature in self-dual form of Seiberg-Witten equation for protein docking

\[
F_+ = 0, \quad D_+^\mu (A_\mu) = 0
\]

for the evolitional field produced by the feedback loop of adaptive changing curvature of secondary protein folding fiber with 3 types of connection, i.e. \( \beta \) sheet for \( A_\mu=1 \), \( \alpha \) helix, \( A_\mu=2 \) and variation loop region, \( A_\mu=3 \) in docking system between viral glycoprotein and host cell receptor.

Let the cell superspace be

\[
\mathcal{M}_X = X_t^N \coprod Y_t^N \coprod X_t^N / Y_t^N \coprod X_t^O \coprod Y_t^O \coprod N_t \coprod O_t \coprod Cyte_t
\]

(24)

where

- \( X_t^N \) inner space of nuclear membrane.
- \( Y_t^N \) outer space of nuclear membrane.
- \( X_t^N / Y_t^N \) space of nuclear pore.
- \( X_t^O \) inner space of double layer organelle membrane.
- \( Y_t^O \) outer space of double layer organelle membrane.
- \( N_t \) space of nucleoplasm.
- \( O_t \) space of matrix inside organelle.
- \( Cyte_t \) space of cytoplasm.

We have 2 types of dimensions, i.e. the first is the dimension of space, the second is the dimension of superspace with a given number of layers. The first is double layers. The second is a single layer of spinor network of genetic code and spinor network of protein secondary structure folding. There exists 2 types of double layers for dbrane and anti-dbrane. Nuclear membrane and some organelle membrane like ER and mitochondria membrane see (Fig. 3 for detail). The last type is a single dbrane of cell membrane. The maps between those 5 layers of cytoplasm define the coordinates of all enzyme as a node in ribbon graph of a supersymmetric support of Dirac network for quantum atomic cell. We give a simple quantum mechanical equation derived from the interaction of protein and gene between organelle and cell membrane for a single cell. We have a modified attach and docking operator for ghost field in protein state + undocking state with sign − in the feed back loop of protein receptor over the cell superspace \( \mathcal{M}_X \). This new Dirac operator is defined as

\[
D_{\Phi}^\pm ([L]^{[\gamma]}_{A\mu}) = \int \mathcal{M} \coprod \prod_k \coprod N_t A \wedge A + A \wedge A \wedge A + \int_{Cyte} A \wedge A \wedge A \wedge A + \int_{X_t / Y_t} \Pi_j D_{\mu}^{\gamma} (\omega_1, \omega_2, \cdots, \omega_n) + E(k)
\]

\[
- \xi \frac{d^\mu}{d^\omega} \left[ \mathcal{N} (\gamma, \rho) \Pi_j W (\Gamma_{\gamma}^{\gamma} (\omega_1, \omega_2, \cdots, \omega_n)) - E^\gamma (k) = J_N (\kappa, q; A_\mu) \right] \Phi_1^\pm ([L]^{[\gamma]}_{A\mu}) .
\]

(25)
FIG. 3: The picture on the left panel represents the superspace of host cell with supercurrent from its genotype. We can separate the supermanifold of cell $\mathcal{M}$ into subspaces with partition function associated with their phase transition in the form of Wilson loop for quantum observables. The Chern-Simons current of DNA can be transferred around the whole subspace as a phase transition in analogy with Kelvin knotted model for cell. The picture on the right panel is a viral replication circle connecting 2 hosts cells with retroposon state in 4 linked between 2 couplings of areplication circle. In the above cell, red dots means junctions between the interaction of parasitism state of viral particle and the host cell. The exact sequence of replication circle induces infinite Khovanov cohomology sequence in immunosystem.

IV. SEIBERG-WITTEN INVARIANT FOR KNOTS AND LINKS IN PROTEINS

The connection $A_\mu$ has also some extra properties related to the behavior of docking and undocking states of protein signals of receptor and transmission along intercellar and intracellular as partition function in form of Chern-Simons current of life energy encryption in underlying methyl transfer of codon in tRNA. We have an expectation of gene expression as quantum gauge observable. The wave function is the orbit of principal bundle with group action while the translation process in gene expression is the fixed point of the gauge group. The mirror symmetry gauge group act on transposon and retrotransposon along the ribbon graph of knotted DNA folding. They dock to each other and the curvature is the strength of connection. We measure the change of curvature by using the modified Dirac docking operator for protein receptor $D_{\rho,\beta,D}^{\pm}: (\Phi,-\Phi+) \mapsto Adj_{\Phi,-\Phi+} = \epsilon_t \in \mathbb{R}$,

$$< \Phi^+(A_\mu) >_k = \frac{1}{Z_k} \int \Pi \omega W_{\rho,\beta,D}^{\pm}(A_\mu) e^{-iS_{CS}},$$

$$= J_k(N; q = e^{\pm \frac{2\pi i}{k}}),$$

where $J_k$ is a Jones polynomial.

**Definition 9.** A Ramanujan-Jones-Laurent knot polynomial in genetic code over protein docking state with connection $A_\mu$ for a modified Wilson loop $\Phi^\pm(A_\mu) := W_{\rho,\beta,K,D}^{\pm}(A_\mu)$ with a knot $\kappa$ of coupling constant between geneon, transposon and retrotransposon with link $L$ is

$$< \Phi^\pm(A_\mu) >_k = J_k(q, W_{\rho,\beta,K,D}^{\pm}(A_\mu); N)$$

where $q = e^{\frac{2\pi i}{k}}$. Let $[L_{A_\mu}^{[k]}]$ be an expectation value of the corresponding modified Wilson loop for the Chern-Simons current of level $k$. The Jones polynomial for the link $L$ in $S^3$ needs to satisfy the
skein relation written in the general form of Khovanov cohomology of link $<L>$,

\[ q_1 < L_+ > + q_2 < L_0 > + q_3 < L_− > = 0 \]  

(28)

where the coefficients $q_1, q_2, q_3$ are given as Verlinde-Laurent-Jones-HOMFLY polynomial $P(q_1, q_2, q_3)$, that is

\[ q_1 = - e^{\frac{-2\pi i}{3(k+1)}}, \quad q_2 = - e^{\frac{\pi i (2h−A^2)}{k(k+1)}} - e^{\frac{\pi i (2h−A^2)}{k(k+1)}}, \quad q_3 = e^{\frac{2\pi i (1−h^2)}{k(k+1)}}. \]

(29)

The coefficient $q_1, q_2, q_3$ are obtained from Verlinde fusion rule [21] for 2d conformal field theories.

From the definition, the modified Wilson loop is a gauge invariant [30] of spinor field in genetic code. Let $G_X$ be a gauge group. We have a orbit space $O_X = A_X / G_X$, with $Φ \in O_X$. Let $β^\text{geneon}_1$ be the cocycle of geneon state of principal bundle of spinor field in gene. Let $β^\text{anti-geneon}_2$ be the cocycle of anti-geneon state in active side of DNA. Let $β^\text{transposon}_3$ be the cocycle of transposon state in inactive side of DNA with momentum $k$ in cycle. Let $β^\text{retrotransposon}_4$ be the cocycle of retrotransposon state in gene with momentum $−k$ in retrotransposon. These 4 cocycles are loop and knot properties in $κ = 4_1$ which induces hidden 8 states in DNA, e.g. the figure 8 hyperbolic knotted DNA in bacteriophage. Each state can have its own knotted state denoted by $κ_1, κ_2, κ_3, κ_4$. They have representations $ρ_1, ρ_2, ρ_3, ρ_4$ of $G$ with link together in form of $L^\text{genotype}$. We define the modified Wilson loop with some extra-property of underlying protein docking and undocking states, measured by $D^+$ and $D^−$, as

\[ Φ(\mu)^± := W_{L^\text{genotype}, D^±}(A_\mu) = W_{ρ_1, κ_1, D^±}(A_\mu)W_{ρ_2, κ_2, D^±}(A_\mu)W_{ρ_3, κ_3, D^±}(A_\mu)W_{ρ_4, κ_4, D^±}(A_\mu), \quad ∀A_\mu ∈ A_X \]  

(30)

The partition function of genotype is a phase transition of gene expression at all level in the cell, primary protein, secondary protein folding and also cell signal gene expression in intercellular transmission between cell membrane. It is a gauge invariant over canonical form in cell. We give $Φ$ as an element in the moduli state space of cell under the secondary protein folding and also cell signal gene expression in intercellular transmission between cell membrane. It state takes the form of Chern-Simons current for life energy

\[ J^μ := S_{CS}(A_\mu) = \frac{k}{4\pi} \int_X tr(A_\mu ∧ dA_\mu + \frac{2}{3} A_\mu ∧ A_\mu ∧ A_\mu) \]  

(31)

where $J^μ$ is a Chern-Simons current, in biology analogy, with free energy of different of spinor fields between starting and end points of parallel transport of geneon along the link $L$ in lattice gauge field $A_\mu$: this is the so called holonomy of ribbon graph in path integral.

Let us define a partition function of these current in all small units of inside cell, i.e. organelle, nucleous, cell membrane and etc. by

\[ Z_k(Φ^±) = \int_{M_X} e^{-iS_{CS}(A_\mu)}Φ^±(A_\mu)DA \]  

(32)

where $Φ^± : (A, s) → \{1, −1\}$ is a quantum observable of genotype in ghost field of docking state with no variation in gene and anti-ghost field of undocking state with induced feedback loop of a genetic variation $κ_k$. For moduli space $F_{CS} : M_X → \mathbb{R}/\mathbb{Z}$ with coupling constant $k$ The expectation value of genotype in genetic code $< Φ^± >_k$ of the observable $Φ^±$ is given by

\[ < Φ^± >_k = \frac{Z_k(Φ^±)}{Z_k(S^3)} = \frac{\int_{M_X} e^{-iS_{CS}}Φ^±(A_\mu)DA}{\int_{M_X} e^{-iS_{CS}}DA}. \]  

(33)

If $X = S^3$ and $G = SU(2)$,Witten obtains the explicit form of partition function of the level $k$

\[ Z_k(S^3) = \sqrt{\frac{2}{k+2}} \sin(\frac{π}{k+2}). \]  

(34)

This expression is the so called normalized Witten invariant $W_{G, k}(X)$ of 2 frames in which the state of geneon is defined by the Jones polynomial with the knotted property of the skein relation in fusion rule, closed, oriented 3-manifold $X$ with link $κ$ where $W_{G, κ}(X) = \frac{Ξ_{G, κ}(X)}{Ξ_{G, κ}(S^3)}$. More details of derivation of this formulas can be found in
FIG. 4: In the picture on the left, we represent a ribbon graph model of nucleotide in genotype. There are many possibilities of knotted form from the quantization of hydrogen bond in peptide chain. It can be visualized as a ribbon graph for protein structure with loop space in time series data. In the picture on the right, we show the peptide bridge in protein. The hydrogen bonding in ribbon graph twists the plane of secondary protein into the principal bundle with connection. In our model, when we connect 2 amino-acids, the ribbon graph has 8 nodes reflected with 8 states with peptide bridge. The node of ribbon graph is an amino-acid molecule with the edge of ribbon graph as hydrogen bonding.

In a previous work [20], we used this representation for 64 states in codon explicitly as partition function of 20 amino-acids over the genetic code in 4 dimensional manifold of living cell.

Here we apply the same theoretical approach to compute the time series of knotted protein with Ramanujan-Witten-Jones-Laurent polynomials in the time series data of secondary structure of protein. Let \( \Phi^\pm(t_0) \) be the ghost field of starting point of the fiber of secondary protein and \( \Phi^\pm(t) \) be the ghost field at position \( t \) in the sequence of amino-acids in the peptide chain. Let \( q_N(P_K; \kappa; \Phi^\pm(t)) = [e^{i\alpha(t-t_0)}/e^{i\beta(t-t_0)}]/|1| \simeq e^{i(\alpha-\beta)(t-t_0)} \). Every ghost field and anti-ghost field of protein is parameterized by the partition function with order parameter \( \beta_{\text{geneon}} \) in protein sequence with associate quantum biological observable as the link operators \( <L_0>, <L_+>, <L_-> \) satisfying the skein relation.

In a ring of Laurent polynomial, we can associate 2 types of loop space with left and right supersymmetry in reversed direction. The change of direction is done by the Wilson loop operator. We have modified the skein relation to recover the relation for parameterized time series of knots and links in proteins, that is

\[
q_N^\pm(t) <L_+> - q_N^{-1}(t) <L_-> = q_N <L_0> (t-1), t = 1, 2, 3, \cdots, n. \tag{35}
\]

This relation start from the first sequence to the end of protein structure. The measurement of the polynomial can be done by using the algorithm of Chern-Simons current for biology over genetic code [A_\mu].

The Seiberg-Witten equation for biology can be used for the protein transport across the cell membrane. We have the following

**Definition 10.** Let \( \mathcal{M}_X \) be the moduli state space of cell membrane with 2 phospholipid layers. Let \( P^* \) be the induced structure of protein in passive hidden state. We have a complex connection for principle bundle of protein receptor embedded in the cell membrane with 2 states, active state \( P \) with connection \( A_\mu \) with the structure of complex principal bundle of protein in hidden state \( P_{C,K} \),

\[
A_\mu = A_\mu(P_K) + iA_\mu(P_{K}^*), \tag{36}
\]
where

\[ A_\mu(P^\kappa_X) \in \Omega^1(M_X) \otimes \text{Ad}(P_K), \]

is an inactive state of channel. We have the Chern-Simons current \( J^\mu(A_\mu) \) of flow of protein through the channel in cell membrane with cocycle of state in geneon described by the Wilson loop of protein \( W_{\kappa,\beta}(A_\mu) \) with

\[ h = -Re(e^{i\beta} J^\mu(A_\mu)). \]

The metric for time scale in time series data of protein transmission is parametrized by

\[ ds^2 = \int_{M_X} \text{Tr} \delta A_\mu \wedge \ast \delta A_\mu. \]

with the modified Seiberg-Witten equation for the cell membrane,

\[ \frac{d\Phi^\pm(A_\mu)}{ds} = \nabla h(\Phi^\pm(A_\mu)). \]

In this situation, the system of receptor protein \( \Phi^+(A_\mu) \) in cell membrane is in equilibrium state of docking between the curvature of active protein from viral particle \( P \) with curvature \( F^{[A_\mu]} = dA_\mu + A_\mu \wedge A_\mu \) and curvature of passive protein \( \Phi^-(A_\mu) \) of host cell receptor in cell membrane \( P^\ast \) with curvature \( \ast F^{[A_\mu]} \). Actually, the Seiberg-Witten equation for biology is a system of 2 equations,

\[ F^{[A_\mu]} = 0, \]

and

\[ D_{\Phi^+(A_\mu)} \Phi^+(A_\mu) \geq 0, \quad D_{\Phi^-(A_\mu)} \Phi^-(A_\mu) \geq 0, \]

if we add extra-dimensions of time scale to the system of \( M_X \times I \) homotopy path of cell membrane with 2 phospholipid layers. Let \( [A_\mu] \) be an equivalent class of genetic code of viral glycoprotein in which attaches the host receptor docking protein. We can define an evolution signal of \( [A_\mu] \) over time scale in which the analogy with genetic shift and genetic drift is

\[ \frac{\partial [A_\mu]}{\partial t} = -\frac{\delta J^\mu([A_\mu])}{\delta [A_\mu]} = -\ast F^{[A_\mu]}, \]

The solution for this equation is solved for the Hitchin system of quantum field in biology by the pair \( (\Phi^\pm(A_\mu), A_\mu(P_K)) \).

V. COMPUTATION IN SYNTHETIC TIME SERIES OF KNOTS AND LINKS IN PROTEINS

Let \( L \) be a superspace of link operator in time series of knots and links in proteins induced by the adaptive behavior of evolutive factor from mutation of crossing in DNA while the recombination process of replication cycle is going on. Let topology of cell be a hyperbolic knot \( \kappa = 4_1 \). Let \( P \) be unknots and links in proteins with principal fiber \( P_K \). The length of amino-acid is assigned to \( n \) with homotopy path parameterized by the time series as short exact sequence. It is \( t_1 \to t_2 \to t_3 \to t_4 \to \cdots \). Let \( [s_1], [s_2], \cdots, [s_8] \) be 8 states of spinor field in time series of genetic code. We use the fact that figure 8 knots generate an hyperbolic octahedral volume where \( [s_i], i = 1, 2, \cdots, 8 \) are in the corner of lattice of the octahedron for codon. In Axiom 7th of quantum field biology, the path \( \alpha_i, i = 1, 2, \cdots, 12 \) in figure 8 knot belong to the zeros cohomology group \( H^0(\text{End}(P_K) \otimes L) \).

This path induces a homotopy path in \( H^1(\text{End}(P_K)) \) of the axioms by the homotopy equivalent under the influence factor of evolution due to the tensor product in superspace \( < L_0 >, < L_+ >, < L_- > \in L \). It is worth noticing that we have the homotopy path in loop over \( 4_1 \) with 4 equivalent classes of loop space in time series data of knotted protein.

\[ [\beta_1], [\beta_2], [\beta_3], [\beta_4] \in H^1(\text{End}(P_K)) \]

where the path in loop is a generator of knotted group for secondary protein structure with

\[ \beta_1 : 0 \to \alpha_2 \to \alpha_3 \to \alpha_5^{-1} \to \alpha_8^{-1} \to 0 \]
The center of 4-torus are $\beta$ to compute the modified Khovanov cohomology for biology. The right picture is a transformation of left picture into the loop representation of modified Khovanov cohomology for biology as the loop space of time series data. We can connect all obstruction components with a 4-loop of knots and links labelled with red dots and blue line. It is a pictorial representation of modified Khovanov cohomology for biology as the loop space of time series data.

$$\beta_2 : 0 \rightarrow \alpha_4 \rightarrow \alpha_5 \rightarrow \alpha_{11}^{-1} \rightarrow \alpha_{10}^{-1} \rightarrow 0$$

$$\beta_3 : 0 \rightarrow \alpha_2 \rightarrow \alpha_3 \rightarrow \alpha_{10} \rightarrow \alpha_{11} \rightarrow \alpha_6 \rightarrow \alpha_7 \rightarrow 0$$

$$\beta_4 : 0 \rightarrow \alpha_1 \rightarrow \alpha_{8}^{-1} \rightarrow \alpha_9^{-1} \rightarrow \alpha_4^{-1} \rightarrow \alpha_5^{-1} \rightarrow \alpha_{12} \rightarrow 0$$

There exists 2 trivial elements in open state for 2 ends terminal of protein secondary structure folding. It is an unknotted state of protein generates from the kernel map in higher dimensional knotted state of protein loop superspace.

$$[\gamma(t_1)], [\gamma(t_{13})] \in H^2(End(P_C)).$$

From this example, we have a time series of link operator parametrized by the underlying ghost and anti-ghost fields of knots and links in proteins with modified Wilson loop over the exact sequence of link operator $< L > (t)$

$$< \Phi^+(A_\mu)>_k(t) : 0 \rightarrow [L_0]^{[s_i(t_1)]}_{A_\mu} W_{4_1,\beta_4}(A_\mu=3; t_1) \rightarrow [L_-]^{[s_i(t)]}_{A_\mu} W_{4_1,\beta_1,\beta_4}(A_\mu=3; t_2) \rightarrow$$

$$\rightarrow [L_0]^{[s_i(t_3)]}_{A_\mu} W_{4_1,\beta_1}(A_\mu=3; t_3) \rightarrow [L_+]^{[s_i(t_4)]}_{A_\mu} W_{4_1,\beta_1,\beta_2}(A_\mu=3; t_4) \rightarrow [L_0]^{[s_i(t_5)]}_{A_\mu} W_{4_1,\beta_2}(A_\mu=3; t_5) \rightarrow$$

$$\rightarrow [L_+]^{[s_i(t_6)]}_{A_\mu} W_{4_1,\beta_2,\beta_3}(A_\mu=3; t_6) \rightarrow [L_0]^{[s_i(t_7)]}_{A_\mu} W_{4_1,\beta_3}(A_\mu=3; t_7) \rightarrow [L_-]^{[s_i(t_8)]}_{A_\mu} W_{4_1,\beta_3,\beta_1}(A_\mu=3; t_8) \rightarrow$$

$$\rightarrow [L_0]^{[s_i(t_9)]}_{A_\mu} W_{4_1,\beta_1}(A_\mu=3; t_9) \rightarrow [L_-]^{[s_i(t_{10})]}_{A_\mu} W_{4_1,\beta_1,\beta_2}(A_\mu=3; t_{10}) \rightarrow [L_0]^{[s_i(t_{11})]}_{A_\mu} W_{4_1,\beta_2}(A_\mu=3; t_{11}) \rightarrow$$

$$\rightarrow [L_+]^{[s_i(t_{12})]}_{A_\mu} W_{4_1,\beta_2,\beta_4}(A_\mu=3; t_{12}) \rightarrow [L_+]^{[s_i(t_4)]}_{A_\mu} W_{4_1,\beta_4,\beta_2}(A_\mu=3; t_{13}) \rightarrow 0.$$
TABLE I: The table below shows artificial viral glycoprotein for synthetic signal of time series in knots and links in proteins according to the definition of first 14-ghost fields in $E_8 \times E_8$ model of artificial capsid VP1, VP2, VP3 viral supermanifold structure of secondary protein.

| Ghost field $\Phi_i$ | site name       | state space variable $x_t$ | type of fiber              |
|----------------------|-----------------|-----------------------------|----------------------------|
| $\Phi_1^+$           | $C'BHA2$        | $x_t$                       | $A_{\mu=3}$, loop          |
| $\Phi_2^+$           | $N'H A1$        | $x_t$                       | $A_{\mu=3}$, loop          |
| $\Phi_3^+$           | $CBHA2$         | $x_t$                       | $A_{\mu=3}$, loop          |
| $\Phi_4^+$           | $siteC$         | $x_t$                       | $A_{\mu=3}$, loop          |
| $\Phi_5^+$           | $Hinge$         | $x_t$                       | $A_{\mu=3}$, loop          |
| $\Phi_6^+$           | $SiteE$         | $x_t$                       | $A_{\mu=3}$, loop          |
| $\Phi_7^+$           | Attachment Site | $x_t$                       | $A_{\mu=3}$, loop          |
| $\Phi_8^+$           | $siteB$         | $x_t$                       | $A_{\mu=3}$, loop          |
| $\Phi_9^+$           | $SiteD$         | $x_t$                       | $A_{\mu=1}$, $\beta$ sheet|
| $\Phi_{10}^+$        | Loop            | $x_t$                       | $A_{\mu=3}$, loop          |
| $\Phi_{11}^+$        | $N'H A2$        | $x_t$                       | $A_{\mu=2}$, $\alpha$ helix|
| $\Phi_{12}^+$        | $C'BHA2$ (Bromelain cleavage) | $x_t$                       | $A_{\mu=3}$, loop          |
| $\Phi_{13}^+$        | Fusionpeptide   | $x_t$                       | $A_{\mu=3}$, loop          |
| $\Phi_{14}^+$        | $C'H A1$        | $x_t$                       | $A_{\mu=3}$, loop          |
| $\Phi_1^-$           | Antigen Binding Site | $y_t$                       | $A_{\mu=1}$, $\beta$ sheet|
| $\Phi_2^-$           | LightChain      | $y_t$                       | $A_{\mu=1}$, $\beta$ sheet|
| $\Phi_3^-$           | Heavy Chain     | $y_t$                       | $A_{\mu=1}$, $\beta$ sheet|

This short sequence can be written as a linear combination of bases,

$$<\Phi_i^\pm ([L_i]^{[\kappa]}_{A_i}; P_C) > k (t) = \sum_{j=1}^{12} \sum_{s=1}^{4} \lambda_{ij} [L_i]^{[\kappa]}_{A_i} \Pi_{\kappa} W_{\nu, \beta} (A_i) (t_j). \quad (51)$$

$$H ([L_i]^{[\kappa]}_{A_i}; P_C) : 0 \rightarrow \cdots \rightarrow H^1([L_i]^{[\kappa]}_{A_i}; P_C) \rightarrow H^2([L_i]^{[\kappa]}_{A_i}; P_C) \rightarrow H^3([L_i]^{[\kappa]}_{A_i}; P_C) \rightarrow H^4([L_i]^{[\kappa]}_{A_i}; P_C) \rightarrow \cdots$$

$$\rightarrow H^2([L_i]^{[\kappa]}_{A_i}; P_C) \rightarrow H^2([L_i]^{[\kappa]}_{A_i}; P_C) \rightarrow H^2([L_i]^{[\kappa]}_{A_i}; P_C) \rightarrow \cdots \rightarrow 0 \quad (52)$$

The short exact sequence of time series of knotted protein induces an infinite sequence of modified Khovanov cohomology with the 3d-cohomology group associated with the volume form of the Chern-Simons current in the protein docking and undocking states.

VI. COMPUTATION OF CHERN-SIMONS CURRENT IN VIRAL CAPSID GLYCOPROTEINS

In this section, we use the notation in Table I for integrate and differentiate over cohomology of loop space in homotopy path along the hidden 14 dimensional model. The ghost fields of 14 glycoprotein sides (see Fig. 8 for details) are adopted in super-integrals to represent the viral attach cell. The 14 dimensional loop space of cell is derived from docking and undocking states of ghost and anti-ghost fields that model the protein-protein interactions. This is just a simple example of how to use the Grothendieck topology to coordinate the protein docking equation in a unified theory $E_8 \times E_8$ model for living organism. We use synthetic ghost fields of protein secondary structure from influenza viral glycoprotein and antibody light and heavy chains of human cell as example for computing the Khovanov cohomology for time series of knots and links in proteins.

Let $\mathcal{A}$ be a superspace for artificial viral particle in $S^{-k, k=14}$ attached with artificial cell structure of mathematical structure of antibody in $S^{k, k=3}$ model.
FIG. 6: The picture on the left shows an influenza viral glycoprotein model from x-ray crystallography. The glycoprotein is
drawing from experiments. An icosahedral group $E_8 \times E_8$ model of ghost field and antighost field for this component is shown
in Table I. The axiom of quantum field for biology is satisfied. We use this glycoprotein to calculate, with a similar algorithm,
other artificial icosahedral viral capsid proteins, i.e. VP1,VP2,VP3, which are particles in hidden 14 dimensional model of super-
statistics in BV-cohomology theory. A glycoprotein of virus with 14 sides with recognized name from x-ray crystallography is
reported. In the right picture, we show the docking system of $D^+ \Phi_+ (x; A_\mu) | \Phi_−(y; A_\mu)$. The viral glycoprotein is denoted by the
ghost field $\Phi_+ (x; A_\mu)$ with the attach docking operator derived from the behavior of gene expression in virus, denoted as $D^+$
operator. We move $\Phi_+$ to dock with static place of $\Phi_−$ in host cell membrane. This situation is specified with the notation
$D^+ \Phi_+$. We specify also the parallel transport of gauge field of docking protein. In this model, we have defined the docking
operator by using the Grothendieck coordinates with continuous co-adjoint functor with their limit
$$\lim_{b \to a} \Gamma_{b\mu}^a (\gamma) \Phi_+^b - \Phi_−^a t_b - t_a = 0,$$
as modified covariant derivative of proteins docking system in principal fiber bundle. This equation of docking is a parts of the
modified Seiberg-Witten equation for biology.

In this example, we have 14 bases (see Fig. 6) for ghost fields 11 bases for anti ghost fields (for detail of definition
of ordering of basis, see table I).

$$< \Phi_1^+(A_\mu) > = \frac{1}{Z_{k=1}} \int_{H^1([L_\pm]^{[v_i]}; P K)} \Pi_\mu W_{\beta_1,\kappa}(A_\mu) e^{-j2\pi \beta_1 (C'H A 2)} e^{-i S^{SC} d \beta_1} D_{\Phi_-(A_\mu)} | \Phi_1^+(A_\mu) > = 0,$$

$$< \Phi_2^+(A_\mu) > = \frac{1}{Z_{k=2}} \int_{H^1([L_\pm]^{[v_i]}; P K)} \Pi_\mu W_{\beta_2,\kappa}(A_\mu) e^{-j2\pi \beta_2 (N'H A 1)} e^{-i S^{SC} d \beta_2} D_{\Phi_-(A_\mu)} | \Phi_2^+(A_\mu) > = 0,$$

$$< \Phi_3^+(A_\mu) > = \frac{1}{Z_{k=3}} \int_{H^1([L_\pm]^{[v_i]}; P K)} \Pi_\mu W_{\beta_3,\kappa}(A_\mu) e^{-j2\pi \beta_3 (C'B H A 2)} e^{-i S^{SC} d \beta_3} D_{\Phi_-(A_\mu)} | \Phi_3^+(A_\mu) > = 0,$$

$$< \Phi_4^+(A_\mu) > = \frac{1}{Z_{k=4}} \int_{H^1([L_\pm]^{[v_i]}; P K)} \Pi_\mu W_{\beta_4,\kappa}(A_\mu) e^{-j2\pi \beta_4 (site C)} e^{-i S^{SC} d \beta_4} D_{\Phi_-(A_\mu)} | \Phi_4^+(A_\mu) > = 0,$$
\[ <\Phi_5^+(A_\mu) > = \frac{1}{Z_{k=5}} \int_{H^1([L_\pm]_{A_\mu}; P_\kappa)} \Pi_{\mu} W_{\beta_5,\kappa}(A_\mu) e^{-j 2\pi \beta_5(Hinge)} e^{-i S_{SC} d\beta_5, D_{\Phi^-}(A_\mu)} |\Phi_5^+(A_\mu) > = 0 \]

\[ <\Phi_6^+(A_\mu) > = \frac{1}{Z_{k=6}} \int_{H^1([L_\pm]_{A_\mu}; P_\kappa)} \Pi_{\mu} W_{\beta_6,\kappa}(A_\mu) e^{-j 2\pi \beta_6(SiteE)} e^{-i S_{SC} d\beta_6, D_{\Phi^-}(A_\mu)} |\Phi_6^+(A_\mu) > = 0 \]

\[ <\Phi_7^+(A_\mu) > = \frac{1}{Z_{k=7}} \int_{H^1([L_\pm]_{A_\mu}; P_\kappa)} \Pi_{\mu} W_{\beta_7,\kappa}(A_\mu) e^{-j 2\pi \beta_7(AttachSite)} e^{-i S_{SC} d\beta_7, D_{\Phi^-}(A_\mu)} |\Phi_7^+(A_\mu) > = 0 \]

\[ <\Phi_8^+(A_\mu) > = \frac{1}{Z_{k=8}} \int_{H^1([L_\pm]_{A_\mu}; P_\kappa)} \Pi_{\mu} W_{\beta_8,\kappa}(A_\mu) e^{-j 2\pi \beta_8(SiteB)} e^{-i S_{SC} d\beta_8, D_{\Phi^-}(A_\mu)} |\Phi_8^+(A_\mu) > = 0 \]

\[ <\Phi_9^+(A_\mu) > = \frac{1}{Z_{k=9}} \int_{H^1([L_\pm]_{A_\mu}; P_\kappa)} \Pi_{\mu} W_{\beta_9,\kappa}(A_\mu) e^{-j 2\pi \beta_9(SiteD)} e^{-i S_{SC} d\beta_9, D_{\Phi^-}(A_\mu)} |\Phi_9^+(A_\mu) > = 0 \]

\[ <\Phi_{10}^+(A_\mu) > = \frac{1}{Z_{k=10}} \int_{H^1([L_\pm]_{A_\mu}; P_\kappa)} \Pi_{\mu} W_{\beta_{10},\kappa}(A_\mu) e^{-j 2\pi \beta_{10}(Loop)} e^{-i S_{SC} d\beta_{10}, D_{\Phi^-}(A_\mu)} |\Phi_{10}^+(A_\mu) > = 0 \]

\[ <\Phi_11^+(A_\mu) > = \frac{1}{Z_{k=11}} \int_{H^1([L_\pm]_{A_\mu}; P_\kappa)} \Pi_{\mu} W_{\beta_{11},\kappa}(A_\mu) e^{-j 2\pi \beta_{11}(N^\prime HA2)} e^{-i S_{SC} d\beta_{11}, D_{\Phi^-}(A_\mu)} |\Phi_{11}^+(A_\mu) > = 0 \]

\[ <\Phi_12^+(A_\mu) > = \frac{1}{Z_{k=12}} \int_{H^1([L_\pm]_{A_\mu}; P_\kappa)} \Pi_{\mu} W_{\beta_{12},\kappa}(A_\mu) e^{-j 2\pi \beta_{12}(C^\prime HA2)} e^{-i S_{SC} d\beta_{12}, D_{\Phi^-}(A_\mu)} |\Phi_{12}^+(A_\mu) > = 0 \]

\[ <\Phi_{13}^+(A_\mu) > = \frac{1}{Z_{k=13}} \int_{H^1([L_\pm]_{A_\mu}; P_\kappa)} \Pi_{\mu} W_{\beta_{13},\kappa}(A_\mu) e^{-j 2\pi \beta_{13}(Fusionpeptide)} e^{-i S_{SC} d\beta_{13}, D_{\Phi^-}(A_\mu)} |\Phi_{13}^+(A_\mu) > = 0 \]

\[ <\Phi_{14}^+(A_\mu) > = \frac{1}{Z_{k=14}} \int_{H^1([L_\pm]_{A_\mu}; P_\kappa)} \Pi_{\mu} W_{\beta_{14},\kappa}(A_\mu) e^{-j 2\pi \beta_{14}(C^\prime HA1)} e^{-i S_{SC} d\beta_{14}, D_{\Phi^-}(A_\mu)} |\Phi_{14}^+(A_\mu) > = 0 \]

Considering the expectation ghost field \( H^3(Y_t)/H^{14}(X_t) \approx H^{-11}(Y_t/X_t) \ni \epsilon_t^* \) with superderivative with respect to anti-ghost field in cell defined by

\[ <\Phi_1^- (A_\mu) > = \frac{d}{dS^1} g^{11} \Phi_1^+(A_\mu) = \frac{g^{11} de^{2\pi i a_2(BindingSite)}}{d\alpha_1}, D_{\Phi^+(A_\mu)} |\Phi_1^- (A_\mu) > = 0 \]

\[ <\Phi_2^- (A_\mu) > = \frac{d}{dS^2} g^{22} \Phi_2^+(A_\mu) = \frac{g^{22} de^{2\pi i a_2(LightChain)}}{d\alpha_2}, D_{\Phi^+(A_\mu)} |\Phi_2^- (A_\mu) > = 0 \]

\[ <\Phi_3^- (A_\mu) > = \frac{d}{dS^3} g^{33} \Phi_3^+(A_\mu) = \frac{g^{33} de^{2\pi i a_3(HeavyChain)}}{d\alpha_3}, D_{\Phi^+(A_\mu)} |\Phi_3^- (A_\mu) > = 0 \]

we have

\[ \alpha_t([y_t]) \beta_t([x_t]) \simeq [\epsilon_t^*] \in H^{-11}(O_{Y_t/X_t}; P_\kappa). \]
If we write the Dirac operator for docking system denoted by $D = D_{\Phi}^{-}(A_{\mu})$ and $d := D_{\Phi}^{+}(A_{\mu})$, when docking state is in equilibrium, all curvatures do not change and equal to each other from duality sites. So we have

$$Ad_{\Phi}^{-}(A_{\mu}) \Phi^{+}(A_{\mu}) := \nabla_{\Phi}^{-}(A_{\mu}) \Phi^{+}(A_{\mu}) := \{ dd\Phi^{1}_{-}(y_{i}) \Phi^{2}_{-}(y_{i}) \Phi^{3}_{-}(y_{i}) \cdot \Phi^{14}_{-}(y_{i}) \} $$

If docking is in equilibrium and viral can penetrate to host cell, that means we have just one part of mirror symmetry of Dirac operator to be zero according to our new definition. Therefore, we have

$$D\Phi^{1}_{-} D\Phi^{2}_{-} D\Phi^{3}_{-} D\Phi^{4}_{-} \cdots D\Phi^{14}_{-} = 0.$$  

(56)

If we defined our adjoint operator with extra properties of algebraic operator by

$$DDDD \cdots DDDD \Phi^{1}_{-} \Phi^{2}_{-} \Phi^{3}_{-} \Phi^{4}_{-} \cdots \Phi^{14}_{-} = D\Phi^{1}_{-} DDDD \cdots DDDD \Phi^{2}_{-} \cdots \Phi^{13}_{-} \Phi^{14}_{-} $$

$$= \cdots = D\Phi^{1}_{-} D\Phi^{2}_{-} D\Phi^{3}_{-} \cdots D\Phi^{13}_{-} D\Phi^{14}_{-}.$$  

(57)

therefore we have a solution for each gene in each ghost field given by the system of equations

$$D\Phi^{1}_{-} = 0, D\Phi^{2}_{-} = 0, D\Phi^{3}_{-} = 0, \cdots, D\Phi^{13}_{-} = 0, D\Phi^{14}_{-} = 0.$$  

(58)

We can factorize the gene in time series of knotted glycoprotein with obstruction components for each gene. It can be solved by using the modified Wilson loop for gene expression.

In the model of protein complex surface, the differential 2 forms induced by the equilibrium $\tilde{d}^{2} = 0$ over 8 states and hidden states generate the codon with 64 bases in exact sequence. Then we use the triplet state over the layer of protein $P$ to generate a Chern-Simons 3 form over the canonical form of exact sequence of triplet state $P$ with its dual $P^{*}$. The computation is as follows. For the equilibrium docking, we have $H^{-k}(O_{A}, s) = 0$, for all $k > 0$. This means that we cannot notice ghost and anti-ghost fields if the system of docking is in equilibrium. There will exists hidden negative dimension area of trash DNA active only when the state of undocking in protein system appears. The immunosystem will induce feedback loops of retrotransposon and transponson by cohomology in negative dimension in feedback path to cohomology in positive dimension to find a new equilibrium point of docking until it holds then the negative path is zeros again recursively. The main expression of gene can be written as a super-regression $[\alpha] \sim [\beta] \in H^{2}(O_{A}; O_{X/Y})$, so we induce an evolutional field in trash area as a hidden field to control the second round of recursive form of induced long infinite exact sequence along superspace of time series data. The super-regression is given by co-states that couple with 2 feedback loop of geneon and retrotransposon state in genotypes, that is

$$\varphi^{\text{retrotransposon}}_{Y} = [\alpha] + [\beta] \varphi^{\text{geneon}}_{X} + [\epsilon_{i}]_{X/Y}.$$  

(59)

The copy process of retrotransposon loop space is a characteristic class of cohomology in negative dimensions induced by a master equation with adjoint functor as cohomology functor. The extended Chern-Simons current for trash DNA is possible by cosaxter number $h$ in the Laurent series of poles of state $[s_{i}]^{*}, i = 1, 2, \cdots, 8$ with icosahedral group $E_{8}$ we get $h = 30$. Therefore we can extend this approach to represent genetic code as Laurent polynomials in the variable $q$ with integer coefficients, that is for trash area with knot $K$ over sheaf cohomology of DNA.

A hyperbolic manifold is a manifold with a metric of constant negative curvature. A system of viral replication cycle in host cell can be visualized as a hyperbolic manifold with 2 states space variables $(x_{i}, y_{i})$ over ghost field $\Phi^{-}(A_{\mu}; x_{i})$ with co-cycle $\beta$ of viral particle and anti-ghost field $\Phi^{-}(A_{\mu}; y_{i})$ over co-cycle $\alpha$ of host cell over protein docking system on the surface of host cell. We give an simple hyperbolic equation of viral attach to host cell with some explanation of transition state between geneon and anti-geneon in docking system as evolutional gauge field of genetic code given as the connection $[A_{\mu}]$.

Let trajectory of path in replication cycle of viral components penetrate to host cell and fuse RNA with DNA of host cell until go out from host cell. It can be parameterized by figure 8 knot $\kappa$ with hyperbolic manifold in host cell $S^{3} - \kappa$ with finite hyperbolic volume $\text{Vol}(\kappa)$. These volumes are invariant in host cell and can be, specifically, thought as invariant volumes of host cell receptor knotted protein if we visualize the viral glycoprotein as a trajectory in time series of knotted docking protein along $\kappa$.

**Definition 11.** Let $\mathcal{M}_{X_{i}/Y_{i}}$ be a moduli state space of parasitism state between host cell with viral replication cycle. It is a configuration space of coupling transition state between geneon and anti-geneon. Let $S$ be spin state span by 8 bases of spinor field $[s_{i}]$ and gauge field $A_{\mu}$ for behavior of underlying genotype in time series data of genetic code. A
TABLE II: The table shows the Chern-Simons current for genetic code of the first 20 peptides. We calculate the average codon of predefined Chern-Simons current for amino-acids considering real values of parameter $k$.

| no. | Amino-acid | Abbreviation | Code | Average Chern-Simons Current | state space(k) | Average state for one pixel |
|-----|------------|--------------|------|-------------------------------|----------------|----------------------------|
| 1   | Alanine    | Ala          | A    | 0.0320                        | 29.30,31.32    | 30.5                       |
| 2   | Cysteine   | Cys          | C    | 0.0120                        | 49.50          | 49.5                       |
| 3   | Aspartic acid | Asp         | D    | 0.0136                        | 41.42          | 41.5                       |
| 4   | Glutamic acid | Glu         | E    | 0.0128                        | 47             | 47                         |
| 5   | Phenylalanine | Phe         | F    | 0.6036                        | 1.2            | 1.5                        |
| 6   | Glycine    | Gly          | G    | 0.0086                        | 61.62,63.64    | 62.5                       |
| 7   | Histidine  | His          | H    | 0.0179                        | 37.38          | 37.5                       |
| 8   | Isoleucine | Ile          | I    | 0.1066                        | 9,10,11        | 10                         |
| 9   | Lysine     | Lys          | K    | 0.0145                        | 43.44          | 43.5                       |
| 10  | Leucine    | Leu          | L    | 0.2305                        | 5,6,7,8        | 6.5                        |
| 11  | Methionine | Met          | M    | 0.0841                        | 12             | 12                         |
| 12  | Asparagine | Asn          | N    | 0.0015                        | 41,42          | 41.5                       |
| 13  | Proline    | Pro          | P    | 0.0367                        | 21.22,23.24    | 22.5                       |
| 14  | Glutamine  | Gln          | Q    | 0.0166                        | 39.4           | 39.5                       |
| 15  | Arginine   | Arg          | R    | 0.0100                        | 53,54,59,60    | 56.5                       |
| 16  | Serine     | Ser          | S    | 0.0352                        | 17,18,19,20,57,58 | 31.5                       |
| 17  | Threonine  | Thr          | T    | 0.0292                        | 25,26,27,28    | 26.5                       |
| 18  | Valine     | Val          | V    | 0.2658                        | 13,14,15,16    | 14.5                       |
| 19  | Tryptophan | Trp          | W    | 0.0112                        | 52             | 52                         |
| 20  | Tyrosine   | Tyr          | Y    | 0.0210                        | 33,34          | 33.5                       |

Coupling parasitism system is the statistical system ($\mathcal{M}_{X,Y}$, $S$) with a transition between $[s_i]$ to $[s_i^*]$ in evolution dual state $[e_i] = <[s_i^*]|[s_i]|([e_i]$) $\in \mathcal{F}(\mathcal{M}_{X,Y}, S)$. The energy $\mathcal{E}_k$ of the system is measured by coupling constant $k \in K$ as the transition level in partition function of internal state of parasitism replication cycle, that is

$$\mathcal{E}_k : \mathcal{F}(\mathcal{M}_{X,Y}, S) \rightarrow \mathbb{R}$$

The partition function of the system is defined as

$$Z_k = \sum \mathcal{E}_k([e_i])\varphi^{\text{geneon}}(t)$$

where $\varphi^{\text{geneon}}(t) : \mathcal{F}(\mathcal{M}_{X,Y}, S) \rightarrow \mathbb{R}$ is a wave function of geneon state of the transition between ground states $[s_i]$ to excited state $[s_i^*]$ in genotypes of docking system.

**Theorem 1.** The state of docking between viral capsid protein and host receptor protein is in equilibrium when the Seiberg-Witten equation for cell membrane of host cell holds, that is

$$F^{[A_\mu]} = 0, D_{\Phi^+}^+|\Phi^+_k(A_\mu; x_i) >= |s_k|\Phi^+_k(A_\mu; x_i) >= 0, \quad D_{\Phi^+}^-|\Phi^-_k(A_\mu; y_i) >= |s_k|\Phi^-_k(A_\mu; y_i) >= 0$$

The solution for Hitchin pair of this equation can be described in hyperbolic equation over 2 variables in moduli state space model of parasitism $(x_i, y_i)$ with parameter $(\alpha, \beta)$ as a coupling co-cycle. The transition function is defined by the holonomy of $\Phi_{\text{in}}^+ (A_\mu)$ and $\Phi_{\text{out}}^+$ between quantum states of in docking system over the cell membrane.

$$\text{Hol}_{\mathcal{M}_{X,Y}}(\delta \Phi^+ (A_\mu) > k) := \Pi_{\mu} W_{\beta, \gamma}(A_\mu) W_{\gamma}, \gamma(A_\mu) = 0 = <\Phi_{\text{out}}(A_\mu) >= <\Phi_{\text{in}}(A_\mu) >= <\delta \Phi > k$$

Proof: Let $[A_\mu] = \Gamma_{ij}^\mu$ be the equivalent class of gauge field gene $[s_i]$ with transition hidden state to $[s_j]^*$. From $F^{[A_\mu]} = 0$, we have $\partial_\mu A_\nu - \partial_\nu A_\mu + A_\mu \wedge A_\nu = 0$ or, shortly, $dA = -A \wedge A$. Let $x_t$ be a state variable of geneon in viral capsid protein genotype and $y_t$ be state variable of geneon in host receptor protein. We choose the connection $A_\mu$ to represent a gauge field where the source of field is a spinor field $[s_i] = \varphi^{\text{geneon}} = [e_i^{\text{geneon}}]$ located at the center of obstruction component in $S^1$. The state spinor variable $x_t - [s_i]$ is a radius of circle $S^1$. We choose a representation
of Wilson loop with connection in principal fiber $P_X$ adopting a Möbius map from the circle to the fiber $F_{[s_i]} \in P_X,[A_{\mu}]$ defined by

$$W_{\beta,P_X,\kappa}(A_{\mu}) = Tr_{\rho}Pe^{f A_{\nu}} = Tr_{\rho}Pe^{\frac{\epsilon}{\pi - i \gamma_0} dx_\mu} = e^{\frac{\epsilon}{\pi - i \gamma_0} dx_\mu}. \quad (64)$$

For a co-cycle, we choose, as above, the connection $A_{\mu}$ to represent a gauge field where the source of field is a spinor field $[s_j]^* = \varphi^{anti-geneon} = [e^{-i\alpha}]$ located at the center of $S^{-1}$ and state spinor variable $y_t - [s_j]^*$ is a tangent to the same unit circle with opposite direction of orientation $S$. So we have

$$W_{\alpha,P_Y}(A_{\mu},\kappa) = Tr_{\rho}Pe^{f A_{\nu}} = Tr_{\rho}Pe^{\frac{1}{\pi - i \gamma_0} dy_j} = e^{\frac{1}{\pi - i \gamma_0} dy_j} \quad (65)$$

and

$$Hol_{M_X/Y}(<\delta \Phi^\pm(A_{\mu})>_k) := W_{\beta,P_X,\kappa}(A_{\mu})W_{\alpha,P_Y}(A_{\mu},\kappa) = e^{\frac{1}{\pi - i \gamma_0} dx_\mu} e^{\frac{1}{\pi - i \gamma_0} dy_j}$$

$$= e^{ln|x_t - [s_i]| + \epsilon_{t},e^{ln|y_t - [s_j]| + \epsilon_{y}} = 0. \quad (66)$$

Hence, we have

$$|x_t - [s_i]||y_t - [s_j]| = 0, \quad (67)$$

so $x_t = \pm [s_i], y_t = \pm [s_j]$. We call 2 hidden states with minus sign from these solutions of docking equation, $-[s_i]$ a transposon state and $- [s_j]$, a retrotransposon state.

From this solution, if we assign $\pm [s_i], \pm [s_j]$, a constant real value by using the projection from spin space to real value and the transition energy function

$$\varphi^{geneon}(t) : F(M_{X/Y},S) \rightarrow \mathbb{R}, [s_i] \rightarrow \varphi^{geneon}([s_i];t) \quad (68)$$

$$\varphi^{anti-geneon}(t) : F(M_{X/Y},S) \rightarrow \mathbb{R}, [s_j]^* \rightarrow \varphi^{anti-geneon}([s_j];t) \quad (69)$$

$$\varphi^{transposon}(t) : F(M_{X/Y},S) \rightarrow \mathbb{R}, [-s_i] \rightarrow \varphi^{transposon}(-[s_i];t) \quad (70)$$

$$\varphi^{retrotransposon}(t) : F(M_{X/Y},S) \rightarrow \mathbb{R}, -[s_j]^* \rightarrow \varphi^{retrotransposon}(-[s_j]^*;t) \quad (71)$$

then we can draw solution into $xy$ plane in $\mathbb{R}^2$. The solution will cut $xy$-axis in 4 points. We use these 4 points as vertices of 2 hyperbolas with the same center point at $(h,k)$. The hyperbolar graph is a simple example of hyperbolic structure of co-state between geneon and anti-geneon, that is

$$\frac{(x_t - h)^2}{\varphi^{geneon}([s_i];t)} = \frac{(y_t - k)^2}{\varphi^{anti-geneon}([s_j]^*;t)} = 1, \quad (72)$$

and hyperbolic structure of co-state between transposon and retrotransposon, that is

$$\frac{(y_t - h)^2}{\varphi^{transposon}(-[s_i];t)} = \frac{(x_t - k)^2}{\varphi^{retrotransposon}(-[s_j]^*;t)} = 1. \quad (73)$$

We can write the hyperbolic equation of solution in a general form as

$$A x_t^2 - B y_t^2 + C x_t + D y_t + E = 0. \quad (74)$$

These 5 parameters can be estimated by an empirical analysis with the Chern-Simons current in genetic code. The partition function can be used to measured transition states between these 4 states with some energy hand gap between ground state and excited state in the hyperbolic curve derived from the estimation of genetic code in genotype.

If we $d^* := D_{\Phi^*}, D^* = D_{\Phi^-}$, we have a mirror symmetry of docking operators for transposon and retrotransposon as repeated obstruction solution since the docking system is not in equilibrium. There exist 2 types of evoloutional field as eigenvalues of life energy induced from adaptation of curvature changing while docking. The first is the evoloutional
field induced from the obstruction component of genetic variation adaptation in genotype of receptor protein in host cell. The docking operator changes direction of spin from adjoint (reversed direction of antiparallel of spin) to co-adjoint direction (parallel direction of spin) from host cell y to dock with viral particle x with ghost field in protein $\Phi^+(x)$. This system is undoing state so virus cannot penetrate the cell anymore since host cells can adapt them and change curvature in transposon transition state with eigenvalue $\varphi_{\text{transposon}}$. In quantum biology, we use Hermitian notation for excitation states $D \rightarrow D^*$. This eigenvalue brings the life ground state of ghost field to an excited state:

$$
D^*|\Phi^+(x_i)> = D_{\Phi_i}^+|\Phi^+(x_i)> = \varphi_{\text{transposon}}|\Phi^+(x_i)> .
$$

In this situation, we induce an evolution feedback loop with reversed evolutional field down to retrotransposon state. The virus needs to survive and changes its spin state switching its direction from $+$ to $-$ sign of docking Dirac operator. From the memory of ghost field of underlying protein state, DNA methylation or RNA methylation can exist in viral particles to switch some part of their inactive gene to retrotransposon states. We have transition from $d \rightarrow d^*$ defined by

$$
d^*|\Phi^-(y_i)> = D_{\Phi_i}^-|\Phi^-(y_i)> = \varphi_{\text{retrotransposon}}|\Phi^-(y_i)>.
$$

Let $\varphi_{\text{retrotransposon}} = \varphi_{\text{transposon}}$ and $\epsilon_i^2 = \varphi_{\text{transposon}} \varphi_{\text{retrotransposon}}$ be an evolution feedback gauge field for docking-undocking system. We define the curvature of docking and undocking system as a function of evolution

$$
F_{\mu\nu} = [\nabla_{\mu}, \nabla_{\nu}] = \text{adj} \{d^*, D^*\} = <\Phi_{\mu}^- d^*| D^* \Phi_{\nu}^+ > = \epsilon_i^2 < \Phi_{\mu}^-| \Phi_{\nu}^+ > .
$$

When docking system is in equilibrium, the host cell will die since viral can penetrate in it with curvature changing to zero. If host cells want to survive, they need to have an evolutional field to change their curvature from zero to eigenvalue of retrotransposon: in this case, the virus cannot dock to host cell in this feedback loop. In trash DNA, there are a lot of repeated patterns of retrotransposon inactive part. They can involve eigenvalues of feedback loop of docking system to control immunosysstem for the defense of virus particle in host cell. This retrotransposon state cannot be reset with DNA methylation from mother and father cell. Since the active part is in reversed direction of ghost field in genetic code, they will increase size more and more from father to son and to descendants of all living organisms induced from the feedback loop of docking system in evolutional field.

**VII. RESULTS OF DATA ANALYSIS**

We use genotype of viral capsid proteins V1, V2, V3 and genotype of their host cell receptor protein genotype. The first download sample is a time series of genetic code of unknotted V1, V2, V3 genotypes in 2 species of Rhinovirus, the so called Echovirus and Coxsackievirus. Second analysis involves their receptor protein, IgCAM in host cell genotype. We want to detect the characteristic of geneon wave function as a Holo-Hilbert spectrum $\xi$ from the trend of super-regression of $(ITD - IMF)_{\text{chain}}(1, n)$ with 3 layers of frequency mode modulation, $FM1, FM2, FM3$, from super-regression of Chern-Simons current in genotype of unknots and links in proteins. We use Rhinovirus and, specifically, perform the data analysis with 2 species, Poliovirus and Escovirus, with 8 samples of different genotype which contain very high genetic variation and Coxsackievirus. We compare the amount of nucleotides in 8 samples from Coxsackievirus and Echovirus nucleocapsid structural glycoprotein V1, V2, V3. They are download from genBank with different lengths of genetic code in their genotypes. The length of sequence is very short compared with genotype in human gene. The capsid protein V4 comes from IA gene and is inside the viral surface protein, therefore we do not perform an empirical analysis for this case in this work. The capsid protein V2 comes from IB gene. The capsid protein V3 comes from IC gene. The capsid protein V1 comes from ID gene. To demonstrate the efficiency of this tool, we perform data analysis with $(IMF - ITD)_{\text{chain}}(1, n)$ of Chern-Simons current in genotype of viral capsid protein genotype with predefined value of one pixel to generate the image for pattern matching and to classify the species of organisms. We use values from Table II to compute the Chern-Simons current for 20 amino-acids, computed from the algorithm of Jones polynomials derived from the Witten invariant tensor correlation between gene tensor network of Chern-Simons current in genotype of viral capsid protein and host receptor protein. The goal is the visualization of pattern recognition. We use a pixel representation of Chern-Simons current in genotype for every amino-acid (see Table II for detail) adopting a spinor network model. For genotype, we use the RGB image of Chern-Simons current for each node of amino-acid. The capsid proteins of icosahedral virus in interaction with host receptor proteins are only V1, V2. The time series of genetic code of V2, V3, V1 are induced from gene 1B, 1C, 1D respectively. The result of computation of $(ITD - IMF)_{\text{chain}}(1)$ and trend of V1 is shown in Fig. 7. In the plot, we notice that time series of $(ITD - IMF)_{\text{chain}}(1)$ of gene of V1 in Coxsackievirus...
FIG. 7: On the left, we plot the time series of $\text{(ITD} - \text{IMF)}_{\text{chain}(1)}$ of gene of $V_P1$ in Coxsackievirus with 8 samples. On the right, we plot the time series of $\text{(ITD} - \text{IMF)}_{\text{chain}(8)}$ of gene of $V_P1$ in Coxsackievirus with 8 samples.

FIG. 8: On the left, we plot the time series of $\text{(ITD} - \text{IMF)}_{\text{chain}(1)}$ of gene of $V_P2$ in Coxsackievirus with 8 samples. On the right, we plot the time series of $\text{(ITD} - \text{IMF)}_{\text{chain}(1, 4)}, \text{(ITD} - \text{IMF)}_{\text{chain}(1, 5)}$ of gene of $V_P2$ in Echovirus with 8 samples, successively.

with 8 samples does not change so much compared to results in $V_P2$ and $V_P3$. The trend of super-regression of $V_P1$ is almost similar with straight line with upper slope where we can estimate the parameter of regression. The last sample is only with parabolic shape. The result of computation of $\text{(ITD} - \text{IMF)}_{\text{chain}(1)}$ and trend of $V_P2$ is shown in Fig. 8. From this result, we find that 8 sample time series of Chern-Simons current with $\text{(ITD} - \text{IMF)}_{\text{chain}(1)}$ of gene of $V_P2$ in Coxsackievirus shows more genetic variations. The $V_P2$ is on docking site to host receptor with high evolutionary field more than $V_P1$ site. The result of computation of $\text{(ITD} - \text{IMF)}_{\text{chain}(1)}$ and trend of $V_P1$ is shown in Fig. 9. From the results, we sum up trend from 8 samples into the geneon wave function with transition state. The result of geneon wave function is shown in Fig. 10.

Based on these results, we generate an image for species classification of Echovirus and Coxsackievirus with tensor network algorithm. The result of image of geneon is shown in Fig. 11. We visualized the tensor network and calculate the closeness centrality for $V_P1, V_P2, V_P3$ in Echovirus. The only result of $V_P2$ in Coxsackievirus is shown in fig. 12. The highest peak of closeness centrality is the site of genetic variation in genotype from this analysis. In order to measure the connection $A_{ij}$ in genotype of $V_P1, V_P2, V_P3$ of Coxsackievirus, we used the Ising algorithm over the image of tensor network produced from geneon state of Coxsackievirus. The detail of algorithm can be found in 30. The result of Ising algorithm over image of geneon in Coxsackievirus is shown in Fig. 14 and Fig. 15.

The image of $FM2, FM3$ in geneon image of $V_P1, V_P2$ is shown in Fig. 16. The Holo-Hilbert spectrum 30 of quantum biology is represented as a spectrum of geneon wave function with different frequency mode modulations. It will be interpreted as hidden transition states of genotype induced from evolution feedback path in protein docking.
FIG. 9: On the left, we plot time series of gene of \((ITD-IMf)chain(1)\) of VP3 in Echovirus by using the average value of Chern-Simons current in genotype. On the right, we plot \((ITD-IMF)chain(6)\) of VP3 with different sizes of genome.

FIG. 10: In the first row on the left, we plot a wave function of geneon in genotype of VP1 in Coxackievirus from the linear combination of 8 species adopting the \((ITD-IMF)chain(1,n)\). In the first row on the right, we plot a wave function of geneon in genotype of VP1 in Echovirus from the linear combination of 8 species adopting the \((ITD-IMF)chain(1,n)\). In the second row, we plot a wave function of geneon in genotype of VP1 in Coxackievirus from linear combination of 8 species adopting the \((ITD-IMF)chain(1,n)\). In the second row on the right, we plot, in red, the wave function of geneon in genotype of VP1 in Echovirus from linear combination of 8 species adopting the \((ITD-IMF)chain(1,n)\) VP2 from 8 samples of Echovirus. The blue line is the geneon of VP2 in Coxackievirus.
FIG. 11: The picture represents the image of geneon in genotype of VP1, VP2, VP3 from 8 samples of Echovirus with tensor correlation network. The picture on the left side is an artificial image for pattern matching generated from tensor correlation network between different layers of \((ITD - IMF)chain(1, n)\) of VP1 between genetic variation among 8 species of Echovirus. The detail of mapping values of one pixel between measurement of Chern-Simons current and artificial pixel value is shown in Table III. The picture in the middle is an artificial image for pattern matching generated from tensor correlation network between different layers of \((ITD - IMF)chain(1, n)\) of VP2 between genetic variation among 8 species of Echovirus. The result of tensor network of VP1 and VP2 are shown in Fig. 12. The result of visualization of VP3 tensor network is shown in Fig. 13. The picture on the right side is an artificial image for pattern matching generated from tensor correlation network between different layers of \((ITD - IMF)chain(1, n)\) of VP3 between genetic variation among 8 species of Echovirus. The dot pattern in image shows tensor correlation between different layers of correlation of different modes in empirical decomposition algorithm. The pattern of dots is fixed for a given species. We can choose the background color for representing the image by adding a constant value to every pixel for increasing the contrast of the image quality. The yellow background comes from adding each pixels with 20. On the right picture, we make a different background for presenting the image with adding each pixels with 40. The resulting value of the background image is the blue color.

FIG. 12: On the left, we visualize the gene tensor network of VP1 in Echovirus with the centrality calculation over genetic variation among 8 samples of species in Echovirus. The maximum peak of centrality measurement shows the side of protein folding for highest genetic variation. On the right, we visualize the gene tensor network of VP2 in Echovirus plotting the centrality.

system. The results can be used to detect hidden patterns inside the protein folding.

For the protein docking behavior, we compare results of VP1, VP2, VP3 with their host protein receptor genotype in antibody of Ig-CAM. The results of data analysis of Chern-Simons current with \((ITD - IMF)chain(1)\) and \((ITD - IMF)chain(8)\) are shown in Fig. 17. The image of tensor network analysis of Ig-CAM with different layer in network of networks is shown in Fig. 18.

VIII. DISCUSSION AND CONCLUSIONS

A configuration space of organism can be represented as the analogue of atomic configurations with valence shell of cycle circle coordinates which constitute the principal fiber bundle of a free electron circulating in free energy level of a global macromolecule of protein enzyme. Due to the metabolism of cell, it rotates with spinor field in ribbon graph of spinor network. The nucleus of cell is analogue with the atomic nucleus with the total number of proton and neutron
FIG. 13: We visualize the gene tensor network of VP3 in Echovirus with the centrality calculation over genetic variation among 8 samples of species in Echovirus. We notice from the plot that the maximum peak of centrality measurement appears in the first area and a small peak at nucleotide number 8-9 of full neocotides sequence. These 2 peaks show the area of highest genetic variation in protein folding structure in VP3.

FIG. 14: The image represents network of networks between next 1-20 layers of Ising algorithm calculation of tensor network of correlation between geneon of VP1 on the left, VP2 in the middle, VP3 on the right from 8 samples of Coxsackievirus.

FIG. 15: The image represents network of networks between next 21-40 layers of Ising algorithm calculation of tensor network of correlation between geneon of VP1 on the left, VP2 in the middle, VP3 on the right from 8 samples of Coxsackievirus.

as the number of chromosomes in genetic code with a first prototype of knot and vortex structure. Historically, it
FIG. 16: The first image from the left side represents the FM2 of geneon of VP1 derived by the Ising algorithm. The second image from the left side is FM3 of VP1. The third image represents FM2 of geneon of VP2. The last image is FM3 of VP2.

FIG. 17: Here, we plot the gene of Ig–CAM-like protein receptor of antibody with 10 samples with spinor field in time series data. On the left, we plot only the first 20 amino-acid sequence. The graph shows highly genetic variation compared to the genetic variation in viral glycoprotein gene.

could be compared with the atomic model first introduced by Kelvin, Thomson and finally Rutherford. We know that this model fails in explaining the atomic structure. Despite this failure, we can still recover the old theory and redefine the wave function of simple cell organism introducing new concepts based on quantum mechanic of "atomic" knotted proteins in cell. Here "atomic" means that we cannot divide the constituents of an organism more than these
FIG. 18: The images represent network of networks between the first 25 layers of tensor network of correlation between geneon of all genes taken from IgACAM − 1, human virus receptor protein gene in antibody for VP1, VP2, VP3 viral capsid glycoproteins. From the result, the image shows the high variation without pattern compared with image of viral capsid protein.

configurations. Roughly speaking, we can separate the superspace of atomic organism in 2 parts. The first part is the nucleus and the second part is the cytoplasm. The orbital is the configuration of valence of organelle that, as the electron, circulates around nucleus in loop space of cell system according to theory of vortex and knot of Kelvin. The difference between cell and atom is that the nucleus is connected with cytoplasm by using the knotted behavior of first atomic prototype introduced by Kelvin and Thomson. The nucleus is in contact to electron orbital by electrostatic force instead of genetic code. For this construction, the genetic code is an artificial movement of current, i.e. the Chern-Simons super-current of life energy flow along coordinate of cell cycle in fiber space [38].

In this paper, we proposed a superspace model of knots and links for time series data of proteins taking into account the feedback loop from docking to undocking states of protein-protein interactions. In particular, the direction of interactions between the hidden states is considered. A $E_8 \times E_8$ unified spin model emerges where the genotype, from active and inactive parts of DNA time data series, is considered. The approach comes from the loop-quantum gravity and quantum field theory and it is adapted to biology. In this sense, we can deal with a quantum field biology. We derive the equations for the gene expression which describe transitions from ground to excited states, and for the 8 coupling states between geneon and anti-geneon transposon and retrotransposon in trash DNA. The construction is essentially based on the modifications, in view of biological applications, of the Grothendieck and Khovanov cohomologies. The final result is a Chern-Simons current in $(8 + 3)$ extradimensions on a given unoriented supermanifold generated by the ghost and anti-ghost fields of protein structures. The 8 dimensions are related to the 8 hidden states of spinor field of genetic code while the extradimensions derive from the 3 types of principle fiber bundle in the secondary protein.

Specifically, we solve a central dogma paradox by using this new modified Grothendieck cohomology to explain why undocking states of proteins induce docking mechanism. The core of this mechanism is related to a new definition of
parallel transport as a connection acting in the quantum gauge group of genotype in genetic code as the representation of gene expression. Implicitly, an equation of gene expression is defined over the coupling state between the gene and anti-geneon. In this picture, an induced analogue gravitational field can be defined related to the curvature of docking.

From the modified Khovanov cohomology, used for the construction of time series of knotted protein folding, it is possible to define knots and links in protein secondary structure. Furthermore, by using the Grothendieck topology in co-adjoint functor between 3 categories of 3 types of biological objects, i.e. DNA, RNA and proteins and with Chern-Simons current, one can plot all gene in active area and in trash area. From a geometrical point of view, one can give a new definition of the superspace of living organism by a unoriented supermanifold generated by the sheaf cohomology. In the framework of this theory, the central dogma is an adjoint functor over the group action which gives a representation of the alphabet code with left and right symmetry.

Based on the fact that the protein docking is a non-equilibrium state, we use the transition state in hidden directions of gene expression in loop-quantum gravity for biology over a modified Seiberg-Witten equation. The transposon induces a loop space in time series data in which unoriented states of knots and twistors appear from the operation of insert and delete a gene. The retrotransposon is an example of genotype in viral capsid protein VP1, VP2, VP3. We give a simple model of moduli state space for the transition of all states and hidden states of geneon, anti-geneon to transposon and retrotransposon. This allows us to construct the wave function of all gene component in trash and in active part of DNA by using differential 2 forms and modified Dirac operators. In particular, we use the Khovanov cohomology to define the time series of knots and links in proteins and we give a new definition for connection on principle bundle of secondary protein by using the Grothendieck topology and modified Atiyah axioms. This construction says us how living organisms can adapt their behavior, in central dogma model, under life energy of ghost and anti-ghost fields as a central unit of sheaf cohomology defined in Grothendieck topology. The Chern-Simons current for active gene and trash DNA can be explained by the retrotransposon state of the gene. The image of tensor network in geneon image of VP1, VP2, VP3 can be explained as the Holo-Hilbert spectrum of quantum biology wave function. It can be interpreted as hidden transition states in genotype induced from evolution feedback path in protein docking system. The results of this approach explain the evolitional band gap between \(IMF−ITD chain(8)\) in 2 parabolic shape merging into the hyperbolic structure of the cell manifold. The spinor field in time series of knotted protein is induced by the Hopf fibration over the loop space of transposon and retrotransposon transition in inactive states over trash DNA.

The information can take off only when we give a definition of the Seiberg-Witten equation for biology by a Dirac operator with Chern-Simons current over cohomology sequence of living organism. We use model of hyperbolic knots of parasitism state in viral replication cycle to solve this new equation which results a hyperbolic equation of transition states in trash DNA. The gene state of central dogma can be induced without transitive layer of protein as principle fiber bundle \(P_{A_{ij}}\). The underlying connection (a gauge potential of genotype) appears as a Yang-Mills field \(F_{\mu\nu}\). We have cycle and co-cycle \(\beta\) of superspace of living organism \(X_t\) defining a Jacobian over the supermanifold fiber \(g_{ij} = \frac{\partial A_j}{\partial A_i}\). The source of gravitational field \(\frac{\partial g_{ij}}{\partial s}\), the Chern-Simons current in codon, is induced from the connection over the parallel transport of co-cycle \(g^{ij}\) and cycle \(g_{ij}\) in analogy with the definition of connection \(F^k_{ij} := [A_k] \) in General Relativity. Furthermore, we define 3 forms over alphabet code by Chern-Simons 3 form over alphabet of gauge field in genetic code. They represent the protein layers as triplet states which induce further 32 states from differential 3 forms with Seiberg-Witten invariant.

Finally, we demonstrated the above construction by simple examples of VP1, VP2 and VP3 genes in 2 species of icosahedral virus with their host receptor gene, Ig – CAM antibody. We used the new algorithm of frequency mode modulation in Holo-Hilbert spectral algorithm over a new adaptive method of data analysis to find a spectrum of transition states in genotype of capsid protein of 2 viruses. The knotted protein time series of curvature in genotype of secondary protein docking state is parameterized by \(k = dt^*\) the order number of amino-acid in form of time series data.

In future works, detailed applications of the present model will be developed considering other examples of genes.

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