บทความวิจัย

สมการกรอบเคลื่อนที่ของเฟรชเนท์-เซอเรอท์ บนระนาบของระบบพิกัด ดี อาร์ พี ของการบิดตัวบนเส้นโค้งของโครงสร้างโปรตีน

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รับบทความ: 18 พฤษภาคม 2564 แก้ไขบทความ: 12 มิถุนายน 2564 ยอมรับตีพิมพ์: 12 มิถุนายน 2564

บทคัดย่อ

เราได้นิยามกรอบเคลื่อนที่บนเส้นโค้งที่ลากไปบนหนึ่งมิติซึ่งเกิดจากการบิดตัวของกาลเวลาและระยะทางบนระนาบการโค้งงอของโครงสร้างทุติยภูมิของโปรตีน งานวิจัยนี้คือส่วนของการแก้ปมปัญหาด้วยการค้นพบทางทฤษฎีที่สามารถตอบคำถามได้ว่าทำไมรูปร่างสามมิติของโครงสร้างของโปรตีนจึงมีลักษณะเหมือนกับเส้นเชื่อกปลายเปิดที่มีค่าความโค้งซึ่งถูกนิยามในระบบพิกัดแบบระนาบดีอาร์พี เราได้เพิ่มคุณสมบัติพิเศษของสนามแรงโน้มถ่วงลงในในโฮโมไครัลของชีวโมเลกุลที่มีภาพสะท้อนในแกนสมมาตรและปราฏการณ์สนามพลังงานยังมิลล์ในรหัสพันธุกรรมเข้าไปในสูตรของกรอบเคลื่อนที่เพื่อเข้าไปนิยามค่าความโค้งงอในกรดอะมิโนซึ่งเกิดจากการตกแบบอิสระของควอนตัมจีโนไทป์ไปตามค่าความโค้งงอของรูปทรงโปรตีน สุดท้ายเราได้พิสูจน์การมีอยู่จริงของปริมาณดีอาร์พีในสูตรของเฟรชเนท์-เซอเรอท์

คำสำคัญ: การบิดตัวของโครงสร้างทุติยภูมิของโปรตีน; กรอบเคลื่อนที่; แรงลอนดอน; คอนเน็กชั่น;

อ้างอิงบทความนี้

กบิล กาญจมาภรณ์กุล, ธัญญดา รุ่งโรจน์มงคล และสุพจน์ หารหนองบัว. (2564). สมการกรอบเคลื่อนที่ของเฟรชเนท์-เซอเรอท์บนระนาบของระบบพิกัด ดี อาร์ พี ของการบิดตัวบนเส้นโค้งของโครงสร้างโปรตีน. **วารสารวิทยาศาสตร์และวิทยาศาสตร์ศึกษา**, 4(1), 38-50.

Research Article

Frenet-Serret Formulas for Moving Frame with (d,r,p)-Layer in Protein Folding

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Received <18 May 2021>; Revised <12 June 2021>; Accepted <12 June 2021>

Abstract

We provide a new definition of one-dimensional model of curve spacetime in a moving frame of protein folding. It is a clue for answers to the question of why proteins have open string shaped with curvature defined in (d,r,p)-layer of the coordinate system of biomolecules. By adding some extra properties of the gravitational field in homochiral of biomolecules with effect of mirror symmetry, and Yang-Mills behavior field in genetic code to the moving frame, the new definition of curvature in amino acids can be defined from the role of coupling behavior field in free falling of the quantum genotype along curved shape of protein folding. Finally, we provide the proof of the existence of (d,r,p)-layer in protein folding with Frenet-Serret formulas for moving frame.

Keywords: Protein folding, Moving Frame, London Force, Connection.

Cite this article:
Kanjamapornkul, K., Rungrotmongkol, T and Hannongbua, S. (2021). Frenet-Serret Formulas for Moving Frame with (d,r,p)-Layer in Protein Folding. **Journal of Science and Science Education**, 4(1), 38-50.

Introduction

Curve shape of protein folding is one of open questions for scientists to be explianed. In fact, it is a result of free falling of graviphoton like hidden particle along the four dimensional manifolds of living organism. One of the commonly found structures of the protein in the living organisms is an open string shape with curvature for functional purpose in the active site of the protein docking system (Ghalami-Choobar and Moghadam, 2018). There exist many open questions such as why most of the protein crystal structures have unique protein folding with open 2 ended points. Moreover, why all proteins in living organisms including viruses commonly found only 20 L-amino acids from among more than 150 amino acids in nature. The number 20 is commonly found amino acids in nature has a deep relationship with geodesic path properties and comes from the properties of the open reading frame, ORF in noncoding area of DNA and some viral RNAs (Cheng et *al*., 2018). It is a result of the evolutional geodesic path from all possibilities of curvature in protein folding in nature from all hidden interaction forces.

The interaction between three types of biomolecules occurs in DNA, while the cohesin flying ring (Merkenschlager and Odom, 2013) is modeled with the knot and link properties (Witten, 2011). In human DNA at the transition between 2 states of DNA in chromosome and transcription, the double strand of DNA molecule is moved inside the cohesin protein (Richterova et *al*., 2017) with DNA folding in unique structure between these 2 transitions (Peters et *al*., 2008). It is one of many phenomena of exchange 2 rings between protein and DNA flying ring. The DNA folding is a projection of a flying ring in biomolecules that appears as Khovanov cohomology (Witten, 2012) in biological time series (Pincak *et al*., 2020). These properties are based on the fact that there exist homochiral molecules in L-amino acids and D-ribose saccharides in RNA and DNA. The length of DNA is very long in order to minimize the internal free energy and transfer the excess momentum as a wave function. At the end of DNA molecules, there exist telomerase enzymes in the area of coupling to each other in form of 3 open strings of supermolecules DNA, RNA, and protein as rotating of a flying ring (Pincak *et al*., 2020). It is a wave function of those three supermolecular orbital in quantum transition states. To be at the state with the lowest the energy, the DNA molecule will release the internal hidden energy by a reduction of the excess momentum in form of DNA-RNA folding in circular DNA and RNA (Soslau, 2018). The assumption is based on the fact from the new theory of quantum biology to replace the original continuous flow of central dogma from $DNA \rightarrow RNA \rightarrow PROTEIN$. What is the smallest subunit used for representing the living organism? The unification between supergravities in hydrogen bonding and London force between $[A]-[T]$ and $[C]-[G]$ along the evolutional path of differential 3 form can be investigated by modified Chern-Simons theory to quantum biology with adding extradimension of Yang-Mills fields in protein docking system. It is the new way for unification between the triplet states of DNA-RNA and protein in supersymmetry effect over 3 alphabet code in codon and anti-codon.

For longtime, many scientists have attempted to understand information encrypt inside in 64 codons (Shinde et *al*., 2018) and real function affected to the cohesin loop exclusion of DNA folding (Borrie et al., 2017). In fact, it is a source of hidden behavior transition state $d^* \in D^*$ in the circular rotational biological clock in d^* state of DNA coupling with their mirror symmetry of circular ring of London force in passive protein state, p^*. There exist 3 coupling behavior fields as basic instinct behavior, ω^-, between junk DNA state, d^* and immaturing behavior field, im^- in noncoding RNA state r^*(Saldana et *al*., 2019) with the role of supersymmetry in the loop space of sequences $CCCTC$ repeats in CTCF with 5 alphabets in junk DNA, d^*. The role of circular ring of cohesin passive protein, p^* (Merkenschlager et *al*., 2016) is an induced behavior field in genetic code by using 6 types of all possible London forces between biomolecules (d, r, p) and their supersymmetry states (d^*, r^*, p^*). It is analogy with gauge group interaction as a source of supergravity in genetic with vanishing behavior gauge field in genetic code along the Wilson loop of parallel transportof gene expression $p^* \rightarrow d^* \rightarrow d \rightarrow r \rightarrow p$ along the exact sequence of cohomology group in principle bundle of cohesin loop exclusion (Nora et *al*., 2020). This process is an example of reversing the flow of genetic code

in central dogma as a hidden dual state, $p^* \to r^* \to d^*$, in supersymmetry theory for biology. Self-diffeomorphism in human telomere is involved with configuration space in a Lagrangian system and the least action principle in the path integral of quantum biology. We can apply the simple model of the geodesic equation to the new theory of quantum biology as a source of observation associated with the Hamiltonian operator in quantum biology. It is a source of the pair of alleles in genetic code over the genotype. On the otherhand, it is important to investigate why the adaptive behavior of immunosystem (Byun et *al*., 2018) is involved with the hidden feedback control mechanism in evolutional feedback loop (Wood and Komarova, 2018) on the trash DNA-like status. As a result of reversed transcription of DNA state, $d^* \in \mathcal{O}_{D^*}$, the extrusion loop of kinesin gives each round only 5 based transcription factor in CTCF (Merkenschlager and Nora, 2016). This number be related to the number of 6 superspaces in root of Lennard Jone potentials. The protein folding is the result of the coupling wave function of these three strings with increasing von Neumann entropy as a result of changing the curvature of the protein docking system. It is measured empirically with a newly quantitative method of the plot the genetic code with Chern-Simons current (Capozziello et *al*., 2018). In this method, the curvature of protein folding is defined as a spacetime curve in the Minkowski cone of the physiology of amino acids with (3+1)D but these dimensions are disjoint to each other, so the line in protein folding does not intersect to each other with a knot and link model (Pincak et *al*., 2020).

This paper is organized as follows. In section 1, the definition and theory of Lagrangian system of $L(d, r, p)$ in quantum biology, we explain and provide a precised definition for the source of curvature in evolutional path in the geodesic equation. In section 2, the result of the construction of the equation to explain the curvature in protein folding with Frechnet-Serret formulas is presented. We also discuss the results. In section 3, we give the conclusion to the work and discuss further studies.

Methodology

$(\boldsymbol{d}, \boldsymbol{r}, \boldsymbol{p})$-Layer in Lagrangian system of DNA, RNA and protein

The application of the model of the link of the string with gauge group operation $SO(3,1)$ in (3+1)D is an extra dimension $\mathbf{t}$ in the spacetime of evolutional feedback path. This structure allows the supersymmetry breaking of the orientation of supermanifold (Witten, 2016) into non-orientation with Hopf fibration for entanglement state of superposition of RNA state and DNA state (Einstein et *al*., 1935) similar to a wormhole in biology (Weyl, 1921). Let $dS^2 : T_pX \to \mathbb{R}_1^4$ be an evolutional path of natural selection with spinor field as the ground state, $\mathbb{H} = \mathbb{R}_1^4$. The genetic code with basis of 4 alphabet codes can span by basis $([A], [T], [C], [G]) = (x, y, z, t) \in \mathbb{R}_1^4 = S^3$ with metric g_{ij} as a cocycle of quantum genotype to transform the alphabet code from $x_i = \sigma_i = ([A], [T], [C], [G])(t_0)$ to $x_j := \sigma_j = ([A], [T], [C], [G])(t_n)$. In this case, the process of gene expression starts from spinor field state σ_i in tangent of supermanifold of living cell, where RNA layer is defined with left translation in $SO(3,1)^+$ and stopped at x_j. It is a source of quantization or transition state in genetic code as cocycle g_{ij} of gauge group action as a left translation with Lorentz invariance. In differential geometry, these Lolentz metric $g_{ij} = -1$ appears as a Minkowski cone of the physiology of the chemical structure of the dihedral angle in the polypeptide chain for hyperbolic geometry (Ohtsuki, 2017).

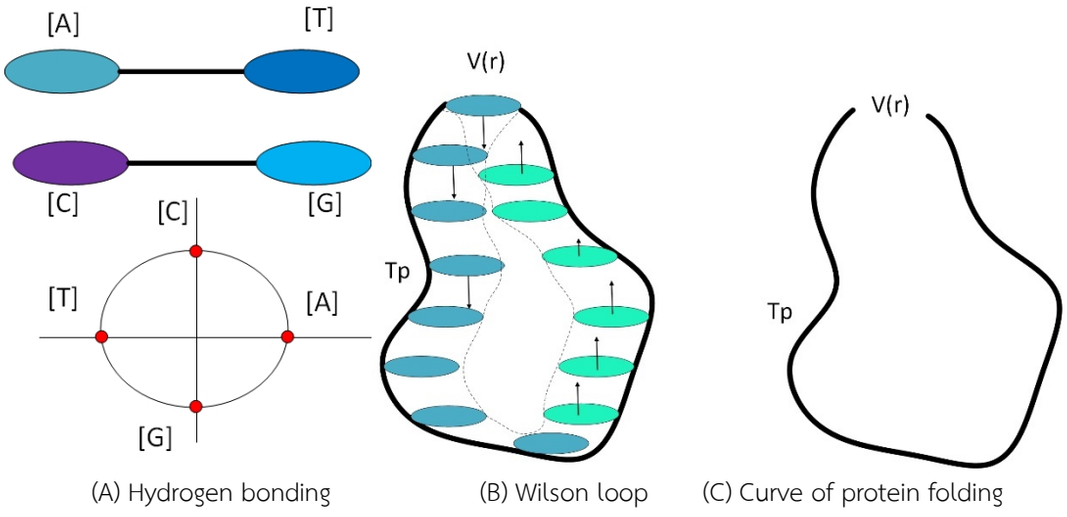

Figure 1. (A) The hydrogen bonding between nitrogen bases in DNA molecules. (B) Localized Wilson loop of behavior field $A(r) = V(r)^{ext}$ along the curve of protein folding. (C) Open string shape of protein folding.

Recently, the new gravitational theory was applied to supersymmetric properties between retrotransposon (Shen et *al*., 2018) and methyl transfer (Cheng et *al*., 2018) in junk DNA and noncoding RNA (Saad, 2018) for better understanding on information in alphabet their noncoding alphabet code (Devi et *al*., 2018). Methylation is an epigenetic modification catalyzed by DNA methyltransferase enzymes for encoding tRNA prior to translation in all living organisms. These enzymes use S-adenosylmethionine as a methyl donor to transfer protons through junk DNA. It is a DNA folding phenomenon in the area of epigenetic in heterochromatin inside the human chromosome. Genetic code on DNA is not the only information that determines how life forms life but also have their old curvature DNA-DNA docking system. If we consider the curvature in genetic code as a connection over the sheave in Groethendieck cohomology. It is a source of Chern-Simons current in biology induced from the coupling of behavior Yang-Mills co-fields $(\mathcal{O}_{[A_\mu]}, \mathcal{O}_{[A^\mu]})$. It is a vierbein element in genetic code for adaptation (Peck and Waxman, 2018). Scientists now consider junk DNA as their unknown function in octamer with an observation system of DNA methylation. It is a source of switching of the gene on when and where the genes work. Information beyond these genetic codes in junk DNA makes each organism in the different environment, differentiated, and expressed. Even twins with genetic code on DNA in all respects, there is no way to be the same in every inch. Biologists characterize the variation caused by genetic factors that epigenetics in DNA folding. One of the most important biochemical processes in epigenetics in junk DNA is DNA methylation, which refers to the process of adding the methyl group to the bases on the DNA strand. Most of which are added to the cytosine base. It makes the proteins involved in tRNA decoding in 3 alphabets in codon in RNA evolutional path (Rezazadegan et *al*., 2018).

The genetic code is independent of coordinate in superspace (Capozziello et *al*., 2017) of DNA, RNA, and protein. There exists a hidden evolutional path in the extra dimension. In this work, we called the curve of protein folding with the geodesic path of information kept in an inertial frame of curvature of protein-protein interaction. The genetic code can be defined by connection over the physiology of the spinor field (Kanjamapornkul *et al*., 2017) hidden 8 states in Grothendieck cohomology theory for biology (Pincak et *al*., 2019). In differential geometry, a source of the geodesic path is a curvature of space with the connection. The connection is a Jacobian flow and analogous with free-falling along with the gravitation in the D-brane theory, in which the source of protein folding is a gravitational effect of supergravity force in massive anti-photon in the D-brane of quantum genotype. The super gravity field is an Yang-Mills behavior field without source and becomes stronger fields in supermolecules with heavy molecular weight that analogy with London repulsive force, e.g. Lagrangian system of transitive interaction of supermolecules, *i.e.* DNA, RNA, and protein.

The one-dimensional curve representing for protein folding is the new model that derives from the free rotation of dihedral angle of amino acids with parallel transport along with the hidden gravitational fields, which means the field from inversed van Der Waals force field (Vedani, 1988). This is because the Casimir effect (Jaffe, 2005) that induced the relativistic effect of London repusive forces (Jones, 1924) in biology to become analogous with gravitational force in physics (Lei Zhang, 2013).

The least action S of co-living organism between virus and host cell is the new quantity in quantum biology. It keeps the information in genetic code in van Der Waals distances between biomolecules in living organisms and viruses. It is a relativistic biological supergravity force that allows the interaction to each other by changing the coordinates between these 3 biomolecules with the Lorentz metric as an inertial frame of reference. The change of frame of this least action is the source of the geodesic of quantum genotype, g_{ij}. It started the record of the adaptive information from the evolution from the ancient historical path in many million years to the present. The result of these least actions is to diversify the curvature in 20 amino acids. The amino acid sequence leads to a curvature of protein appear from the genetic code with hidden biological supergravity denoted as the connection of genetic code in form of supermolecular orbital of DNA, RNA, and protein folding as well as the interaction between them. The DNA molecule is very long because of the lowest of external potential energy from adaptation and keeps in hydrogen bonding as a bridge of $[A]-[T]$ and $[C]-[G]$ (Fig. 1) with biological qubit memory in quantum biological entanglement state (Kanjamapornkul and Pincak, 2016) of spin up, $[1]\in\mathbb{Z}/2$, and spin down, $[0]\in\mathbb{Z}/2$, states that can superposition to each other and change state by the process of DNA-RNA transcription and junk DNA folding in epigenetic with van Der Waals interaction to chromatin. The source of the Yang-Mills field in genetic code implies the existence of Schrödinger's cat with the superposition of living and death state (Einstein et *al*., 1935). Let the Lagrangian system of protein docking between the active protein p and the passive protein p^* is defined by $L(A_\mu)^{protein}=\frac{1}{2}g_{ij}p_ip_j^*=\frac{1}{2}g_{ij}(r)r_i{}'r_j{}'$. The external potential $V(r)^{ext}=0, r\neq r_i,r_j$. If r_i is a van Der Waals distance of amino acids p_i, and r_j is a van Der Waals distance of amino acids p_j, then there exists an external potential force field between the interaction of 2 proteins in docking system between positions at amino acid number i from the active protein and amino acid number j in the passive protein. It allows the chain sequence of Lagrangian system of loop space in path connected hydrogen bonding between $[A]-[T]$ and $[C]-[G]$ for r_i with r_j. In traditional biology, the genetic code of DNA, RNA, and protein are represented by the alphabet code but we use a homotopic path to connect the phase transition between them as deformation of supermolecular bonding between them as a curve in $SO(3,1)$ spacetime model. Therefore, this new approach allows the new usage of algebraic operation as a path integral over a summation of span alphabet code as a compact basis set in evolutional path with continuous phase parameter r of fiber space of viral RNA with the ground field of $\mathbb{R}_1^4$. The unification of 3 London force between DNA, RNA and protein comes from the Hopf fibration between 3 forces in hexagonal shape of the bridge between hydrogen bonding in $[A]-[T]$ and $[C]-[G]$. We can generalize this simplicial complex approach into the interaction between 3 types of supermolecule in hexagonal model of London force. The London force can unify into connection over S^3 by glueing 2 torus together in mirror supersymmetry (Fig. 2).

Definition 1 Let a DNA molecule be path of a pointed space of RNA molecule in a trajectory of evolutional path $\mathrm{S^d}$ along the time dimension of DNA is RNA molecule. The $\mathrm{t=r}$ is a state of RNA independent state. It is an independent variable in chain of central dogma, $\mathrm{r\rightarrow p\rightarrow d}$, with only one protein dependent variable $\mathrm{p_i(r)}$ state per one nitrogen base represented in DNA supermolecule as a location for protein $\mathrm{p_i}$. Let $\mathrm{p_i=V_i^{-1}(V_j^d(p_i)), p_j=V_j^{-1}(V_i^d(p_j)), g_{ij}^d(p)=\frac{\partial p_i}{\partial p_j}}$ be the rate of change of hydrogen bonding between amino acids $\mathrm{d_i=p_i{}'}$ connecting with $\mathrm{d_j^*=p_j{}'}$. Let $\mathrm{g\in\mathcal{G}}$ be a gauge group of roots of inversed Lennard-Jones force field. It is defined by a cocycle of quantum genotype $\mathrm{g^d=g_{ij}^d(p)}$ with curvature $\mathrm{A_{London}^d(g^d)}$ in other hydrogen bonding $\mathrm{p_k}$ in extradimension of fiber bundle of protein molecule.

Definition 2 The state of RNA $\mathrm{r_i}$ is defined by hydrogen bonding in nitorgen base of DNA molecule $\mathrm{[A],[T],[C],and\ [G]}$. Let $\mathrm{d_i = V_i^{-1}\left(V_j^r(d_i)\right), and\ d_j = V_j^{-1}(V_i^r(d_j)), g_{ij}^r(d) = \frac{\partial d_i}{\partial d_j}}$ be the rates of change of hydrogen bonding between nitrogen bases $\mathrm{r_i = d_i{}'}$ connecting with $\mathrm{r_j^* = d_j{}'}$. Let $\mathrm{g^r \in \mathcal{G}}$ be a gauge group of roots of inversed Lennard-Jones force field. The London force of RNA-RNA interaction is defined by a cocycle of quantum genotype $\mathrm{g^r = g_{ij}(r)}$ with curvature $\mathrm{A_{London}^r(g^r)}$ in other hydrogen bonding $\mathrm{r_k}$ in extradimension of fiber bundle.

Definition 3 Let a protein molecule be a trajectory of pointed space in evolutional path $\mathrm{S^p}$ along the time dimension of DNA state in transcription process. The $\mathrm{t = d}$ state is of biological clock in protein with independent variables in chain of central dogma, $\mathrm{d \to r \to p}$, with only one state per one nitrogen base in RNA supermolecule $\mathrm{r_i}$. The state of RNA $\mathrm{r_i}$ is defined by hydrogen bonding in nitorgen base of RNA molecule $\mathrm{[A],[U],[C],and\ [G]}$ Let $\mathrm{r_i = V_i^{-1}(V_j^p(r_i)), r_j = V_j^{-1}(V_i^p(r_j)), and\ g_{ij}^p(r) = \frac{\partial r_i}{\partial r_j}}$ be the rates of change of hydrogen bonding between amino acids $\mathrm{p_i = r_i{}'}$ connecting with $\mathrm{p_j^* = r_j{}'}$. Let $\mathrm{g \in \mathcal{G}}$ be a gauge group of roots of inversed Lennard-Jones force field. It is defined by a cocycle of quantum genotype $\mathrm{g = g_{ij}(r)}$ with curvature $\mathrm{A_{London}^p(g^p)}$ in other hydrogen bonding $\mathrm{r_k}$ in extradimension of fiber bundle.

The Jacobian flow of group action $\mathcal{G} \times F \to F, (g, r_i) \mapsto r_j$ on fiber bundle is the permutation of cocycle act on these tangent space of distance of hydrogen bonding as an effect of protein folding. The distance of hydrogen bonding, $S = \frac{\epsilon}{i} ln\Psi$ is a twistor on arc length of circle appear as flying rings to exchange the energy and momentum between 3 supermolecules in quantum biology. The least action is the evolutional path between the Lagrangian systems of internal energy of superposition between live and death states in three cyclic coordinates of anti-self dual form in 3 superstring states of unification of 3 forces in DNA RNA and protein. Let $L_{DNA}^{Type-I}, L_{RNA}^{Type-II}, L_{PROTEIN}^{Type-III}: TX \to R, TX = \coprod_{i=}^{n} F_i$ where X is a manifold of living organism.

Definition 4 Let $\mathrm{S^d}$ be the least action in the biological system. It is a dynamical system of supermolecular DNA, RNA, and protein folding that can allow the van Der Waals force and hydrogen bonding in these three types of supermolecules to interact with each other. It is a weak interaction of intermolecular orbitals appeared as the maximum principle of the Hamilton-Jacobi equation for control gene expression by minimizing the free energyalong the exact sequence $\mathrm{r \to p \to d}$ in the Lagrangian system of DNA folding,

$$S^d = \int_{r=r_0}^{r=r_n} L_{DNA}^{Type-I}(r, p(r), d(r))dr. \quad (1)$$

Definition 5 Let $\mathrm{S^r}$ be the evolutional path in the biological system. It is a dynamical system of supermolecular DNA, RNA, and protein folding that can allow the van Der Waals force and hydrogen bonding in these three types of supermolecules to interact with each other. It is a weak interaction of intermolecular orbitals appeared as the maximum principle of the Hamilton-Jacobi equation for control gene expression by minimizing the free energy along the exact sequence $\mathrm{p \to d \to r}$ in the Lagrangian system of RNA folding state parametrized by protein state,

$$S^r = \int_{p=p_0}^{p=p_n} L_{RNA}^{Type-II}(p, d(p), r(p))dp. \quad (2)$$

Definition 6 Let $\mathrm{S^p}$ be the least action in the biological system. It is a dynamical system of supermolecular DNA, RNA, and protein folding that can allow the van Der Waals force and hydrogen bonding in these three types of supermolecules to interact with each other. It is a weak interaction of intermolecular orbitals appeared as the maximum principle of the Hamilton-Jacobi equation for control gene expression by minimizing the free energy along the exact sequence $\mathrm{d \to r \to p}$ in the Lagrangian system of protein docking,

$$S^p = \int_{d=d_0}^{d=d_n} L_{PROTEIN}^{Type-III}(d, r(d), p(d))dd. \quad (3)$$

Definition 7 In system of protein docking, the Lagrangian is $\mathrm{L_{Protein}^{type-III}(d, r, p)}$ with evolutional path S. The biological clock is parametrized along the DNA molecules with hidden state d. The virus RNA state r is the change in the distance of the viral RNA lines from the past to the present, resulting from adaptation compared

to the change in the curvature of the viral protein with evolutional path S. We use symbols as derivatives relative to the variable p,

$$r = \frac{\partial S}{\partial p}. \tag{4}$$

Definition 8 Let $\mathrm{r}' = \frac{\mathrm{dr}}{\mathrm{dd}}$. Let $\mathrm{g_{ij}}$ be cocycle of quantum genotype protein folding. Let $\mathrm{L} = \frac{1}{2}\mathrm{g_{ij}} < \mathrm{r'_i}, \mathrm{r'_j} >$, $\mathrm{dS} = \mathrm{L(d, r(d), r'(d))dd}$ be least action in evolutional path in protein folding according to geodesic equation, where $\mathrm{g_{ij}}$ is hydrogen bonding between RNA molecules $\mathrm{r_i}$ and $\mathrm{r_j}$. The p state is defined by rate of change of evolutional path with respect to the rate of change of degree of disorder in hydrogen bonding of RNA $\mathrm{r}' = \frac{\mathrm{dr}}{\mathrm{dd}}$ with biological clock d,

$$p = \frac{\partial S}{\partial r'}. \tag{5}$$

The ratio of $\frac{S}{\epsilon_t} = \theta$ is an invariant properties so-called biological quantum principle number, because we can have a non-degenerate state with canonical quantum number $2\pi n$ with n round of rotation, $\Psi(d) = e^{2\pi n i\theta}$. The evolutional path S is the same quantity with von Neumann entropy in discorder degree of physiology of biomolecules. It was used to measure the disorder degree in DNA molecule with $n = 1,2,\cdots$ transitions,

$$0 \leq \theta = \frac{\mathrm{S}}{\epsilon_t} \leq 2n\pi. \tag{6}$$

It is implied that the evolutional path is positive entropy and increasing along with the rotational of the unit circle with periodic condition with period $2\pi n, n = 1,2,3,\cdots, 0 \leq S \leq 2\pi\epsilon_t n$. Therefore, the fluctuation of von Neumann entropy is the source of the quantum state. In one dimensional model of protein folding, we define $p(d) = \frac{dr}{dd}, \text{and } r(d) = \frac{dd}{d\alpha}$ for $\alpha(t) > 0$.

Let $\Gamma_{ij}^{\mu}(g) \in \Omega^1(\wedge TX \otimes \mathbf{R})$ be connection appeared as a quantum genotype in fiber bundle of tangent of manifold of amino acid sequence in protein folding. Let p_i be a protein state i at amino acid subunit i. We can interpret g_{ij}^{p} as cocycle of quantum genotype induced from van Der Waals-gravitational field between amino acids p_i connecting with p_j, because the the explicit form of force field of van Der Waals force and gravitational field are similar to each other.

Result and Discussion

The Proof of existence of (d,r,p)-Layer in Frenet-Serret Formulas

There exists a relationship from RNA state to transform their coordinate system into protein state by using the process of gene expression in codon with open reading frame, ORF. Mathematically, we write these relationship by using compact notation of equivalent relation $\sim$

$$d = r \sim p. \tag{7}$$

In general form, we introduce the tensor field for this equivalent relation by wedge product, $d = r \wedge p$. In vector field, the wedge product is a cross product of 2 vectors, tantent and normal vector, to the phase transition of hidden curve spacetime in (3+1)D protein folding,

$$\mathbf{d} = \mathbf{r} \times \mathbf{p}. \tag{8}$$

It means RNA, r transition to protein, p or p induced by r, or DNA is an coadjoint map from RNA state to protein state. We change from d to the pullback function of $\mathcal{O}_d \ni L(r,p) = r \wedge p$ state along coadjoint product of central dogma, $d \to r \to p$. It is an inner product with cocycle appeared as a source of genotype in pullback function $\mathcal{O}_d \ni L(r,p) = g_{ij} < r,p >, g_{ij} \in SO(3,1)$. The open reading frame (ORF) in central dogma over the exact sequence of manifold of living organism X can be shifted by (Lag) operator $L_g, L_g^3 = 1$ along $L_g: d \to r \to p \Longrightarrow r \to p \to d$, and $L_g^2 = L_g L_g$ shifts to $p \to d \to r$, with $L^{Type-II}(d(p), r(p))$ over the cyclic coordinate in (d,r,p)-layer. Let $x(t) \in C_0(X)$ be a pointed space. It is an approximation of fixed coordinate of hydrogen bond in biomolecule $[A], [T], [C]$ or $[G]$ to a point in generalized coordinate over deformed phase space(Fig. 2C). In exact sequence of vertical transcription, $d(t) = x'(t), r = x''(t), p =$

$x^{(3)}$ is in chain complex. In horizaontal coordinate of protein folding moving frame, we set intial condition $x(t_0) = x_0 = 0$ (Muangchoo-in et *al*., 2021), while the coordinate is not only (d, r, p)-layer but it can be generalized to n −derivative over $n-$ amino acids approximated by the recursive coordinate by moving frame with $x_n = x'_{n-1}(t), x_1 = x'(t), x_2 = x'_1 = x''(t), x_3 = x^{(3)}(t), \cdots, x_{\mathrm{n}} = x^{(\mathrm{n})}(t)$ (Fig. 2B). Let the chain sequence of biological cohomological sequence be

$$0 \to C_0(X) \xrightarrow{d} C_1(X) \xrightarrow{d} C_2(X) \xrightarrow{d} C_3(X) \to 0. \tag{9}$$

The tangent vector in three dimensional model in the above chain sequence is $\mathbf{r(t)} = \frac{dx_t}{dt}$, where $x_t = (cos\theta(t), sin\theta(t), t)$. Let the coordinate of genetic code in unit circle be

$$x_{[A]}(\mathrm{t}) = (cos0, sin0, t),\ x_{[C]}(\mathrm{t}) = \left(cos\frac{\pi}{2}, sin\frac{\pi}{2}, t\right), x_{[U]}(\mathrm{t}) = \left(cos\frac{2\pi}{2}, sin\frac{2\pi}{2}, t\right),$$

and $x_{[G]}(\mathrm{t}) = \left(cos\frac{3\pi}{2}, sin\frac{3\pi}{2}, t\right)$. In general form, we have

$$\mathbf{r}(t) = \frac{d}{dt}(cos\theta(t), sin\theta(t), t) = (-sin\theta(t), cos\theta(t), 1) = \left(-sin\frac{S}{\epsilon_t}(t), cos\frac{S}{\epsilon_t}(t), 1\right). \tag{10}$$

The normal vector is $\mathbf{p}(t)$ state with

$$\mathbf{p}(t) = \frac{d\mathbf{r}}{dt} = \left(-cos\frac{S}{\epsilon_t}(t), -sin\frac{S}{\epsilon_t}(t), 0\right), \mathbf{d}(t) = \mathbf{r}(t) \times \mathbf{p}(t). \tag{11}$$

In unit circle with constant evolutional constant in raduis of circle $\epsilon_t = 1$, the tangent vector will become normal vector when the evolutional path shifts with phase transition $\frac{S}{\epsilon_t}(t) = \frac{\pi}{2}$. Therefore, there exists a pair of genetic code by [A]-[T] and [C]-[G](Fig 2(A)).

In the the chain sequence of open reading frame, ORF in vertical transcription from DNA to RNA and to protein, the pullback map is induced by $d_t \in C_1(X), C_1(X) \to C_2(X) \to C_3(X) \to C_3(X)/C_2(X) = C_1(X)$. It is source of cyclic coordinate in a biological Frenet-Serret formulas for (d, r, p) moving frame of protein folding because $\mathbf{d} = \mathbf{r} \times \mathbf{p}$,

$$\frac{d\mathbf{d}(t)}{dt} = -\beta\mathbf{p}(t), \tag{12}$$

$$\frac{d\mathbf{r}(t)}{dt} = \kappa\mathbf{p}(t), \tag{13}$$

$$\frac{d\mathbf{p}(t)}{dt} = -\kappa\mathbf{r}(t) + \beta\mathbf{d}(t), \tag{14}$$

or in general form, one writes,

$$\begin{bmatrix} \frac{d\mathbf{d}(t)}{dt} \\ \frac{d\mathbf{r}(t)}{dt} \\ \frac{d\mathbf{p}(t)}{dt} \end{bmatrix} = \begin{bmatrix} 0 & \kappa & 0 \\ -\kappa & 0 & \beta \\ 0 & -\beta & 0 \end{bmatrix} \begin{bmatrix} \mathbf{d}(t) \\ \mathbf{r}(t) \\ \mathbf{p}(t) \end{bmatrix}, \tag{15}$$

where $\mathbf{d}$ is bivector of DNA state transition with inversed map of transition of protein induced by RNA. There exists a torsion vector in DNA state $\mathbf{d}' = -\beta\mathbf{p}(t)$. We called 2 types of quantum genotype β, κ. $\mathbf{r}$ is a tangent vector to the curve of 3D model of protein folding. $\mathbf{p}$ is a normal vector for induced curvature. Hence, there exists three types of the system, $L^{Type-III}(d, r(d), p(d)), L^{Type-II}(r, p(r), d(r)), L^{Type-I}(p, d(p), r(p))$. The covariant derivative represents the state of parallel transport for gene expression in genetic code along the geodesic path in central dogma, $d \to r \to p$, or $r'_i \to r'_j \to r'_k$(Fig. 3A),

$$\nabla_{r'_i} r'_j = \frac{\partial^2 r_k}{\partial t^2} + A^d_{London} < r_i', r_j' >, \tag{16}$$

where $\kappa(t) = \left|\frac{\partial^2 r_k}{\partial t^2}\right|$ is a curvature of protein folding.

In the system of protein docking between active protein state p and passive protein state p^*, there exists a quantum genotype defined by the curvature in protein folding $\frac{\partial^2 r_k}{\partial t^2} = F^{g^p} = -A^p_{London}$, if $< p, p^* > = 1$ (Fig. 3B and Fig. 3C). The protein docking system in equilibrium induces the parallel transport from p to p^*,

$$\nabla_p\, p^* = 0. \tag{17}$$

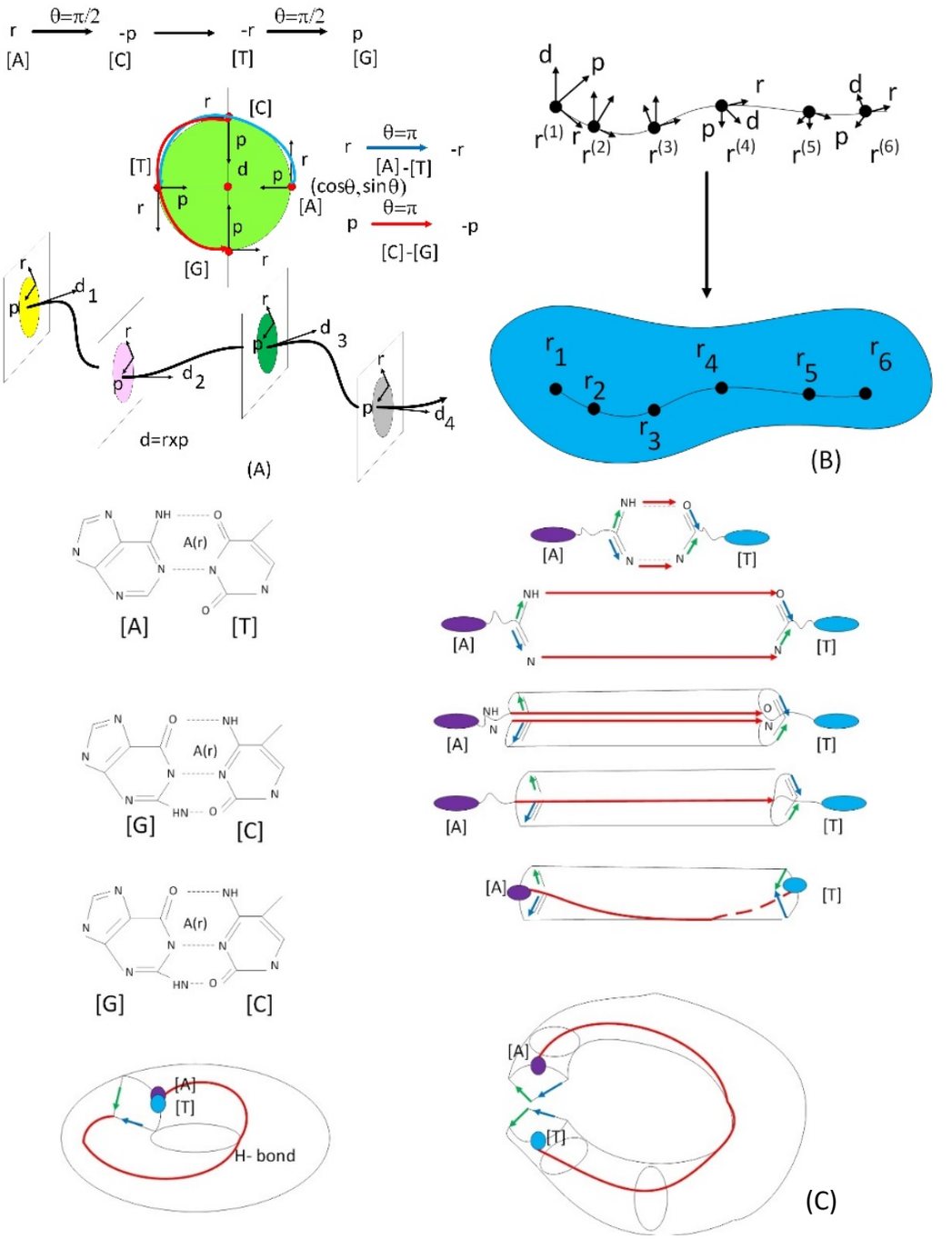

Figure 2. (A) The circle in the middle is the cross-section of (d,r,p)-Layer in moving frame with d state at the center and perpendicular r and p in the plane. The circumference is a topological invariance property with an evolutional constant as a radius. The evolutional path in curve-shaped protein folding is defined by a unit circle with tangent vector r and normal vector $\boldsymbol{p}$. The above panel shows the invariant properties of shift a tangent vector from [A] to [T], the tangent vector $\boldsymbol{r}$ is equal to mirror symmetry of $-\boldsymbol{r}$. If a normal vector moves from [C] to [G], then $\boldsymbol{p}$ is equal to mirror symmetry of $-\boldsymbol{p}$. (B) The demonstation of covering space of manifold of living organism spaned by protein with 6 amino acids. The moving frame in Hopf fibration of tangent of manifold with 6 fiber spaces of $(\boldsymbol{d},\boldsymbol{r},\boldsymbol{p})$-layer. (C) A pair of hydrogen bonding in DNA is defined by a point in the torus. It is a place where information is stored in the adaptive behavior field in the genetic code. The nitrogen base is topological equivalent to torus by using a topological invariant property. If we transform from hexagonal by gluing their cells complex, then the pair of the hydrogen bonds is contractable to a point in torus by using homotopic equivalent class.

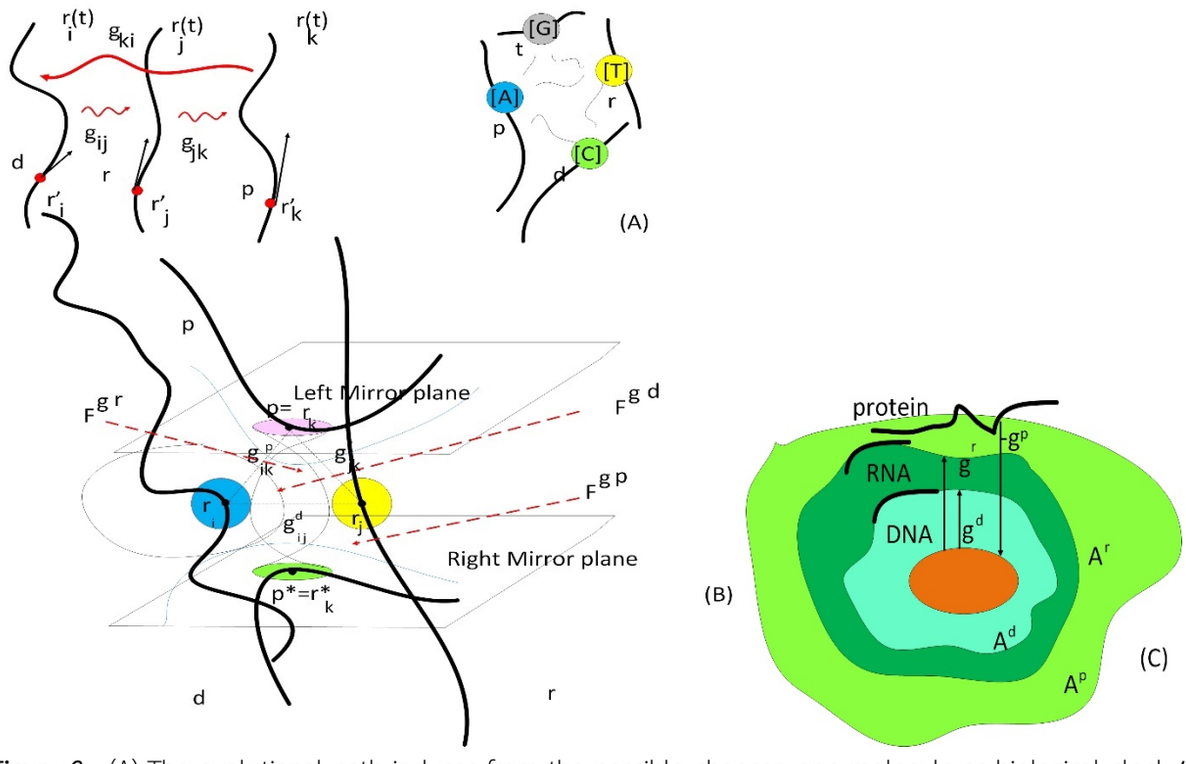

Figure 3. (A) The evolutional path induces from the possible choosen one molecule as biological clock t and the other molecules will be (d,r,p)-triplet state with van Der Waals-supergravity in transition between them. In this picture the nucleobases, $([C],[T],[A]) = (d,r,p)$ and $[G] = t$. Although, the choice of basis is cyclic coordinate and can choosed any based to be a time scale. (B) The transition between $d = r'_i$ to $r = r'_j$, and to $p = r'_k$. F^g is a van Der Waals-supergravity force in transition between them. It is specified by a Yang-Mills field to deformed the curved spacetime in loop space of supermolecular orbital. There exists a mirror symmetry between protein state p and their dual state of hidden parity protein state p^* in the mirror symmetry plane of the protein docking system. (C) The ground state is d state with induced Yang-Mills behavior field A^d. It is a DNA state in nucleus of host cell. While r and p are excited states with induced Yang-Mills behavior field A^r and A^p. When the transition is in protein state p, the cell system will try to reduce the excited steate energy by docking to other protein analogy with transition back to ground state.

Conclusion

In this theoretical investigation and new more precise definitions, there exist many potential applications to the studying of the genetic code of SARS-CoV-2 (Andersen *et al*., 2020) viral state by using moduli state space in RNA molecule to visualize the trajectory of pointed space in evolutional path S^r along the time dimension of their own RNA nonstructural protein, e.g. viral polymerase protein state in the replication process of the open reading frame ORF1ab. The p state of protein state in both virus and host cell are independent variables in the chain of the central dogma, $p \to d \to r$, with only one state per one nitrogen base in RNA supermolecule r_i. Let A_μ be behavior field in genetic code. It is a curvature in differential geometry with more extra properties of the gravitational field in genetic code. This field connects two amino acids into a curve of blend line of polypeptide sequence in (1+3) dimensional Minkowski cone of quantum biology with the application of plotting the genetic code into the graph of curvature. The new definition of DNA, RNA, and protein can adopt this idea as principles of anti-self dual, but the mathematical structures are the not same as Yang-Mills theory in physics, because biologists and physicists study different objects. Therefore, for the new definition of the structures of unification of DNA, RNA, and protein, we need to add some more properties of living things to this new structure in the form of extra properties in the extra dimensions of Chern-Simons theory models from (2+1)D in physics to (3+1)D in biology. The results are implied that DNA d, RNA, r, and

protein p states have their own anti-symmetry partner in hidden dimensions, we called (d^*, r^*, p^*) hidden anti-particle of biomolecules of (d, r, p) - layer of biomolecular chain complex in six hidden dimensions in the root of Lennard-Jones potential field of London force in a superfluid. From this new theory of quantum biology, there exists a fifth force in all living organisms and viruses in which analogy with dark matter in physics. It is a unification of those 6 states from 3 existed forces in their interaction, London forces, Yang-Mills force, and supergravity force in quantum biology as a new research area with strong application to the system of viral mutation detection with more precise mathematical definitions and equations for plot the genetic code. The Frechet-Serret moving frame has direct application in differential geometry of curvature in protein folding compared to experimental biology and biophysics of condensed matter theory.

Acknowledgements

K.K. thanks to Chulalongkorn University Graduate Scholarship to Commermorate the 72nd Anniversary of his majesty King Bhumibol Adulyadej. KK. TR and SH are grateful for computational resources supported by NSTDA Supercomputer Center (ThaiSC) for this work.

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