

Extensive Quantum Theory of DNA and Biological String

Yi-Fang Chang

ABSTRACT

Assume that quantum elements of DNA are A-T and G-C. According to basic thinking of *NeuroQuantology*, the extensive quantum theory of DNA is researched and corresponding quantum theory and its many mathematical methods are applied to DNA and molecular biology. From this we discuss symmetry and supersymmetry of DNA, and the quantum theory and equations of DNA, in particular, the $SU(2)$ gauge theory and some solutions of equation. Further, we propose the string theory of DNA and general biological string. Some solutions and functions of these theories may describe probably DNA, biological things and their motions. Finally, we propose quantitatively a universal entropy theory on evolution of any natural and social systems.

Key Words: biology, quantum theory, DNA, string, supersymmetry, entropy, evolution

DOI Number:10.14704/nq.2014.12.3.738

NeuroQuantology 2014; 3: 356-363

1. Introduction

DNA is an important basis of molecular biology (Micklos *et al.*, 2003). Fitchet *al.* (1983) discussed mapping the order of DNA restriction fragments. Waterman *et al.* (1986) discussed interval graphs and maps of DNA. Goldstein *et al.*, (1987) used stochastic relaxation to mapping DNA. Head (1987) analyzed the generative capacity of specific recombinant behaviors from formal language theory and DNA.

Peyrard and Bishop (1989) investigated the statistical mechanics of a simple nonlinear lattice model for the denaturation of the DNA double helix. This PB model consists of two chains connected by Morse potentials

representing the H bonds. Then Peyrard *et al.*, studied effective breather trapping mechanism for DNA transcription (Ting *et al.*, 1996), and generation of high-energy localized vibrational modes in nonlinear Klein-Gordon lattices (Bang *et al.*, 1996). Further, Peyrard (1998) proposed an experiment using micro-mechanical stretching of DNA to probe nonlinear energy localization in a lattice.

Brown *et al.* (1993) provided an introduction to the use of mathematical models in biology, the statistical techniques for fitting and testing them, and associated computing methods, which includes comparison of DNA sequences, neural networks, analysis of patterns in space and time, generalized linear models, nonlinear models and multiple regression.

Benham, *et al.* (2009) edited a book “*Mathematics of DNA Structure, Function and Interactions*”. It includes 16 chapters: mathematical methods in DNA topology, conformational statistics of DNA and diffusion equations on the Euclidean group, differences between positively and negatively supercoiled DNA that topoisomerases may distinguish, analysis of high-order DNA-protein assemblies

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Relevant conflicts of interest/financial disclosures: The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

Received: 24 February 2014; **Revised:** 14 April 2014;

Accepted: 2 May 2014



by difference topology, topological analysis of DNA-protein complexes, closing the loop on protein-DNA interactions, four-way helical junctions in DNA molecules, micromechanics of single supercoiled DNA molecules, statistical-mechanical analysis of enzymatic topological transformations in DNA molecules and so on. In 14 Chapter *Mathematics of DNA Structure, Mechanics, and Dynamics* (pp.293-320), Swigon discussed topology, elasticity, electrostatics, statistical mechanics and dynamics, etc. It includes the notions of the linking number, writhe, and twist of closed DNA, elastic rod models, sequence-dependent base-pair level models, etc. In the first approximation, a closed DNA molecule can be treated as a single closed in space.

Pratt (2003) searched consciousness, causality and quantum physics. Shan (2003) proposed a possible quantum basis of panpsychism. Bernroider (2003) discussed quantum neurodynamics and the relation to conscious experience. Tarlacı (2005) discussed quantum brain dynamics, general quantum neurodynamics, quantum field theory and consciousness. Tarlacı (2010b) discussed a historical view of the relation between quantum mechanics and the brain, and assumed to be a quantum mechanical many-body system interacting with the macroscopic neuron system. Tarlacı (2010a) proved we need quantum physics for cognitive neuroscience, and researched the probabilistic quantum thinking and obtained experimental results that are of basic significance in the fields of neuroscience and of psychology (Tarlacı, 2010c; 2013) used the expression consciousness-brain, and discussed terms of the soul, or something that existed other than the material body, and developments on mind-body duality, mind-brain and consciousness-brain. This is symbolized in the psi-phi problem. Li (2013) investigated a timeless and spaceless quantum theory of consciousness.

At present mathematics of DNA are mainly statistics, topology, etc. In this paper, according to basic thinking of *NeuroQuantology*, we research the extensive quantum theory of DNA. Then corresponding quantum theory and its many mathematical methods may be applied to DNA and molecular biology.

2. Basic Quantum of DNA and Its Extensive Quantum Theory

Based on the extensive quantum theory in which the formulations are the same with the quantum mechanics and only quantum constant h is different, we proposed the extensive quantum theory (Chang, 1993; 2002; 2006) and the extensive quantum biology (Chang, 2012a). Further, we discussed the fractal, chaos and soliton in nonlinear biology and neurobiology, in which soliton may keep the integrality and veracity of information in neural transfer. The nonlinear mechanism of memory is researched (Chang, 2012a).

In the extensive quantum biology, gene, cell, man and any live individual as the smallest live element in various levels are all different live quantum (Chang, 2012a). It is known that genes of most eukaryotes are interrupted genes, and DNA is also interrupted. The model of DNA is a well-known double helical structure. Its basic elements are A-T and G-C. For RNA the basic quantum elements are the corresponding A-U and G-C. Assume that A-T and G-C are the basic quantum of DNA, or assume nucleic acid has five types of base quantum: A, T, G, C and U, but usual case A-T, G-C form double; therefore, we research the extensive quantum theory of DNA.

The basic equation of quantum mechanics is Schrödinger equation:

$$\frac{d^2\psi}{dr^2} + 2m(E - U)\psi = 0. \quad (1)$$

If U is a potential of the harmonic oscillator:

$$U(r) = \frac{1}{2}m\omega^2r^2. \quad (2)$$

The solution of Eq.(1) is:

$$\psi_n(r) = \sqrt{\frac{m\omega}{\pi}} \frac{1}{\sqrt{2^n n!}} e^{-m\omega r^2/2} H_n(r\sqrt{m\omega}). \quad (3)$$

Here $H_n(x)$ is Hermite function. From the solution (3) a cycle form may be obtained (Landau *et al.*, 1977). It probably corresponds to DNA. For different potentials the solutions are also different.

In the molecular biology, the movement of DNA double helices may be described by a set of coupled sine-Gordon equations (Zhang, 1987). Peyrard *et al.* investigated the vector nonlinear Klein-Gordon equation of helicoidal DNA model, whose envelope soliton solutions are described by a radial and an angular degree of freedom for each site (Cocco *et al.*, 1999; Barbi

et al., 1999). They discussed nonlinear dynamics of DNA, its statistical mechanics, and researched the fundamental properties of nonlinear lattices and their applications in condensed matter and biomolecular physics (Terraneo *et al.*, 2002). We investigated the neural synergetics, Lorenz model of brain whose fractal dimension $D \approx 2.06$, soliton-chaos double solutions and physical neurobiology (Chang, 2013a).

Erol (2010) researched basics and concise relations between Schrödinger wave equation and consciousness/mind. Vimal (2009a; 2009b; 2010a; 2010b) researched systematically the subjective experience aspect of consciousness as an integration of classical, quantum and subquantum concepts for emergence hypothesis, and discussed a theory of everything as introduction of consciousness in Schrödinger equation, standard model, and loop quantum gravity and string theory and unification of experiences with fundamental forces.

Generally, biomechanics should be nonlinear. Usually, the fractal, chaos and soliton will appear in the nonlinear biology, and there are soliton-chaos double solutions (Chang, 2013a). Further, the Schrödinger equation, and Dirac equation, Klein-Gordon equation can be developed to nonlinear, and Higgs equation is already nonlinear.

3. Symmetries of DNA and Supersymmetry

In DNA there is the replacement symmetry for A and T, G and C. We may suppose A-T as a “particle”, so T-A as an “anti-particle”. Further, there is an extensive supersymmetry between A-T and G-C. In a matrix of DNA

$$M_{DNA} = \begin{pmatrix} A & T \\ G & C \end{pmatrix}, \quad (4)$$

there are the left-right symmetry of single element and up-down symmetry of double elements. Eq.(4) is analogue with the supermultiplet (a multiplet of super-particles)

$\Phi = \begin{pmatrix} \phi \\ i b \bar{\epsilon} \psi \end{pmatrix}$ (Chang, 2003), in which ϕ are bose fields (they may be various scalar fields, vector fields, tensor fields and so on.) and ψ are fermi spinor fields.

The supersymmetry is connected with superspace, superfield and super-

transformation, etc (Salam *et al.*, 1975; 1978). It arouses the supergravity in the gravitational theory. Combining a string model, a well-known superstring is derived (Gribbin, 1999). Weinberg (2000) introduced systematically supersymmetry in his book “*The Quantum Theory of Field*”.

Some directions in supersymmetry are discussed: Yang-Mills gauge theory (Leibundgut *et al.*, 1998; Hashimoto *et al.*, 1998; Naik 1999; Csaki *et al.*, 1999), the supersymmetry breaking and dark matter (Nelson 1998; Arnowitt *et al.*, 1998) and so on.

The generators t_a of a Lie Algebra satisfies commutation relations

$$[t_a, t_b] = i \sum_c C_{ab}^c t_c.$$

Supersymmetry is expressed in terms of symmetry generators t_a that form a Graded Lie Algebra (GLA) (Fayet *et al.*, 1977; Weinberg, 2000), embodied in commutation and anticommutation relations of the form:

$$t_a t_b - (-1)^{n_a n_b} t_b t_a = i \sum_c C_{ab}^c t_c. \quad (5)$$

GLA are extensions of usual Lie Algebras. Based on new representations and the supposition, GLA of bosons and fermions can be unified (Chang, 2003).

Based on the symmetry in biology we may research the biological groups. For example, A-T and G-C components in DNA are similar with the atomic nuclei composed of proton and neutron. Such we assume that DNA possesses SU(2) symmetry, and is consistent with Yang-Mills gauge theory (Chang, 2012b; 2013a). Of course, both forms and interactions are different. DNA as the double helix is analogue with an entangled string, and nucleus is analogue with a sphere.

4. Quantum Equations in DNA

Based on the inseparability and correlativity of the biological systems, we proposed the nonlinear whole biology and four basic hypotheses (Chang, 2012b). It may unify reductionism and holism, structuralism and functionalism, and belongs to systems biology (Oltvai *et al.*, 2002; Macilwain, 2011). Further, the loop quantum theory, which constitutes a very small discontinuous space, as new method is applied to biology. From this we proposed the model of protein folding and lungs, and



obtained four approximate conclusions: their structures are quantized, their space regions are finite, various singularities correspond to folding and crossed points, and different types of catastrophe exist (Chang, 2012b).

Different sensation systems are usually independent each other. Based on the open out the potential of blind children and other research, we proposed a hypothesis: The neural excitable cell is continuously induced and excited, then grow out new synapse and dendrite, and the feeling system, hearing system, smell system, etc., may joint to visual system, and form a new neural network, and achieve finally a transformation among vision and other sensations. Further, we proposed some possible tests, for example, for trained mammal, etc., and researched possible theories. This is a testable application of the nonlinear whole neurobiology, and may build a bridge between modern science and traditional culture, religion (Chang, 2013c).

NeuroQuantology should be nonlinearity and quantization, and may relate to quantum chaos, quantized matrix, etc. We discussed biofield and some nonlinear theories in biology and researched chaos in biology and its application to cancer, and searched fractal and complex dimension in biology. We proposed the matrix representations of hypercycle theory. Its fuzzy element corresponds to that each element is fractal (Chang, 2013d).

We researched the possible applications of the Yang-Mills gauge theory in biology (Chang, 2012b; 2013a). The equation of the Yang-Mills gauge theory is:

$$D_\nu F_a^{\mu\nu} = \partial_\nu \partial^\mu A_a^\nu - \partial_\nu \partial^\nu A_a^\mu + g C_{abc} [\partial_\nu (A_b^\mu A_c^\nu) + A_{\nu b} (\partial^\mu A_a^\nu - \partial^\nu A_a^\mu)] + g^2 C_{abc}^2 A_{\nu b} A_b^\mu A_c^\nu = J_a^\mu. \quad (6)$$

Here C_{abc} are different structure constants of various gauge groups. Actor (1979) reviewed comprehensively some classical solutions of SU(2) gauge theories. The solutions with U(1) gauge invariance have Jukia-Zee (1975) dyon:

$$h(r) = \alpha r / \sinh \alpha r, \quad (7)$$

$$f(r) = \sinh \beta [-1 + \alpha r \cosh \alpha r / \sinh \alpha r], \quad (8)$$

$$g(r) = \cosh \beta [-1 + \alpha r \cosh \alpha r / \sinh \alpha r], \quad (9)$$

where α and β are arbitrary constants. For Euclidean solutions the one-meron solution is:

$$eW_i^a = -\varepsilon_{ian} (x_n / r^2) [1 - x_o / \sqrt{x_o^2 + r^2}]. \quad (10)$$

Belavin-Polyakov-Schwartz-Tyupin instanton is:

$$eW_o^a = \mp 2x_a / (x^2 + v^2), \quad (11)$$

$$eW_i^a = -\varepsilon_{ian} [2x_n / (x^2 + v^2)] \pm \delta_{at} [2x_o / (x^2 + v^2)]. \quad (12)$$

And it is self-dual:

$$eB_n^a = \pm eE_n^a = \delta_{an} 4v^2 / (x^2 + v^2). \quad (13)$$

Moreover, there are dilaton solution, monopole solution, and vortex solution, etc. The formation of DNA is possibly the origin of the magnetic field.

Bodnar (1998) proposed that telomere shortening is the molecular clock that triggers senescence. In the biological chirality, left-hand and right-hand circular things should correspond to the opposite spins in quantum mechanics, or to the spinor with isospin-1/2 doublets. Perhaps, both may apply the extensive GLA and supersymmetry. Further, instantons in Yang-Mills gauge theory are related to chiral symmetry breakdown (Actor, 1979). Therefore, they may describe the biological chirality.

5. Biological String

In particle physics, Nambu and Nielson, *et al.*, in 1969 proposed the string model. Its vibration may obtain linear Regge trajectory, whose development is Veneziano (1968) model with the duality, the analyticity and the crossing symmetry, etc. Regge amplitude is (Feld, 1969):

$$A_R(s, t) = \frac{[2\alpha(t) + 1][1 \pm e^{-i\pi\alpha(t)}]}{\Gamma(\alpha(t) + 1) \sin \pi\alpha(t)} \beta(t) \left(\frac{s}{s_0}\right)^{\alpha(t)-1}. \quad (14)$$

Veneziano amplitude derived result (Collins, 1977):

$$V(s, t) \xrightarrow{s \rightarrow \infty} g \frac{\pi\alpha(s)^{\alpha(t)} e^{-i\pi\alpha(t)}}{\Gamma(\alpha(t)) \sin \pi\alpha(t)}. \quad (15)$$

Based on the general oscillation and rotation of string we proposed that a corresponding equation of the emergence string may be:



$$\frac{d^2\psi}{dr^2} + \left[-\frac{K(K+1)}{r^2} + 2m(E-U)\right]\psi = 0. \quad (16)$$

Here ψ is a wave function or other functions. This equation (16) may also regard one of a scalar field in the gauge theory derived from emergence string (Konopka *et al.*, 2008). The potential of the anharmonic oscillator U is (Landau *et al.*, 1977; Flugge, 1999):

$$U(r) = \frac{1}{2}m\omega^2 r^2 + \alpha r^3. \quad (17)$$

Usual string should possess two moving states: oscillation and rotation. Assume that hadrons are formed from the emergence string, so we derived corresponding potential and the equation of the emergence string, whose energy spectrum is namely the GMO mass formula and its modified accurate mass formula (Chang, 2012c):

$$M = M_0 + AS + B[I(I+1) - S^2 / 2]. \quad (18)$$

These are some relations between the string and observable experimental data.

We proposed that the extensive quantum biology may combine string and superstring theories, and apply their mathematical forms and physical meanings. Such we may develop the extensive superstring and the extensive loop gravity theory by a method extended c or/and h , and which are applied to biology (Chang, 2012a). Moreover, the string may spin, bifurcate and be reversed, be entangled, etc. The solutions of $SU(2)$ gauge theory are related to the Dirac string (Actor, 1979).

Culik II and Harju (1991) introduced semigroups of dominoes as a tool for working with sets of linked strings, in particular, splicing semigroups of dominoes and DNA.

At present the most successful string theory is a hybridized string model with $E(8) \otimes E(8)$. Masip *et al.* (2006) researched the relations between the supersymmetric models and Higgsino dark matter.

The string model is generally 26 dimensional spaces. The superstring combining Kaluza-Klein theory is 10 dimensional spaces. Various supersymmetry theories are in higher dimensional space (Nelson, 1998). Weinberg (2000) discussed supersymmetry algebras in higher dimensions in Chapter 32 of “*The Quantum Theory of Field III*”.

We propose that DNA and various living things with string states and their motions may be described by the superstring and the extensive string theory. They can include some biological macromolecules, neurons, RNA, genes, proteins, even sperm and the channels in traditional Chinese medicine, etc. Various loops and nets of living things may be described by the closed string, for example, neural networks. They form namely the biological string. Their symmetries and groups may be researched. Perhaps, these solutions (Equations. 3, 7-13) and functions (Equations. 14 and 15) may describe some biological strings and their motions.

6. Universal Entropy Theory on Evolution of Any Systems

In the statistics a basic principle is statistical independence: The state of one subsystem does not affect the probabilities of various states of the other subsystems, because different subsystems may be regarded as weakly interacting (Landau *et al.*, 1980). It shows that various interactions among these subsystems should not be considered. But, if various internal complex mechanism and interactions cannot be neglected, a state with smaller entropy (for example, self-organized structure) will be able to appear under some conditions. In this case, the statistics and the second law of thermodynamics should be different (Chang, 1994; 1997; 2005; 2012d; 2013b). The internal interactions often are related with nonlinearity (Chang, 1997). Because internal interactions bring about inapplicability of the statistical independence, entropy decrease in an isolated system is possible for physics (Chang, 1997; 2012d; 2013f), chemistry (Chang, 2009; 2013e), biology (Chang, 2013b,d), astronomy (Chang, 2013g) and social sciences (Chang, 2013h). In particular, it has a possibility for attractive process, system entropy, transformation of internal energy (Chang, 2014) and so on.

Cramer (1988) proposed the evolution field. We proposed a universal formula for any isolated system (Chang, 2005):

$$dS = dS^a + dS^i, \quad (19)$$

where dS^a is an additive part of entropy and is always positive, and dS^i is an interacting part of entropy and can be positive or negative. Eq.(19) is similar to a well-known formula:

$$dS = d_i S + d_e S, \quad (20)$$



in the theory of dissipative structure proposed by Prigogine. Two formulae are applicable for internal or external interactions, respectively. Further, based on the Eq.(19), a sufficient and necessary condition of entropy decrease in isolated system may be expressed quantitatively (Chang, 2012d):

$$0 > dS^i > -dS^a, \text{ i.e., } |dS^i| > dS^a \text{ (for negative } dS^i \text{).} \quad (21)$$

In usual cases, the condition corresponds to that in isolated systems there are some stronger internal attractive interactions. Negative temperature is based on the Kelvin scale, we found that it derives necessarily entropy decrease. The known negative temperature is a fallacy in thermodynamics, and is contradiction with usual meaning of temperature and with some basic concepts of physics and mathematics (Chang, 2012d). The new self-repairable plastics are classical material with a process of entropy decrease in closed system through internal interactions.

In the dissipative structure theory, the total change of entropy for an open nonequilibrium system is a formula (20), in which $dS_i \geq 0$ is the entropy production inside the system, and dS_e is the entropy flow, which may be positive or negative, such $dS_e = dS_e^+ - dS_e^-$. Therefore, the total entropy can decrease when input entropy flow is negative, and is given as

$$S = S_0 + dS = S_0 + dS_i + dS_e^+ - dS_e^- > 0, \quad (22)$$

which and the entropy production are always positive. Then the maximum entropy is

$$S_{\max} = S_0 + dS_i + dS_e^+ \geq S_0 \geq dS_e^- > 0. \quad (23)$$

The maximum entropy defines a quantitative range of moderate degree on input negative entropy flow for any open system, whose absolute value is always greater than zero, but the total entropy can never become negative (Chang, 2013b).

We combine the universal formula (19) for any isolated system (Chang, 2005) and the

moderate degree on input negative entropy flow for any open system (22). Assume that in the sufficient and necessary condition of entropy decrease in isolated system (23) dS^i divides two parts of positive (internal repulsive interactions) and negative (internal attractive interactions) $dS^i = dS_+^i - dS_-^i$, and we obtain a total formula of entropy change:

$$dS = dS^a + dS_+^i - dS_-^i + dS_i + dS_e^+ - dS_e^-, \quad (24)$$

When

$$dS^a + dS_+^i + dS_i + dS_e^+ > dS_-^i + dS_e^-, \quad (25)$$

entropy increase $dS > 0$, the system tends to disorder. When

$$dS^a + dS_+^i + dS_i + dS_e^+ < dS_-^i + dS_e^-, \quad (26)$$

entropy decrease $dS < 0$, the system tends to order. Both differences are determined by the input negative entropy flow in open system and the internal attractive interactions in isolated system $dS_e^- + dS_-^i$. This conclusion and formula may be applied to any natural and social system.

Generally, biological evolutions are increases of complexity and bio-information. They should correspond to entropy decrease. In biology the neuroscience, the permeable membrane, enzyme, adenosine triphosphats (ATP) and the molecular motor, etc., are all some internal interactions. Any organism all is a typical self-organized system, and must be an order process of entropy decrease. As long as this process is isolated at least in a certain time, it all is a violation for the second law of the classical thermodynamics (Chang, 2013b).

In a word, the complex biological systems provides a wide region for research of entropy decrease in various isolated systems, which has possibly different levels in biological systems. If entropy decrease in any isolated system may be proved, it will promote greatly development of all modern science and society.

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