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Quantum Neural Networks are Modeled Using Biological Lattice Gauge Theory

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Abstract: We suggest using the biological lattice gauge theory to model quantum brain networks, drawing on biological gauge field theory and quantum biology. The double helical structure of DNA and the violation of chiral symmetry in biology may be described by this method, which fully applies the same lattice theory in quantum fields but has two anomaly concerns. We also go over the quantum neutral networks and neural network (NN) models, which are connected to biological loop quantum theory. Lastly, we investigate some potential advancements in the ways of networks given by the comprehensive graph theory and their novel mathematical forms.

Keywords: biology, neurobiology, modeling, quantum mechanics, lattice gauge theory, network, graph theory.

1. Introduction

All biological systems are extremely intricate. Their descriptions typically use some simplified modeling techniques from the popular Hodgkin-Huxley model to model collective signaling behavior in a networked oscillator model [3], spontaneous emergence of modularity in a model of evolving individuals [2], and spiking-bursting neural behavior using a two-dimensional map [1]. We presented the Lorenz model of the brain based on neural synergetics [4]. Gorbachev and Abramova, on the other hand, used a modified neuro-fuzzy model to analyze the global economic and technical development trajectory [5]. We put out the nonlinear entire biology and four fundamental hypotheses [6] based on the inseparability and correlativity of biological systems. We suggested the extended quantum biology [7] based on the extensive quantum theory. DNA may use the vast field of quantum biology if it is assumed that the fundamental quantum constituents of DNA are A-T and G-C [8]. Furthermore, the Bessel equation could be derived from the Schrödinger equation with the linear potential. The double helical helix of DNA in three dimensions may be formed by its solutions, which are Bessel functions [9]. In this study, we suggest modeling quantum neutral networks using the biological lattice gauge theory, and we investigate newly disclosed network types.

2. Biological Lattice Gauge Theory

The hypothesis of quantum biology is widely recognized. For instance, quantum mechanics is commonly used in neurobiology. Tarlaci demonstrated that quantum physics is necessary for cognitive neuroscience [10], investigated probabilistic quantum thinking, and produced experimental findings that have fundamental implications for the study of psychology and neuroscience [11]. Erol studied the fundamentals and the connections between consciousness/mind and the Schrödinger wave equation [12]. We looked into how the Yang-Mills gauge theory might be used in biology [6,13]. We specifically covered the SU(2) gauge theory of DNA, along with related equations and some of its solutions [8]. The biological lattice gauge theory, which fully applies the same lattice gauge theory in quantum fields, is the result of our combination of the two elements. Additionally, it is the vast field of quantum biology [7].

Wilson put out the lattice gauge theory, which substitutes a discrete set of points for space-time [14]. The theoretical Hamiltonian model was then covered by Kogut et al. [15]. This theory becomes a significant quantum field theory since it provides qualitative nonperturbative information about QCD [16,17].

In lattice gauge theory the simplest lattice is defined with equal lattice spacing *a*. When the limit $a \to 0$, it reduces to the usual Yang-Mills gauge theory, i.e., it is the discrete gauge field theory, and there is an effective largest momentum of order 1/*a* as an ultraviolet cutoff [17]. Two neighboring sites of the lattice denote $(n, n+\mu)$. A member of SU(3) is [16]:

$$U(n, n+\mu) = \exp[iag \frac{\lambda^a}{2} A^a(n)] . \tag{1}$$

Here *g* is the coupling constant, λ^a is the generator of SU(N), and $A_\mu^a(n)$ is the gauge field.

The scalars on the lattice must make the substitution:

$$\partial_\mu \phi \to \frac{1}{a}(\phi_{n+\mu} - \phi_n). \tag{2}$$

Such the scalar action becomes:

$$S = \sum_n [\frac{a^2}{2} \sum_{\mu=1}^{4} (\phi_{n+\mu} - \phi_n)^2 + a^4 (\frac{m^2}{2} \phi_n^2 + \frac{\lambda}{4!} \phi_n^4)]. \tag{3}$$

Here ϕ_n replace its Fourier transform $\phi(k)$, and insert the Fourier expansion of ϕ_n into the free action of the scalar field on the lattice. On the lattice, the propagator is generated [16]:

$$k^2 + m^2 \to m^2 + \sum_\mu \frac{4}{a^2} \sin^2(ak_\mu / 2). \tag{4}$$

Therefore, the properties of the expression are examined by a formula [16]:

$$\frac{1}{a^2} \sin^2(ak_\mu) + m^2. \tag{5}$$

Eq.(4) and (5) are similar to biological helical structures. The lattice gauge theory may derive two anomaly problems [16]: 1) Every space-time dimension has an unphysical double. However, it appears to only match DNA's double helical shape. 2) The anomaly violating chiral symmetry is associated with another issue. However, the violation of chiral symmetry in life is a commonly accepted natural phenomenon. Consequently, the double helical helix of DNA and the violation of chiral symmetry in biology should be explained by the biological lattice gauge theory. Furthermore, quark confinement is described by the lattice gauge theory, which also explains biological inseparability.

3. Quantum Neural Networks

Complex networks were studied by Watts and Strogatz [18], and networks of linked dynamical systems have been used to describe brain networks, genetic control networks, biological oscillators, and numerous other self-organizing systems. They looked at basic network models that can be adjusted using this compromise: regular networks that have been "rewired" to add more disorder. They discovered that these systems can have tiny typical path lengths, like random graphs, and be heavily clustered, like regular lattices. Specifically, these are "small-world" networks [18, 19]. Complex networks have certain topological statistical characteristics, such as being scale-free [20], meaning that their power function distribution is precise or nearly so, having group structures [21–25], and having a corresponding network evolutional model. It has to do with topological thermodynamics, where the Tellegen theorem and Kirchhoff law can be used in neurobiology. A violation of Kirchhoff's current law will result in a brain infarction.

Hopfield [26,27] proposed a type of neural networks model, whose basic nonlinear equations are:

$$C_i \frac{du_i(t)}{dt} = -\frac{u_i(t)}{R_i} + \sum_{j=1}^{N} T_{ij} g_j(u_j(t)) + I_i. \tag{6}$$

Bishop and neural networks for pattern recognition were addressed by Christopher [28]. Wolfram discovered that there are four distinct outcomes from cellular automata: chaos, period states, stable states, and complicated states [29]. Additionally, there exist random and quasiperiod states. We talk about the quantum neutral network, which could be connected to quantum theory of biological loops [6].

Random networks and scale-free networks are examples of networks [30]. The general bionetwork is not a random network; instead, it frequently forms "small-world" networks with the shortest path length and network clusters, which are defined by the clustering coefficient [18]. Network motifs can be built by bionetworks using feed-forward, bi-fan, bi-parallel, and three-chain forms [31, 32], as well as modularity [33].

Statistics physics, which is associated with the average field and renormalization theory, is a key instrument in networks. The statistical description of complex networks was covered by Ravasz et al. [34, 35]. In phase transition, a phenomenological rule of order parameter is:

$$\xi \propto |t - t_c|^\beta. \tag{7}$$

It is a nonlinear formula, and β is fractal dimension. The scale-free network has stronger robustness, and obeys also the power law [22]:

$$p(k) \sim k^{-n}. \tag{8}$$

It is the degree distribution formula with a fractal dimension $D = -n$. The scale-free and clustering in bionetworks coexist, and emerge the new hierarchical networks, whose formations [34] are some classical fractals, for example, Eq.(8). Further, the fractal dimension may be developed the complex dimension in both aspects of mathematics and physics [36-38]:

$$D_z = D + iT\,. \tag{9}$$

The fractal dimension changes with time, energy, etc. when the complex dimension is coupled with relativity, which has three real spaces and one imaginary time as dimensions. It's common in biology [39]. We talked about how the fractal describes the structure of particles, medicine, meteorology, seismology, etc. [36,38,39]. The neurobiological system is recognized to be a highly intricate nonlinear system. Neural networks (NN), the foundation of the neural system, are built by many neurons. They can use discrete or continuous models. The pan-brain level and the pan-brain relation are combined in the pan-brain network. It consists of intricate microcircuits and macrocircuits. These can be used to study the mechanisms and functions of neurons and neurobiology, as well as to form their theoretical models.

A connection model of Artificial Neural Networks (ANNs) is:

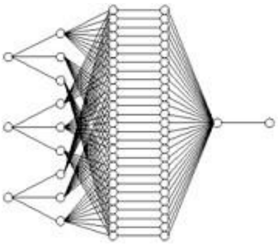

Fig. 1. A connection model of ANNs

Neural network perception is one of them. They might be self-organizing and self-adapting, which is consistent with learning. Information can be used for learning, control, memory, and storage. A three-layer connected model of NN is:

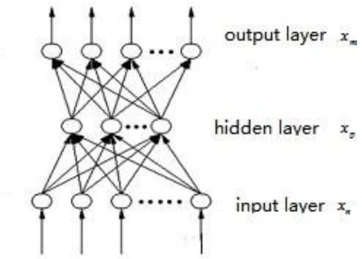

Fig. 2. A three-layer connected model of NN

In this model input layer x_n has *n* neurons, hidden layer x_p has *p* neurons and output layer x_m has *m* neurons. While x and y are not direct connection.

Barabasi and Albert [20] proposed the average field equations of evolutionary model on scale-free network:

$$\frac{\partial k_i}{\partial t} = mk_i / \sum_{j=1}^{N-1} k_j\,. \tag{10}$$

When time t is enough long, a solution is $k_i = m(t/t_i)^{\beta}$. When network increases with complete random, the average field equations are:

$$\frac{\partial k_i}{\partial t} = \frac{m}{m_0 + t - 1}\,. \tag{11}$$

Their solution is $p(k) \propto e^{-k/m}$, which is the same with Eq.(8)

Metabolic networks, such as amino acid biosynthesis, carbohydrate metabolism, lipid metabolism, nucleotide metabolism, etc., were studied by Jeong et al. [40] and Tanaka [41]. The small world property is theirs. Additionally, protein networks that interact are scale-free [42, 43]. They have fractal structures and small world properties, just like the channels in traditional Chinese medicine.

If the relation between the clustering coefficient C(k) and scale k is $C(k) \propto k^{-\alpha}$, it will explain networks with the level structure. Networks possess clustering and hierarchical characters [33,34]. Group structures are present in social networks [43–46,22,2]. Different tribes and communities are represented by distinct biological sense systems. Assortativity is a crucial statistical metric that Newman suggested [47, 48]. For example, it is equivalent to the same sense system.

Clustering in the scale-free network Holme-Kim model is adjustable [45,49]. In addition to forming the coevolution network model [53,54], adaptive network model [55], self-organized network model [52], and other models, networks can exhibit dynamics with scale-free structures and network nodes [50–52].

For structures of functional networks [56] the memory function is defined by the edge weight function f(e) in networks flow. When $f(e) \geq f(e_c)$, threshold value is namely long memory. It is related with initial conditions. Entropy of degree distribution is defined by formula:

$$H = -\sum_{k} P(k) \lg P(k)\,. \tag{12}$$

Regular networks correspond to the minimal entropy, while uniform random networks correspond to the maximum entropy. It demonstrates that the small-world network method's degree distribution is comparable to the random figure's degree distribution [19].

In several isolated biological systems, such as the brain, the permeable membrane, the molecular motor, etc., we suggested that internal interactions may be the cause of an entropy decrease. Moreover, a quantitative expression for a sufficient and necessary condition of entropy decrease is provided [57]. No complicated system can ever be derived by entropy rise. Furthermore, we put out a universal entropy theory of evolution for all natural and social systems in a quantitative manner [8].

Kuramoto suggested a phase model with an average field for the synchronization model [58]. Universal synchronization was covered by Pikovsky et al. [59]. Numerous linked nonlinear oscillators and synchronization systems are studied for phase clustering and the transition to phase synchronization [60,61]. Each item may be described as a nonlinear oscillator using this technique, and networks have a clustering structure [47,62]. Further, the networks model of synchronization may be constructed [1,3]:

$$x_{n+1}(i) = f[x_n(i), y_n(i)] + k[1-\delta(i,n)] \sum_{j \in S(i)} \delta(j, n-\tau(d_{ij}))\,, \tag{13}$$

$$y_{n+1}(i) = y_n(i) - \mu(x_n(i)+1) + \mu\sigma\,, \quad (i = 1,2,\ldots,N_1). \tag{14}$$

Here k is a key, which is bigger, and more synchronized. This is also a phenomenological field (as the thought field, religion field and Qi field, etc).

Hierarchical structure and the prediction of missing links in networks were recently studied by Clauset et al. [63]. Structure and inference in annotated networks were examined by Newman and Clauset [64]. Bionetworks and biological topology are related, and both can be represented by a matrix with nodes representing order and edges representing element values. The entire incidence matrix is made up of points and edges. Conduction directions are the directed graph, whereas biological networks are typically the non-directed graph.

We looked into chaos in biology and how it relates to cancer, and we talked about biofield and other nonlinear theories in biology. In biology, fractal and complex dimensions are looked for. Possible entropy loss is examined in nonlinear biothermodynamics. We put forward the hypercycle theory's matrix representations. Quantized matrices, quantum chaos, and other concepts may be related to the nonlinearity and quantization that characterize quantum brain biology [39]. The matrix formulation has connections to both quantum biology and neural biology and is a type of quantum mechanics.

As a neuron and matrix element, the weighted values for the neuron structure can create different matrices. Positive weighted values in this matrix indicate an increase in influence, while negative values indicate a drop in effect. It should be four matrices (np, pn, pm, mp). They may be unified by one matrix:

$$(H_{np} + H_{pn}') + (H_{pm}' + H_{mp}) = H_{2(n+m)\,p}\,. \tag{15}$$

$$H_{2(n+m)\,p} = \begin{bmatrix} H_{np} \\ H_{pn}' \\ H_{pm}' \\ H_{mp} \end{bmatrix}. \tag{16}$$

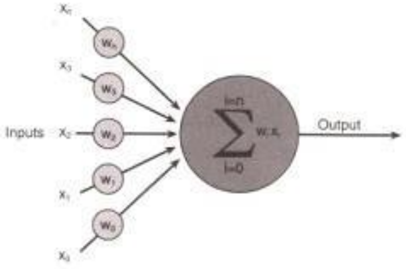

Fig. 3. Figure on inputs and output

General output is:

$$X_i = \sum_{j=1}^{n} w_j x_j + s_i \,. \tag{17}$$

Here s_i is the feedback information. From this forms the cycle mode. Its dynamic model is:

$$\frac{dH}{dt} = F_{ip} \,. \tag{18}$$

It connects with Hopfield model.

Research on networks whose status varies over time is known as network dynamics [65–67]. The least action principle might serve as its foundation, and network architectures could be derived from selection principles [68–71]. We believe that an ancient network theory, in which the channels are specifically the special networks, forms the foundation of Chinese medicine. Systems biology is the generalization of bionetworks. Furthermore, the biological lattice gauge theory may be used with quantum neural networks.

4. New Research on Described Networks

According to Hartwell et al. [72], contemporary biology should create new research techniques and look into how biological molecules interact as well as the corresponding network dynamics, structures, and functions. The whole biology is nonlinear, as demonstrated by biological networks [6].

Graph theory is one of the primary mathematical tools for networks. Graph theory and its vast scope can be used to bionetworks, brain networks, and general networks [38]. For instance, nodes and fields linked to complexity are represented by the neural elements in neural networks. Different levels of hierarchical networks can be formed by nodes and fields. In this case, several centralities may be used to reflect the nodes' importance [73]. Hierarchical networks can be made simpler by it [34]. There are several hierarchical interregional circuits in the brain system, including microcircuits and local circuits. They might be some lattices in biology. Graph spectra and the detectability of community structure in networks were recently studied by Nadakuditi and Newman [74].

We presented a new development in graph theory based on the combination of Feynman diagrams and the tree-field of graphs. This new development contains five sorts of fundamental elements: vertices, fields (which are a collection of numerous little trees), dotted lines, wavy lines, and varied solid lines. We then looked into their potential uses in the social sciences, physics, etc. [75].

The possible meanings of these elements are mathematically: solid lines represent connections with fixed values, dotted lines represent possible connections, wavy lines represent changed connections by function f(x), and fields represent complexity by sum formula $\sum_{i=1}^{n} f_i$ and integral $\int f(x)dx$ or by product formula $\mathop{S}_{i=1}^{n}(f_i)$ in different levels, etc.

Because biological systems include more intricate joins and structures, the new extensive graph may be applicable to a variety of biological systems. Lines and tubes make up bones. Assume that different fibers correspond to different lines, and cells to fields. The intestine is a line and three-dimensional tube, and the stomach is a field. We put forth the general biological string theory and the string theory of DNA [8]. For a graph, a string is also a distinct line. Lines, vertices, and a field are used to depict Fig. 3.

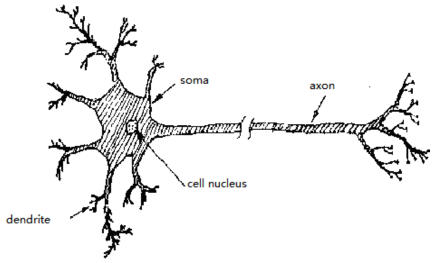

Fig. 5. Structure of neuron

Axon, dendrite, and synapse represent different lines in the neuron's structure (Fig. 5), whereas the cell soma and neuron represent fields. The superstring and higher dimension correspond to each cell body as the modeling Calabi-Yau manifold [76]. We might also look into the Feynman rules of biology. The three-dimensional form of hydrodynamics may be used in the primary model of neural transmission. Assume $A \propto C^{D/(D+1)}$ [69]. For D=3, so $A \propto C^{3/4}$.

Theoretical Theoretical justification of DNA as a biophoton source

Popp et al. have shown emission [77]. The exciplex model states that the standing vibration waves (photons) in the DNA lattice must meet the requirements for biophoton emission to be permitted at all. The stacking interaction in the DNA staircase is thought to be the source of photons in the DNA lattice.
Additionally, the loop quantum gravity theory [6], general relativity, twistor theory [78], and other theories may be combined in this theory.

5. Conclusions

We suggest the biological lattice gauge theory, which is based on quantum biology and is modeled by the lattice theory in quantum fields. Its two anomaly problems might simply explain the double helical helix of DNA and the violation of chiral symmetry in biology. We also go over quantum neutral networks, which are connected to the quantum theory of biological loops. Research is done on some potential advancements in the network approaches defined by the extensive graph theory and their new mathematical representations. In a nutshell, generic bionetworks and quantum neutral networks may integrate different mathematical techniques and theories. It may be a branch of biology and neurobiology that is always being refined and advanced.

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