Natural Selection and Random Matrix Theory

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Abstract

We will study the relationship between two well-known theories, genetic evolution and random matrix theory in the context of many-body systems. It is suggested that genetic evolution can be described by a random matrix theory with statistical distribution in which natural selection acts as a Gross-Witten-Wadia phase transition.
1 Introduction

Genetic evolution [1, 2, 3, 4] occurs through changes in the heritable characteristics of a population over successive generations. Individuals with traits that are advantageous for survival and reproduction are more likely to pass those traits to the next generation. Over time, these advantageous traits become more common in the population, leading to evolutionary changes. It happens when a creature undergoes unexpected natural stresses and then it naturally selects the more stable state. It strongly correlates with external environmental conditions such as air pressure, temperature, food resources, cosmic rays, etc. It also depends on the occurrence of natural phenomena like earthquakes, asteroids, and hurricanes.

The basic question one can ask is on what scale does evolution happen? We want to discuss the subject on a special scale where the quantum dynamic is dominant and all the dynamic is represented by probability laws. If the evolution happens quantum mechanically, then the phase space describing the dynamics is the space of possible states or Hilbert space which contains finite possible states to be observed by the observer. The observed states are our observables in daily life but this does not mean that other states do not exist. This is due to the fundamental nature of uncertainty principle. This scenario points out that a cell can choose between an infinite number of possible states with random distribution each with a specific probability weight. This is known as Quantum Darwinism [5]. We consider these states to be chosen from a hermitian random matrix ensemble by the use of Random Matrix Theory (RMT).

RMT is a strong and useful tool to classify and describe the energy spectrum of many-body chaotic quantum systems with strong coupling between its partitions which are usually thermal systems. It has been intended to study statistical behaviors in quantum regime. This theory is used in various fields, such as string theory, two-dimensional gravity [6, 7], conformal field theory, number theory, condensed matter [8], integrable systems, glass theory, [9], stochastic processes [10], economics [11] and RNA folding [12, 13, 14, 15, 16, 17, 18]. For useful reviews on this context see [29, 30, 31, 32].

Evolution can be observed as changes in the ensemble of genes. The state of a living cell before the decomposition can be considered as a variable taken from a random matrix ensemble with Gaussian distribution. When the decomposition starts, it will pick other random variables from a possible set of ensemble samples by a phase transition. This is what we call in this paper natural selection and it does not always lead to an evolutionary change in the DNA structure. If the order of matrices is $L \times L$, where $L \rightarrow \infty$, and if we consider a two-dimensional living system evaluates such that it goes from a weaker state to a stronger one, then this phase transition is very similar to the one proposed by [40] and [41] for QCD. By weak and strong we mean the stability of the cell against external effects. Just if the environmental conditions change intensely the decoupling may get a genetic disorder after the decomposition as we expect from a strongly coupled chaotic system. We will show this could be possible through the Gross-Witten-Wadia phase transition by defining an effective coupling constant $g$ for DNA. The phase transition occurs at double-scaled limit $g \rightarrow g_c$ and $L \rightarrow \infty$ leaving 'tHooft parameter $\tau = g^2 L$ fixed where $g_c$ is a critical coupling, depending on the conditions of the system.

We will discuss cellular fission and compare it with a Gaussian distribution. The outcome state from the decomposition is picked randomly between many possible states on a random ensemble with a given probability. The main goal of the paper is the possible phase transition in RMT and its relation to genetic evolution, for a general set of random matrix distributions. Depending on the symmetries of the system, these ensembles could be Gaussian Unitary Ensemble (GUE), Gaussian Orthogonal Ensemble (GOE), Gaussian Symplectic Ensemble (GSE), or other class of distributions [31]. We will discuss the case of GUE.
2 RMT, Phase Transition and Evolution

A single DNA is constructed of two sugar phosphate backbones and four nucleotides namely Adenine (A), Thymine (T), Cytosine (C), and Guanine (G) (fig. (1)). The DNA is made up of two base pair bindings AT and GC. GC content of a DNA segment, which is the percentage of nitrogenous bases in a DNA, can affect the stability of the DNA molecule. GC base pairs are held together by three hydrogen bonds, compared to two AT base pairs, making GC-rich DNA more thermally stable. This stability plays a role in the structure and function of genomic DNA, influencing aspects like gene expression and chromatin organization.

We consider that each AT or GC bond in the DNA represents a force with a random value on a specific distribution with zero mean and determined variance $\mathcal{V}$. These forces are related to the potential energy $F = -\nabla U$, therefore each covalent bond carries a random amount of potential energy. In DNA, the energy can differ from one bond to another. For example, an AT bond on one part of the DNA can have slightly different energy than the AT bond on the other part. That is possible since this energy depends on the location of the nucleotides and many other side effects of the potentials of other objects. By seeing this bond energy as a random variable, the DNA can have statistical distribution in terms of energy eigenvalues.

One can define a theory with Hamiltonian $H$ as a unitary matrix with random entries of the size of the number of DNA bonds $L$, in which the energy eigenvalues show the amount of the potential energy of each bond in each generation step in the whole ensemble. One can find the energy

![Figure 1: The structure of DNA (up, right), the nucleotide base pairs (up, left), and the chemical structure of the fundamental nucleotides (down).](image)
eigenvalues of each cell’s DNA by diagonalization of $H$:

$$\text{diag}(H) = \begin{pmatrix} 
\lambda_{AT}^{(1)} & 0 & 0 & \ldots \\
0 & \lambda_{GC}^{(2)} & 0 & \ldots \\
0 & 0 & \lambda_{GC}^{(3)} & \ldots \\
0 & 0 & 0 & \ldots
\end{pmatrix}_{L \times L} \quad (2.1)$$

Where $\lambda_{AT}^{(i)}$ and $\lambda_{GC}^{(i)}$ is the energy of AT and GC for the $i$th binding respectively. Note that the structure of this theory is unknown and we are only extrapolate the general results by considering a system with such Hamiltonian. The ensemble is made of a large number of such matrices known as samples. Another picture would be an $n$ copy of DNA sequences (see fig.(2)). The values of entries in each sample could follow Gaussian or other random distributions. The randomness and the statistical behavior would be manifest at the limit $L \to \infty$. We discuss a hermitian system in this limit with a unitary matrix of Gaussian distribution.

For such a system with finite and constant coupling $g$, there is Columb-like force that causes the eigenvalues to repel at short energy spacings and a long-range spectral rigidity at large energy spacings [30]. In genetics, the bonds also have some similar correlations among each other and this shows that both systems may appear to have the same universal features. For example, In the context of bacterial genomes, a study has shown that there is often a negative correlation between AT and GC biases, meaning that as the proportion of AT base pairs increases, the proportion of GC base pairs tends to decrease, and vice versa. This correlation can vary among different organisms and can be influenced by factors such as the replication mechanisms of DNA [33].

In cellular fission, the DNA will separate into two branches to construct two other cells from the same gene. In the whole process, the matrix elements will be generated randomly, each bond in a specific variance, and that will lead to completely different values of bindings for both produced cells. The cell will randomly choose one of the $m$ possible states (see fig. (3)) to start the replication process. Each state has its probability weight and the one which has greater probability is more likely to be naturally selected.
Figure 3: If the mechanism of decomposition of the living cell is assumed quantum mechanically then there are \( m \) possible states for the cell to choose. Each has its binary growth and probability weight. The states \( 1, 2, \ldots, m \) can be represented by an RMT ensemble with a Gaussian distribution. It can be thought of as an ensemble of \( n \gg 1 \) copies of DNA each with \( L \) bindings.

### 2.1 GWW phase transition

The main question of this paper is when genetic evolution occurs in the decomposition process. Before answering this question, let us see when evolution happens from a biological point of view. As a naive expression, When the cell starts to decouple into two individual cells, most of the time it will preserve the original gene. The story becomes interesting when one nucleotide (like A) exchanges with another nucleotide (like C) and causes an error in the replication which in turn changes the features of the living cell. This is what is referred to as genetic evolution. Now the change \( A \to C \) or \( T \to G \) can generate a drastic gap in the energy spectrum of the DNA (a gap on the Gaussian distribution) to put the cell in a more stable state since GC bounds are stronger. This means one eigenvalue has changed the statistics of RMT which can slightly deviate the shape of the density of eigenvalues \( \rho(\lambda) \).

This evolution can be related to the phase transition concept in RMT since it describes a variation between two phases, weak (more AT) and strong (more GC). This is also possible through studying the distribution of the maximum eigenvalue or Tracy-Widom distribution [37, 38, 39]. This has been widely studied in [36] and we are not going to go through the complete details in this paper.

To support this idea, It has been argued in [35] that any random complex interacting system will remain stable\(^2\) if the largest eigenvalue of the random distribution is less than an inverse of the coupling constant of the system \( g \):

\[
\lambda_{\text{max}} < (g)^{-1}
\]

Hence there is a critical value for \( g \) in which at that point the system would experience a phase transition. A similar phase transition occurs in two-dimensional large-\( L \) lattice gauge theories\(^3\) in critical coupling constant which is known as Gross-Witten-Wadia (GWW) phase transition [40, 41].

Using the steepest-descent method [19], Gorss and Witten solved the large \( L \) limit of the two-dimensional lattice gauge theory and observed a possible 3rd order phase transition. They showed

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\(^2\)The stability here means the perseverance of the species against external conditions. The system is unstable when the species goes toward extinction or the system is not prepared to preserve its heredity by evolution. Natural selection is an action against this process.

\(^3\)For a useful review of large-\( L \) gauge theories see [42].
for a general unitary RMT, the behavior of the density of eigenvalues for weak and strong coupling regimes is described by different analytical functions [40]:

$$
\rho(\lambda) = \begin{cases} 
\frac{2}{\pi \tau} \cos \frac{\lambda}{2} \left( \frac{\tau}{2} - \sin^2 \frac{\lambda}{2} \right)^{1/2}, & \tau \leq 2 \\
\frac{1}{\pi \tau} (1 + \cos \lambda), & \tau = 2 \\
\frac{1}{\pi \tau} (1 + \frac{2}{\pi} \cos \lambda), & \tau \geq 2
\end{cases}
$$

(2.3)

a phase transition is observed (for very large L) at \( \tau = 2 \), marking a boundary between weak and strong coupling regimes. For \( |\lambda| \leq \sqrt{2\tau} \) and \( \tau \to 0 \), the distribution is given by Wigner’s semi-circle law:

$$
\rho(\lambda) \simeq \frac{1}{\pi \sqrt{1 - \lambda^2}}
$$

(2.4)

The phase transition takes place exactly when the eigenvalues completely occupy the entire circle. When the value of the coupling is significantly large, the theory would induce a repulsion among the eigenvalues, leading to a uniform distribution. For very small coupling, the distribution will be as random as possible.

A string model [43] describing the large \( L \) perturbative expansion of QCD could also arise within the lattice framework of this theory. Adjusting the lattice spacing \( a \) and the coupling constant in such a way that the string tension remains constant would help to define an effective coupling. Using this coupling, [40] showed that the \( \beta \)-function of the theory does not vanish at \( \lambda = 2 \), meaning that this phase transition is of a higher order than two, otherwise the string tension must vanish. It is of third order since the third derivative of the free energy experiences a discontinuity at \( \lambda = 2 \).

Figure 4: The density of eigenvalues for (2.3) and (2.4) is plotted. Semi-circle law and small coupling distributions are drawn for \( \tau = 0.125 \). For very small couplings, the semi-circle and \( \tau \leq 2 \) distributions almost behave the same close to \( \lambda_{\text{max}} \) which is a sharp edge with so many random values. As the coupling gets bigger, the distribution becomes uniform until it reaches \( \tau = 2 \) where the phase transition occurs.

Similarly, for a DNA system with random entries for bindings chosen from a unitary random matrix ensemble of \( H \). We consider each DNA on a 2d lattice that its interactions are mainly
electron-electron random columb forces, to be analogous to a $U(L)$ lattice gauge theory. In analogy to the string model, we also consider the bindings as strings with finite tension $\kappa$ with an average spacing $\bar{\pi}$. We adjust the average spacing $\bar{\pi}$ and the coupling $g$ in such a way that the tension of each bound remains fixed. Therefore we define an effective coupling $g(\bar{\pi})$ for DNA bindings such that $\kappa[\bar{\pi}, g(\bar{\pi})] = \kappa$.

When the cell decouples in several steps, the structure of DNA may encounter some disorders from external unwilling effects that put the life of the cell in danger of extinction or cause an error in the replication. Therefore, the nucleotides will encounter such instabilities and decide to choose a stronger structure for the next steps of decoupling. Hence one of the nucleotides, for instance, A, exchanges with other nucleotides which provide more powerful binding, and the DNA will turn into a more stable phase. The coupling constant does not always change in that system just if the system undergoes certain circumstances and tries to preserve its tension. Since there is an obvious interaction between nucleotides, this change transforms the coupling constant to a new value which just at the transition phase reaches its critical value.

At the moment of decomposition, one specific binding should not necessarily have the exact value of previous energy and it gets picked randomly in later steps $^4$. We assume that the amount of energy of each bond $\lambda_{\text{AT}}$ and $\lambda_{\text{GC}}$ can not exceed a minimum and a maximum value. If so, the binding would lead to the destruction of one part of the DNA and the tension vanishes which we are not interested in.

Statistically, if the number of AT and GC energy bindings is equal (with $\lambda_{\text{GC}} > \lambda_{\text{AT}}$), changing A $\rightarrow$ C will change the distribution from the equilibrium point. Therefore, the interaction between AT and GC will turn into a new regime with a less coupling constant between molecules since $\lambda \sim g^{-1}$. That means the larger the population of GC can get, the easier and more accessible it can interact with neighboring eigenvalues. In other words, we tune the coupling such that the structure remains stable. This is similar to the GWW phase transition from weak to strong coupling phase which can turn the DNA into a more stable regime. Since this phase transition occurs randomly in the fission process, it is somehow equivalent to natural selection.

### 2.2 Tracy-Widom distribution

Tracy-Widom distribution is the distribution of the maximum eigenvalue. It is applied near the edge of the semi-circle and it helps us to find the crossover functions between the two weak and strong phases in the double-scaling limit (for finite but large $L$).

The probability distribution and its derivative are depicted in Fig. (5) and (6) (see [36]). We are interested in a large $L$ case where the phase transition can occur on a gap of order $L^{-2/3}$. The probability distribution of the hill in the gap region is described by Tracy-Widom distribution however the tails connected to that hill from the left and right sides are not and they are given by certain functions that satisfy the Painlevé II equations (see [37, 38, 39]). GWW phase transition separates the left and the right tail.

The Colomb-like force between eigenvalues can differ by changing the coupling constant of the theory that will cause a slight deviation to the effective potential where the eigenvalues condensated. Therefore $g^{-1}$ can be seen as a potential wall where we can move it on the real axis line of the energy. When the potential wall is located out of the semi-circle (fig. (a) of (8)), no phase transition will appear. Just as the potential hit the edge, it can affect the eigenvalues and change the Wigner distribution to another distribution close to that region, as shown in fig. (b) of (8) (for more details see [36]). That could cause a 3rd order phase transition from stable to unstable regime and vice versa. When the coupling constant gets smaller, $g^{-1}$ gets bigger and the potential wall will move away from the semi-circle. One can expect that the energy cost of the potential wall to get out of the semi-circle density is equal to the energy of exchanging A with C.

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$^4$To see this, one can also write the density of energy eigenvalues $\rho(\lambda)$ and $\rho(\bar{\lambda})$ in a Gaussian ensemble and calculate the pair correlation function $\rho_c(\lambda, \bar{\lambda}) = \langle \rho(\lambda)\rho(\bar{\lambda}) \rangle$ and take the limit $\lambda - \bar{\lambda} \rightarrow 0$. 

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Figure 5: The probability of having $\lambda_{\text{max}} < (g)^{-1}$ between $L$ eigenvalues in terms of $g^{-1}$. The three solid lines are for small $L$ and the dashed line is for large but finite $L$. There is a critical value for $g$ where the continuous phase transition can occur from the unstable (red line) to the stable (green line) phase. For large $L$, there is a small central region near $g_c^{-1}$ with a width of order $L^{-2/3}$ where the Tracy-Widom distribution applies.

Figure 6: The probability density function for $\lambda_{\text{max}}$ gives us the Tracy-Widom density around the critical value (blue region). The left and right tails are described by two different functions.

Figure 7: Wigner semi-circle law for density of eigenvalues (blue curve). The red curve shows the Tracy-Widom distribution near the edge (yellow bar) which is a perturbation around $\lambda_{\text{max}}$. 

7
Since the interaction between nucleotides changes randomly in each time step, this can transform the coupling constant to a new value which in a specific step, could be the critical value where the phase transition can occur. This phase transition can change the distribution for a short time and then keep the primary form of the distribution invariant. GWW phase transition leads to a change in specific energy eigenvalue which must be preserved in the whole process. The change in one energy eigenvalue directly changes the other eigenvalues due to the correlation and the repulsion force between each pair of eigenvalues.

3 Conclusion

We showed that in a certain toy model with random interactions, the time evolution of a spin operator is similar to the binary cellular growth where the energy bindings of base pairs of DNA sequences are chosen from a random matrix Hamiltonian of a unitary ensemble.

The cell selects a state in which the base pair bindings take random and independent energy values in each time step. This is just one state between many other possible states in the ensemble. Each cell has many states to choose and evaluate, so there are an infinite number of states, each with its probability weight. Environmental parameters such as temperature can play a role in the probability value. We can conclude that the behavior of the cell is a random chaotic phenomenon that can be described in classical and quantum mechanical viewpoints by random matrix theory. Through the idea that has been presented here, one can probe the exact statistical parameters of the cell for a long period and that is possible thanks to Tracy-Widom distribution. The change in DNA bindings can directly change the overall coupling constant which leads to a GWW phase transition from unstable to stable regime and vice versa which we conjecture is similar to natural selection.

It is of significant importance to calculate the free energy of DNA in large $L$ so that it can be compared with the main results obtained for the string model [43]. Connecting the effects and mechanisms inside the cell to the mathematical developments of the random matrix theory, can take a great step in tracking the number of lost circles in nature and drawing a historical map of different evolutions. By analyzing the spectrum and calculating the energy change in the GWW phase transition one expects to see in what exact statistical circumstances the cells have more chance to survive.
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