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Natural Selection and Random Matrix Theory

Mehdi Ameri¹

*Department of Physics, Faculty of Science, Ferdowsi University of Mashhad
P.O.Box 1436, Mashhad, Iran*

Abstract

We will study the relationship between two well-known theories, genetic evolution and random matrix theory in the context of many-body systems. We show that the time evolution of certain quantum mechanical toy models is similar to that of a living cell. It is also 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.

¹mameri@mail.um.ac.ir

1 Introduction

Genetic evolution [1, 2, 3, 4] works in the direction of modifying the mechanism of the entire physical living system to a new more advanced system to protect the living being from external intense conditions. 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 systems with strong coupling between its partitions which are usually thermal systems. It has been intended to study statistical behaviors whether in classical or quantum regimes. 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].

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 n 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.

As a starting point, we will discuss cellular fission and compare it to a specific quantum mechanical toy model with a Gaussian distribution. We will see that the time evolution of both systems shares common properties:

(a) They both have a binary fission that grows exponentially with time until the system reaches a stable state. (b) The outcome state from the decomposition is picked randomly between many possible states on a random ensemble with a given probability. (c) Both systems are sensitive to the temperature and initial conditions. This would motivate us to suspect other universal features of RMT to exist in the DNA structure.

Next, We discuss the main goal of the paper which 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 Cellular Fission and SYK Model

We present a quantum mechanical toy model suitable to describe the time evolution of a living cell, focusing on the binary proliferation of cells and bacteria. This model, known as the Sachdev-Ye-Kitaev (SYK) model, was introduced in [21, 22, 23], and it describes all-to-all and random interactions of q fermions among all other degrees of freedom N of the system. It is an exactly solvable model at large N and its conformal symmetry emerges in the infrared limit. It has gained attention for its potential insights into quantum chaos, strongly correlated materials in condensed matter [24], and its connections to quantum gravity via the AdS/CFT correspondence [23, 26, 27]. The model is defined in $(0 + 1)$ dimensions and It has the following general Hamiltonian,

$$H_{\text{SYK}} = -(i)^{\frac{q}{2}} \frac{1}{q!} \sum_{1 \leq i_1 < i_2 < \dots < i_q < N} j_{i_1 i_2 \dots i_q} \psi_{i_1} \psi_{i_2} \dots \psi_{i_q} \quad (2.1)$$

where $1/q!$ is a normalization factor and ψ_{i_q} are interacting Majorana fermions² which are matrices of order $L \times L$ where $L = 2^{N/2}$. They satisfy the Clifford algebra $\{\psi_i, \psi_j\} = \delta_{ij}$. The factor i is necessary for $q = 2 \pmod{4}$ to be hermitian. This factor means that the system with odd $q/2$ is not invariant under time reversal transformation. The couplings $j_{i_1 i_2 \dots i_q}$ are real and independent numbers that are chosen randomly in a Gaussian distribution and variance

$$\langle j_{i_1 \dots i_q}^2 \rangle = \frac{J^2 (q-1)!}{N^{q-1}}, \quad \langle j_{i_1 \dots i_q} \rangle = 0 \quad (2.2)$$

We see that for a given coupling j we would have a Hamiltonian as a random matrix with eigenvalues in the Gaussian distribution. Therefore, (2.1) is an ensemble of random interactions.

To describe the binary evolution of cells using this model, we make two assumptions: First, we assume that the decoupling of a cell into two cells happens in a quantum mechanical or semi-classical scale where this model is valid. Second, we define the cells as matrices S_i in analog to the original SYK model and assume that S_i inherit the spin operator properties of fermions that constitute the DNA in which the quantum mechanical algebra applied.

We consider the special case $q = 3$ and denote the couplings with γ :

$$H_{\text{cell}} = \frac{i\kappa}{3!} \sum_{i < j < k} \gamma_{ijk} S_i S_j S_k, \quad (2.3)$$

where κ is an arbitrary constant for normalization and i is for the sake of hermiticity. According to the above assumptions, If we let one operator evaluate with time, by using the Baker-Hausdorff lemma we can write

$$S_j(t) = e^{iHt} S_j(0) e^{-iHt} = \sum_{k=0}^{\infty} \frac{(it)^k}{k!} [H, [H, \dots, [H, S_j]]], \quad (2.4)$$

Where t is time and k is the order of expansion (time step) and the number of Hamiltonian commutations with ψ_j . According to figure (1a) in every time step, by commutating the operator ψ_j with the Hamiltonian (2.3), the particle first interacts with the other two particles ($k = 1$), then with the other four ($k = 2$), and this rate will grow binary with time.

Note that in each step there are a bunch of spinor matrices that are random and independent due to the choice of γ_{ijk} . The indices of the coupling depend on N and therefore, at each step, we have many possible states for the descendents. In other words, we have an ensemble of binary fissions like the one shown in fig.(1a). As stated before, these are quantum states with different outcomes

²The model can also be built of Dirac fermions, in that case, it is known as complex SYK and its insights and applications are well developed [28].

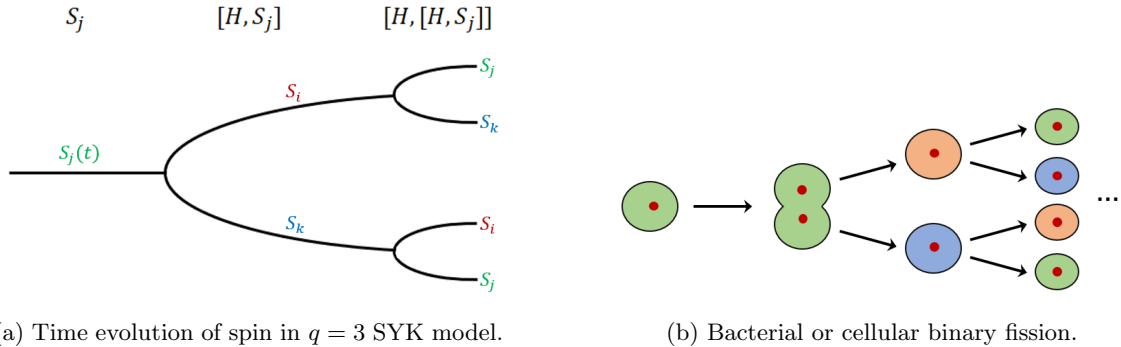


Figure 1: In fig.(1a), based on equation (2.4), the spin interacts with two particles, and this behavior will grow exponentially with time until it interacts with the N th particle of the system in t_* . Albeit it is an ensemble of such fissions, here we depicted only one random coupling. Fig.(1b) shows a similar mechanism to fig. (1a). Each color corresponds to a different random matrix.

and the cell will choose a state with a more possible chance of survival. This choice is proposed to be analogous to natural selection and will be described by a phase transition used in describing the confinement of QCD in the two-dimensional large N lattice gauge theory [40]. This will be explained in detail in the next section.

If we consider the system is compact on a circle or a sphere and all particles have the same distance from each other, the question one may ask is when does S_j interact with (or decay to) the N th particle? In other words, how long does it take for the information to be spread on the entire system? It is clear from figure (1a) that the operator growth is exponential and the time should be equivalent to the logarithm of the number of particles in base two for each temporal step. Therefore for a thermal system with temperature T in such binary evolution, this time would be

$$t_* = c\beta \log_2(N/N_0) = c\beta \log_2(S), \quad (2.5)$$

which is known as the *scrambling time*. Where N is the total number of particles that is directly proportional to the entropy S and N_0 is the number of particles that are interacted with at $t = 0$ ³. β is the inverse of temperature which is added to maintain the dimension of time and c is a proportionality constant factor that can be experimentally determined by the data of cellular growth. This behavior in k temporal steps is also referred to as *k-locality* or *operator growth*. Since γ_{ijk} depends on the order of indices and N , this growth will stop at the scrambling time (2.5).

Moreover, we know that as the temperature increases, the growth rate of the organism is also increased *i.e.* the scrambling time gets shorter when the temperature gets higher. However one has to be careful about the amount of the temperature since in very high temperatures the growth can drastically drop down and this shows the side detrimental effects on the living system. Also, In the extremal temperature $T = 0$, the scrambling time tends to infinity meaning that the growth does not happen.

This exponential growth was one feature of the systems that were described by random matrix theory, however, in the next section, we will give another perspective that shows a genetic deformation can occur randomly at each generation step through DNA reconstruction in the replication process. Considering the DNA bindings as random entries taken from a Gaussian unitary ensemble distribution, we try to explain how the genetical essence of each cell may change in each time step by a *phase transition* and produce different cells through changing the genetic codes. This is not a stable phenomenon and can reproduce early cells again in the next generations (fig. (1b))⁴.

³For our case, one can conventionally set $N_0 = 1$.

⁴This would be trivial due to our first assumption, stating that such behavior is quantum mechanical.

3 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. (2)). 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.

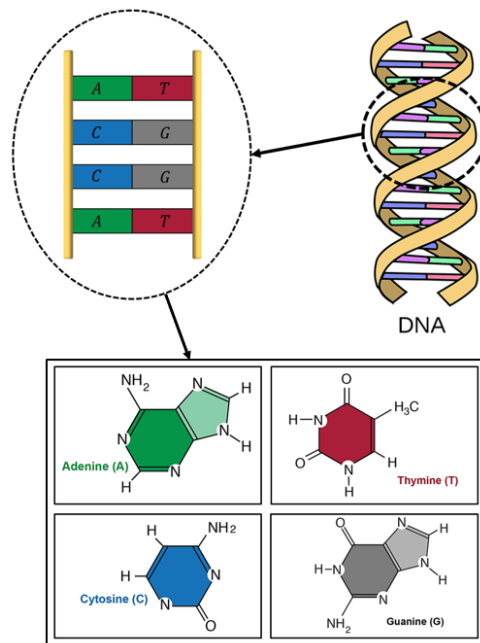


Figure 2: The structure of DNA (up, right), the nucleotide base pairs (up, left), and the chemical structure of the fundamental nucleotides (down).

In analogy to sec.(2), 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 eigenvalues of each cell's DNA by diagonalization of H:

$$\text{diag}(H) = \begin{pmatrix} \lambda_{AT}^{(1)} & 0 & 0 & \dots \\ 0 & \lambda_{GC}^{(2)} & 0 & \dots \\ 0 & 0 & \lambda_{GC}^{(3)} & \dots \\ 0 & 0 & 0 & \dots \end{pmatrix}_{L \times L} \quad (3.1)$$

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.(3)). 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 $L \rightarrow \infty$. We discuss a hermitian system in this limit with a unitary matrix of Gaussian distribution.

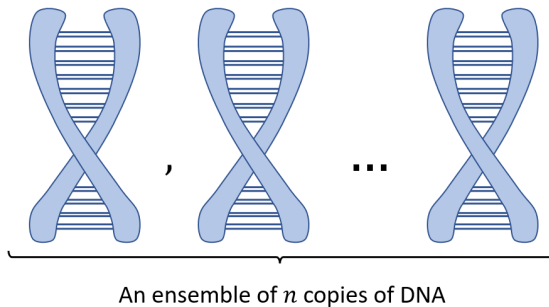


Figure 3: Here we consider an n copy of DNA sequences each with L bounds, as samples of a random matrix ensemble. Each sample represents AT and GC bounds with random energy eigenvalues taken from an $L \times L$ matrix (3.1) with positive and random entries.

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. (4)) 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*.

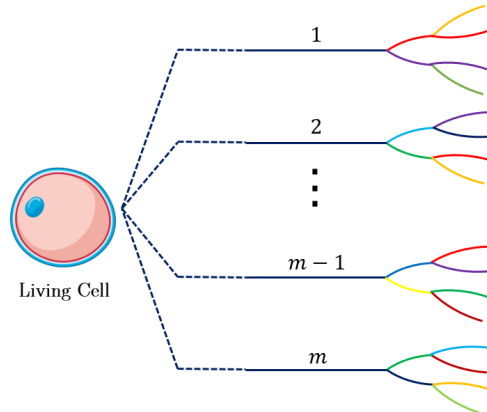


Figure 4: If the mechanism of decomposition of the living cell is assumed quantum mechanically then there are m possible states for the cell to choose. Each has its growth and probability weight. The states $1, 2, \dots, m$ have a growth analogous to fig.(1a) and can be represented by an RMT ensemble with a Gaussian distribution. It can be thought of as an ensemble of $n \gg 1$ copies of DNA each with L bindings.

3.1 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 $A \rightarrow C$ or $T \rightarrow G$ 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 stable⁵ if the largest eigenvalue of the random distribution is less than an inverse of the coupling constant of the system g :

$$\lambda_{max} < (g)^{-1} \quad (3.2)$$

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 theories⁶ in critical coupling constant which is known as Gross-Witten-Wadia (GWW) phase transition [40, 41].

⁵The 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.

⁶For a useful review of large-L gauge theories see [42].

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 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]:

$$\rho(\lambda) = \begin{cases} \frac{2}{\pi\tau} \cos \frac{\lambda}{2} \left(\frac{\tau}{2} - \sin^2 \left(\frac{\lambda}{2} \right) \right)^{1/2}, & \tau \leq 2 \\ \frac{1}{2\pi} (1 + \cos \lambda), & \tau = 2 \\ \frac{1}{2\pi} \left(1 + \frac{2}{\lambda} \cos \lambda \right), & \tau \geq 2 \end{cases} \quad (3.3)$$

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 $\tau \rightarrow 0$, the distribution is given by Wigner's semi-circle law:

$$\rho(\lambda) \simeq \frac{1}{\pi} \sqrt{1 - \lambda^2} \quad (3.4)$$

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 β -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 $\lambda = 2$.

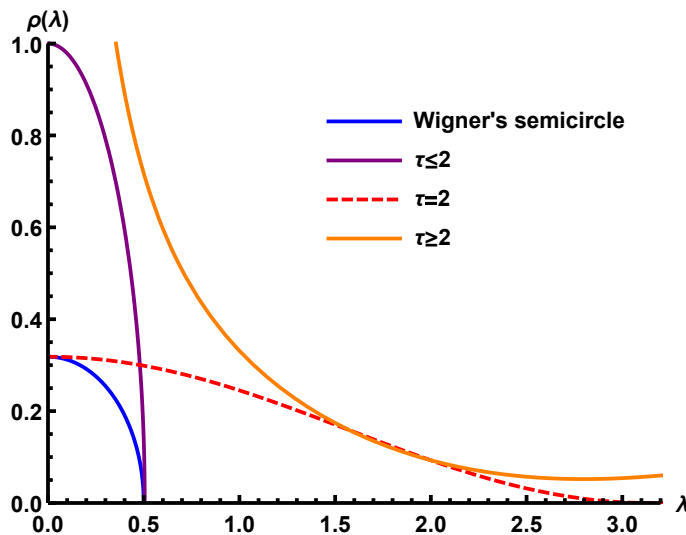


Figure 5: The density of eigenvalues for (3.3) and (3.4) is plotted. Semi-circle law and small coupling distributions are drawn for $\tau = 0.125$. For very small couplings, the semi-circle and $\tau \leq 2$ distributions almost behave the same close to λ_{max} which is a sharp edge with so many random 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 coulomb 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 κ with an average spacing \bar{a} . We adjust the average spacing \bar{a} and the coupling g in such a way that the tension of each bound remains fixed. Therefore we define an effective coupling $g(\bar{a})$ for DNA bindings such that $\kappa[\bar{a}, g(\bar{a})] = \kappa$.

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 ⁷. We assume that the amount of energy of each bond λ_{AT} and λ_{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 $\lambda_{GC} > \lambda_{AT}$), 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.

3.2 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. (6) and (7) (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 and 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 (9)), 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 (9) (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

⁷To see this, one can also write the density of energy eigenvalues $\rho(\lambda)$ and $\rho(\tilde{\lambda})$ in a Gaussian ensemble and calculate the pair correlation function $\rho_c(\lambda, \tilde{\lambda}) = \langle \rho(\lambda)\rho(\tilde{\lambda}) \rangle$ and take the limit $\lambda - \tilde{\lambda} \rightarrow 0$.

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.

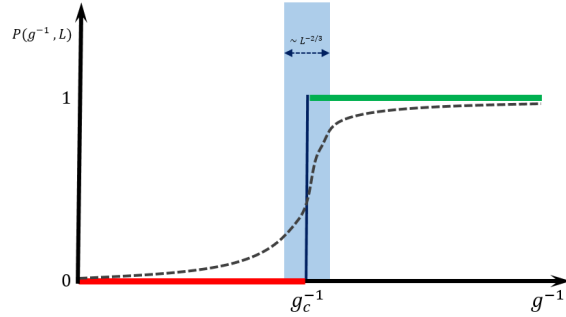


Figure 6: The probability of having $\lambda_{max} < (g)^{-1}$ between L eigenvalues in terms of g^{-1} . The three solid lines are for small L and the dashed line is for large but finite L . There is a critical value for g where the continuous phase transition can occur from the unstable (red line) 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.

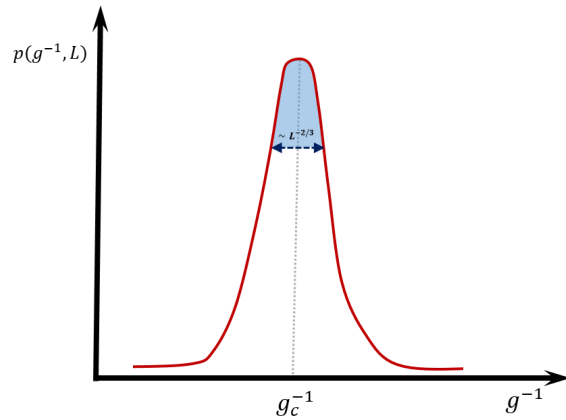


Figure 7: The probability density function for λ_{max} gives us the Tracy-Widom density around the critical value (blue region). The left and right tails are described by two different functions.

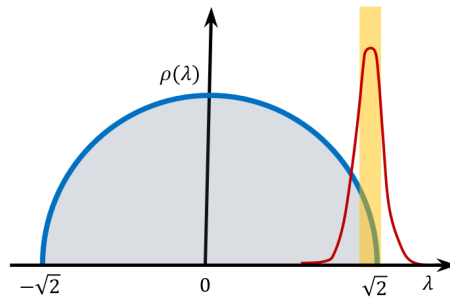


Figure 8: Wigner semi-circle law for density of eigenvalues (blue curve). The red curve shows the Tracy-Widom distribution near the edge (yellow bar) which is a perturbation around λ_{max} .

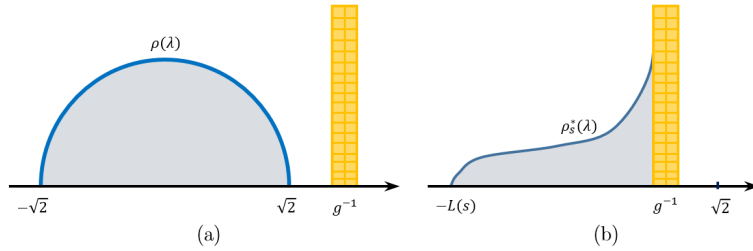


Figure 9: (a) Far away from the edge, the potential well does not affect the distribution and there would be no phase transition. (b) As the coupling changes, the potential will hit the semi-circle and cause a phase transition to a different distribution.

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.

4 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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