Statistical mechanics of DNA mutation using SUSY quantum mechanics

Kadiri Haritha and K V S Shiv Chaitanya

Department of Physics, BITS Pilani, Hyderabad Campus, Jawahar Nagar, Kapra Mandal, Medchal Dist, Hyderabad, Telangana 500 078, India
E-mail: chaitanya@hyderabad.bits-pilani.ac.in

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Abstract
This paper investigates the deoxyribonucleic acid (DNA) denaturation through statistical mechanics and demonstrates that the exceptional polynomials lead to DNA mutation. A DNA model with two chains connected by the Morse potential representing the H bonds is considered and the partition function for this model is computed. The partition function is converted into a Schrödinger-like equation. The techniques of SUSY quantum mechanics are used to model the DNA mutation. The thermal denaturation of DNA for each mutated state is also computed.

Keywords: Peyrard and Bishop model, SUSY quantum mechanics, DNA denaturation, DNA mutation

1. Introduction

The deoxyribonucleic acid (DNA) is a complex molecule composed of two nucleotide chains that form a spiral called double helix. In a nucleotide, the base is attached to a sugar and a phosphate molecule. The base is constituted of chemicals adenine (A), guanine (G), cytosine (C), and thymine (T). The sequence of these bases encodes instructions that determine the information available for building and maintaining an organism. DNA is a common molecule, that is present in all living organisms. Every cell contains a full set of DNA which directs the cell about the kind of proteins to be prepared this in turn is responsible for the functioning, growth and reproduction of all known organisms and many viruses. A noteworthy property of DNA is that it can replicate itself. A mutation may occur during this process. Damaged DNA can be mutated either by substitution, deletion or insertion of base pairs. The mutation that occurs due to substitution arises when the sequence of DNA is altered, while the deletion mutation occurs when one or more base pairs are lost. Insertion mutation being the reverse of deletion, occurs when one or more base pairs are inserted in a DNA sequence [1].
The significant field of study regarding the DNA is its thermal denaturation. It refers to the melting of double-stranded DNA into two single strands. The unwinding occurs when hydrogen bonds between the bases in a duplex break due to elevated temperatures. The study of thermal denaturation becomes crucial since it is considered the preliminary step for DNA transcription. The DNA helix stability is due to the packing of the bases on top of one another. In order to denature DNA, one must overcome these packing energies providing bond between the adjacent base pairs. Several models have been proposed in the literature to analyze the DNA denaturation; the original one uses soliton-like solutions [2]. Other popular model is by studying the DNA denaturation from a statistical mechanics point of view. DNA denaturation and non-linear excitation of bases are presented as a simple model by Peyrard and Bishop [3]. This model analyzed the variation of interstrand separation as a function of temperature. The degrees of freedom of DNA strands and the thermodynamics of non-linear DNA dynamics are explored [4]. The parameters that are used to derive the DNA denaturation temperature by statistical methods are determined experimentally [5]. The thermodynamic properties of DNA under the influence of hump-Morse potential are determined [6]. The helicoidal model of the DNA is reviewed by [7]. In the work done by El Kinani et al., the q-deformed Morse potential is regarded to describe the DNA denaturation and its statistical properties [8]. The Peyrard–Bishop (PB) model is extended to PB–Dauxois model [9] which has a rich literature on nonlinear physics with insight into the statistical approach; however, many revisions of the model have arrived to correlate with the results of the biological experiments [10] and references therein.

This paper presents a mathematical model for statistical mechanics of the DNA mutation employing supersymmetric quantum mechanics (SUSY-QM). The three types of mutations, viz substitution, deletion and insertion of base pairs, are interpreted in terms of SUSY-QM. The SUSY-QM can be classified into two types: (1) SUSY-QM with shape invariant potentials [11], (2) SUSY-QM without shape invariant potentials, which is defined in the literature in terms of codimension exceptional family [12]. SUSY-QM with shape invariance arises when the two Hamiltonians with potentials, known as partners, involve ordinary Laguerre/Jacobi polynomials or both involve exceptional Laguerre/Jacobi polynomials. However, in general the same holds good for other polynomials as well [13, 14]. SUSY-QM without shape invariance occurs when the two Hamiltonians with potentials, one partner having the solution as ordinary Laguerre/Jacobi polynomial and the other having exceptional Laguerre/Jacobi polynomial [15]. The same applies for other orthogonal polynomial families also [16, 17]. For a review of SUSY and more details, the reader may refer to [18, 19]. In supersymmetry, the superpotential $\mathcal{W}(x)$ is defined in terms of the intertwining operators $\hat{A}$ and $\hat{A}^\dagger$ as

$$\hat{A} = \frac{d}{dx} + \mathcal{W}(x), \quad \hat{A}^\dagger = -\frac{d}{dx} + \mathcal{W}(x). \quad (1)$$

The equation (1) allows one to define a pair of factorized Hamiltonians $H^\pm$ as

$$H^+ = \hat{A}\hat{A}^\dagger = -\frac{d^2}{dx^2} + \mathcal{V}^+(x) - E, \quad (2)$$
$$H^- = \hat{A}^\dagger\hat{A} = -\frac{d^2}{dx^2} + \mathcal{V}^-(x) - E, \quad (3)$$

where $E$ is the factorization energy. The partner potentials $\mathcal{V}^\pm(x)$ are related to $\mathcal{W}(x)$ by

$$\mathcal{V}^\pm(x) = \mathcal{W}^2(x) \mp \mathcal{W}'(x) + E. \quad (4)$$
where prime denotes differentiation with respect to \(x\). The equations (2) and (3) imply

\[
H^+ \hat{A}^\dagger = \hat{A}^\dagger H^- , \quad \hat{A}^+ H^+ = H^- \hat{A} .
\] (5)

From the above, one can see that the operators \(\hat{A}\) and \(\hat{A}^\dagger\) act as intertwining operators. These allow one to go from one wave function \(|\psi^+\rangle\) to the other \(|\psi^-\rangle\) and vice versa.

The discovery of new exceptional polynomials in the last decade by Gómez Ullate et al has given rise to a rich structure in SUSY quantum mechanics. The classification of exceptional orthogonal polynomials is given in terms of codimension exceptional family [12]. Codimension of the exceptional family is defined as the total number of the missing degrees in the polynomial sequence. These missing degrees in the polynomial put constraints on the Sturm–Liouville equation and in turn, on the Bochner theorem. It is shown that every exceptional orthogonal polynomial system is related to the respective classical orthogonal polynomials by a sequence of Darboux transformations. Further, every exceptional orthogonal polynomial system is related to classical orthogonal polynomial system by a sequence of Darboux transformations. Gómez Ullate et al showed that the exceptional orthogonal polynomial systems emerge as eigenfunctions of Sturm–Liouville problems [12, 20]. The reference [21] shows that the quantum mechanical problem which admits classical Laguerre/Jacobi polynomials as solutions for the Schrödinger equations, will also admit exceptional Laguerre/Jacobi polynomials as solutions having the same eigenvalues, but with the ground state missing after the modification of the potential. These new polynomials can be classified based on codimension. Quesne constructed the Darboux transformation for the family of polynomials of codimension-two [15, 22]. Later Odake and Sasaki constructed exceptional polynomials for polynomials of arbitrary codimension [23, 24]. In an earlier work done by [25], the application of exceptional potentials to the relativistic hydrogen atom and the Dirac oscillator has led to some exciting results. In the present case, both the Hamiltonians’ wave functions are known, the operator \(\hat{A}\) can be constructed from the following relation:

\[
\hat{A}^+ |\psi^+\rangle = E_\nu \hat{A} |\psi^+\rangle = E_{\nu+1} |\psi^+_{\nu+1}\rangle = H^- |\psi^-_{\nu+1}\rangle.
\] (6)

Using the operator \(\hat{Q} [12, 20, 22]\), which connects the ordinary Laguerre polynomials to the exceptional Laguerre polynomials,

\[
\hat{Q} L_{\nu+1}^k(x) = L_{\nu+1}^k(x),
\] (7)

where \(\hat{Q} = (x + k)(\frac{d}{dx} - 1) - 1\). The superpotential \(W(x)\), can be obtained by replacing \(\frac{d}{dx}\) in \(\hat{A}\) in terms of \(\hat{Q}\). Therefore, it should be clear to the readers that SUSY-QM has two Hamiltonians known as partners, mathematically related by an intertwining operator. In quantum mechanics, these two Hamiltonians correspond to two different states of the system; for instance, one is the ground state and another, the first excited state. But, in the study of statistical mechanics of DNA, the partition function of the DNA model with the Morse potential is converted into an Schrödinger-like equation using transfer integral (TI) method; here, no quantum mechanics is involved. Hence, there are no different quantum states. So the two partner Hamiltonians should correspond to the different sequencing of the base chemicals bonded by the hydrogen atoms. Therefore, a substitution DNA mutation in SUSY-QM is defined, as the two partner potentials that are related by shape invariance. The deletion mutation occurs when the shape invariance does not relate to the two partner potentials.
1.1. PB model

The DNA breathing dynamics are investigated by the PB model, where the base pairs are treated as coupled oscillators. The longitudinal displacements of bases are neglected as their amplitude of vibrations is much smaller than the amplitude of transverse vibration. A harmonic potential connects two neighboring nucleotides of the same strand. Later on, this term is modified by Dauxois to an anharmonic potential [9]. For those belonging to different strands, the Morse potential is used [3] to represent the transverse interaction of the bases in a pair. It represents the attraction between base pairs and the repulsion between the two phosphate groups on the opposite strands. A DNA model with transverse displacement in an $n$th nucleotide is considered. A harmonic potential is assumed to connect the two neighboring nucleotides of the same strand and the Morse potential for those belonging to different strands [3], to represent the transverse interaction of the bases in a pair indicating the hydrogen bonds. The model includes two degrees of freedom corresponding to the two bases of the base pair. Let the in-phase symmetrical mode coordinates are represented by $x_n$ and the out of phase anti-symmetrical mode coordinates are represented by $y_n$. They are computed as

$$x_n = (u_n + v_n)/\sqrt{2}, \quad y_n = (u_n - v_n)/\sqrt{2}, \quad (8)$$

here $u_n$ and $v_n$ indicate the transverse displacements of the bases from their equilibrium positions. A Hamiltonian is derived for the harmonic coupling between the neighboring bases.

$$H = \sum_{n=0}^{N} \left[ \frac{1}{2} m (\dot{u}_n^2 - \dot{v}_n^2) + \frac{1}{2} k [(u_n - u_{n-1})^2 + (v_n - v_{n-1})^2] + V(u_n - v_n) \right], \quad (9)$$

with $m$ being the reduced mass of the bases. This paper aims to model DNA mutation and compute the thermal denaturation for each mutated state by applying statistical mechanics. The classical partition function for the Hamiltonian is given by [3]

$$Z = Z_x Z_p Z_y Z_q = \int_{-\infty}^{+\infty} \prod_{n=1}^{N} e^{-\beta H(x_n, y_n, p_n, q_n)} \, dx_n \, dy_n \, dp_n \, dq_n. \quad (10)$$

The partition function can be decoupled. The momentum terms, being Gaussian integrals, can be integrated to yield

$$Z_p = Z_q = (2\pi m k_B T)^{N/2}. \quad (11)$$

The $X$-coordinate partition function can also be readily integrated

$$Z_x = \left( \frac{2\pi k_B T}{K} \right)^{N/2}. \quad (12)$$

The $Y$-coordinate partition function involves the potential term. Only the nearest neighbor interactions and one-dimensional system are considered

$$Z_y = \int_{-\infty}^{+\infty} \prod_{n=1}^{N} e^{-\beta f(y_n, y_{n-1})} \, dy_n, \quad (13)$$

where $f_{(n,n-1)}$ represents the potential energy component of $H_y$ and is given by

$$f_{(n,n-1)} = k \frac{1}{2} (y_n - y_{n-1})^2 + V_q(y_n). \quad (14)$$
The integral (13) is solved exactly in the thermodynamic limit ($N \to \infty$) by using the TI technique [26, 27], the eigenfunctions given by

$$Z_y = \int \bar{d}y_{n-1} e^{-\beta f(y_{n-1})} \phi_i(y_{n-1}) = e^{-\beta \epsilon_i} \phi_i(y_n).$$

(15)

An equation identical to the Schrödinger equation is obtained [27, 28]

$$-\frac{1}{2\beta^2 k} \frac{\partial^2 \phi_i(y)}{\partial y^2} + V(y) \phi_i(y) = (\epsilon_i - s_o - D) \phi_i(y),$$

(16)

with the Morse potential given by

$$V(y) = V_0(\exp(-2\beta y) - 2 \exp(-\beta y)).$$

(17)

here $\beta = 2a$ and $V_0 = D$ is taken. The comprehensive analysis of DNA breathing dynamics is carried out in the reference [29], where they have discussed the following drawbacks of PB model. In the PB model, the nucleotides are considered to be the beads tied with two types of non-linear springs representing the interactions between the bases within the base pair. The stacking interaction between the adjacent base pairs along the DNA chain in which the water encompassing the DNA chain is disregarded entirely. Dynamic equations are framed for the model treating the DNA chain to be in a vacuum. This paper gives the mathematical model of DNA mutation and it is well known that a mutation occurs when the DNA interacts with the environment. It is established in the physics literature, that the interaction of the system with the environment is modeled as a 'system plus bath', in terms of a master equation [31]. One way of solving the master equation is by converting it into Fokker–Planck or Langevin equations [31].

In the DNA literature, one model which includes these features is the Poland–Scheraga model. Below, a brief description of the Poland–Scheraga model, where the Fokker–Planck equation is reduced to Schrödinger equation [32] is given. Thus our modeling of the DNA dynamics reduced to Schrödinger equation incorporates mutation.

1.2. Poland–Scheraga model

Poland and Scheraga [30, 33] developed a simple model of the DNA denaturation transition. In this model, the equilibrium DNA double-helix structure stability is provided by the hydrogen bonding between the base pairs along the opposite strands called transverse interaction. The base stacking is along the same strand, longitudinal interaction. This double-stranded DNA gradually denatures by altering the temperature or the pH value. The temperature at which half of the DNA molecule has undergone denaturation is called the melting temperature $T_m$.

At room temperature, the double helix opens up into small denaturation zones due to thermal fluctuations [34]. This work aims at modeling DNA by a Schrödinger-like equation, therefore Poland–Scheraga model is followed in reference.

The DNA bubble comprises flexible DNA single strands and their size fluctuates step-wise fastening and unfastening of the base pairs. The on and off fluctuation of DNA bubble, in due course, closes below the melting temperature. The existence of intermittent bubble domains is crucial since the DNA base pairs’ opening by breaking the hydrogen bonds between complementary bases disrupts the helical stack. The ordered stack of the unpaired bases thus flips out, permitting the binding of specific chemicals or proteins by accessing the bases’ reactive sites, which otherwise would not have been possible [34, 35]. The size of the bubble stretches over a wide range, and above $T_m$, the individual bubble size steadily rises. The bubble merges with the neighboring bubbles till the denaturation is completed.
The DNA denaturation can be interpreted as a one-dimensional random walk with the assumption that the bubble fluctuations occur slower than the equilibrium of DNA single-strand bubbles. The experiments on DNA structure support such an assumption. Various models can be found in the literature where the DNA denaturation is modeled statistically. For instance, in [36], a sequence of bound segments and denatured loops represent the molecules. The excluded-volume interactions between the denatured loops are considered and a first-order phase transition in $d_2$ dimensions was identified, which is in agreement with the experimental results. Kafri and Mukamel [37] demonstrated a model which displays Griffiths singularity. This singularity is achieved in the limit of strong binding sites tending to infinity. At this temperature, the corresponding melting of long low-binding energy domains are finite and very large $\nu$, the model displays an additional unbinding transition at a high temperature. Fogedby et al [38] have derived the dynamics of DNA breathing based on the Poland–Scheraga model. The Fokker–Planck equation is analyzed in two regions. Low temperature limit presenting a canonical phase space approach defines the stochastic dynamics. The low temperature region below the transition temperature then corresponds to the continuum states of a repulsive Coulomb potential, while the region above $T_m$ corresponds to the lowest bound state in an attractive Coulomb potential. Thus, bubble lifetime distributions and the associated correlation functions were calculated below, at and above $T_m$. At $T_m$ the DNA bubble fluctuations correspond to a one-dimensional finite time singularity.

The model assumes a Grand canonical ensemble where the total length of the chain is allowed to fluctuate. The grand canonical partition function is given by

$$Z = \sigma_0 \mu^m (1 + m)^{-\epsilon},$$

where $m$ indicates the number of broken base pairs and $u = e^{-\gamma \beta}$ where $\beta = \frac{1}{kT}$, the Boltzmann factor, $\sigma_0 = \exp(-\beta \gamma_0)$ is the cooperativity factor, $\gamma_0$ is the boundary energy $\approx 8000$ cal mol$^{-1}$. In literature, the Poland–Scheraga model for DNA breathing is studied via continuous Fokker–Planck equation [10, 39]. The fluctuation dynamics of DNA denaturation are modeled by the Fokker–Planck equation which is converted into the Schrödinger equation with Coulomb potential. Through this model the bubble lifetime distributions and the associated correlation functions were calculated below, at and above $T_m$. At $T_m$ the DNA bubble fluctuations correspond to a one-dimensional finite time singularity.

The model assumes a Grand canonical ensemble where the total length of the chain is allowed to fluctuate. The grand canonical partition function is given by

$$Z = \sigma_0 \mu^m (1 + m)^{-\epsilon},$$

$$\frac{\partial \tilde{P}}{\partial t} = -\frac{1}{2} \frac{\partial^2 \tilde{P}}{\partial x^2} + \left( \frac{\mu}{x} - \epsilon \right) \tilde{P} + \frac{1}{2} \frac{\partial^2 \tilde{P}}{\partial x^2},$$

where $D$ is the kinetic coefficient and sets the time scale. The Fokker–Planck equation for the equation (19)

$$\frac{\partial P}{\partial t} = \frac{\partial}{\partial x} \left( \frac{\mu}{x} - \epsilon \right) P + \frac{1}{2} \frac{\partial^2 P}{\partial x^2}$$

close to $T_r$, reference temperature $= 37$ $^\circ$C $\mu \approx 1$ and $\epsilon \approx 2 (T/T_m - 1)$. Substituting $P = e^{\epsilon x} x^{-\mu} \tilde{P}$ in equation (20) gives

$$-\frac{\partial \tilde{P}}{\partial t} = \frac{1}{2} \frac{\partial^2 \tilde{P}}{\partial x^2} + \left( \frac{\mu(\mu + 1)}{2x^2} - \frac{\mu \epsilon}{x} + \frac{\epsilon^2}{2} \right) \tilde{P}.$$
This represents the imaginary time Schrödinger equation of unit mass particle in the potential \( V(x) = \mu (x + 1) / 2x^2 - \mu x + e^2 / 2 \) subjected to a centrifugal barrier \( \mu (x - 1) / x^4 \) for an orbital state with an angular momentum \( \mu \) and Coulomb potential \(-\mu x / x\). Coulomb potential can be mapped to Morse potential by a point canonical transformation \( x = \exp(\alpha r) \)

\[
V_\text{coul}(r) = \frac{\epsilon^2}{2} + \mu (\mu + 1) \exp(-2\alpha r) - \mu \epsilon \exp(-\alpha r).
\]

In the next section, the simple model of DNA mutation is presented.

### 2. The simple model of DNA mutation

The mathematical model of DNA mutation is studied using the PB model. Damaged DNA can be mutated either by substitution, deletion or insertion of base pairs. The mutation that occurs due to substitution generally happens when the sequence of DNA is altered. In order to demonstrate the substitution mutation mathematically the techniques of SUSY-QM are used. The dynamics of PB model reduces to the Schrödinger-like equation

\[
-\frac{1}{2} \frac{d^2 \phi_i(y)}{dy^2} + V(y) \phi_i(y) = (\epsilon_i - s_0 - D) \phi_i(y),
\]

with the Morse potential given by

\[
V(y) = V_0(\exp(-2\beta y) - 2 \exp(-\beta y)),
\]

the wave function \( \phi_i(y) \) corresponds to the \( i \)-th eigenstate, with the corresponding eigenvalue \( \epsilon_i \) and \( s_0 = \frac{1}{\beta} \ln \frac{a}{b} \) being the lowest eigenvalue. In the analysis of DNA denaturation, finding the eigenstate of finite norm is the only interest. The Schrödinger-like equation (23) is solved using the methods of SUSY-QM [18, 19]. The ground state wave function for the Morse potential is obtained by \( A \psi_0 = 0 \), where \( A \) is defined in equation (1) which is true up to a multiplicative constant. The superpotential for the Morse oscillator is given by

\[
\mathcal{W}(x) = a - be^{(-\alpha x)},
\]

then the potential is given by

\[
V_0(x, a) = W^2(x, a) - W'(x, a) = a^2 - 2b \left(a + \frac{1}{2} \alpha \right) e^{-\alpha x} + b^2 e^{-2\alpha x}.
\]

The partner potential is obtained by scaling \( a \) to \( a - \alpha \)

\[
V_1(x, a) = W^2(x, a) + W'(x, a) = a^2 - 2b \left(a - \frac{1}{2} \alpha \right) e^{-\alpha x} + b^2 e^{-2\alpha x}.
\]

Thus, the eigenfunctions are computed as

\[
\psi_0(x, a) = \left( \frac{2b}{\alpha} e^{-\alpha x} \right) \frac{\alpha}{\pi} e^{-\frac{1}{2} \frac{\alpha}{b} e^{-\alpha x}} = y(x) \frac{\alpha}{\pi} e^{-\frac{1}{2} y(x)},
\]

and the first excited state is computed as

\[
\psi_1(x, a) = (E_1 - E_0) \frac{1}{\pi} A^* (x, a) \psi_0(x, f(a))
\]

\[
= \left( \frac{2a}{\alpha} - 1 \right)^{\frac{1}{2}} y(x) \frac{\alpha}{\pi} e^{-\frac{1}{2} y(x)} \left( \frac{2a}{\alpha} - 1 - y(x) \right).
\]
In general, any state is computed as

\[ \psi_m = \prod_{i=1}^{m} \left( (E_m - E_{i-1}) \frac{1}{2} \left( -\frac{d}{dx} + W(x, f^{(i-1)}a) \right) \right) \psi_0(x, a - \alpha m) \tag{30} \]

\[ = y(x) e^{-\frac{1}{2} \gamma(x)} L_{m}^{(\frac{1}{2} - m)}(y(x)), \tag{31} \]

where

\[ E_m = \sum_{k=1}^{m} (a - (k - 1)\alpha)^2 - (a - k\alpha)^2 = a^2 - (a - m\alpha)^2, \tag{32} \]

with \( y(x) = \frac{2b}{\alpha} e^{-\alpha x} \) and \( L_{m}^{(\frac{1}{2} - m)}(x) \), the Laguerre polynomials \([18, 19] \). In this case \( a^2 = b^2 = D \) and \( \alpha = \beta \), with \( m = m_{\text{max}} < \infty \) for the Morse potential. The energy eigenvalues \( E_{m=m_{\text{max}}} \) form a finite set, \( E_{m_{\text{max}}} \) is the maximum allowed physical energy. Hence the partition function \((15)\) becomes

\[ Z_\gamma = \sum_{i=1}^{m} \int dy_{n-1} e^{-\beta \left( (E_n - E_{i-1}) \frac{1}{2} \left( -\frac{d}{dy} + W(y, f^{(i-1)}a) \right) \right) \phi_i(y_{n-1})} = e^{-\beta \alpha} \phi_0(y_n). \tag{33} \]

The eigenvalues are given by

\[ \epsilon_n = \frac{1}{2\beta} \ln \frac{\beta k}{2\pi} + \frac{a}{\beta} \sqrt{\frac{2D}{k} - \frac{a^2}{2\beta^2 k}}, \tag{34} \]

and

\[ s_\gamma = \frac{1}{2\beta} \ln \frac{\beta k}{2\pi}. \tag{35} \]
The normalized eigenfunction for the ground state is calculated to be

\[ \phi_0(y) = (\sqrt{2}a)^{1/2} \frac{2d^{(d-1/2)}}{[I(2d - 1)]^{1/2}} \exp(-d e^{\sqrt{2}ay}) \exp(-d - 1/2)\sqrt{2}ay. \]  \hspace{1cm} (36)

The free energy for the ground state is computed as

\[ f = \epsilon - K_b T \left[ N \ln(2\pi mK_bT) + \frac{N}{2} \ln \left( \frac{2mK_bT}{K} \right) \right]. \]  \hspace{1cm} (37)

The first excited eigenfunction of the Morse potential is given by

\[ \phi_1(y) = (\sqrt{2}a)^{1/2} \frac{(2d)^{d-3/2}}{[(2d - 2)(2d - 3)Γ(2d - 3)]^{1/2}} \exp(-d e^{\sqrt{2}ay}) \exp(-d - 1/2)\sqrt{2}ay(1 - \sqrt{2d} \exp(-2ay)). \]  \hspace{1cm} (38)

The free energy is defined by

\[ f = -K_b T \ln(Z_xZ_yZ_xZ_y). \]  \hspace{1cm} (39)

The free energy of the first excited state is given by

\[ f = \epsilon \ln \left[ \frac{(\sqrt{2}a)^{1/2} (2d)^{d-3/2}}{[(2d - 2)(2d - 3)Γ(2d - 3)]^{1/2}} \exp(-d e^{\sqrt{2}ay}) \right. \\
\left. \times \exp \left( - \left( d - \frac{1}{2} \right) \sqrt{2}ay \right) \left( 1 - \sqrt{2d} \exp(-2ay) \right) \right] \\
- \frac{N K_b T \ln(2\pi m K_b T \pi)}{\sqrt{\pi K}}. \]  \hspace{1cm} (40)

The denaturation temperature is evaluated as average stretching of base pairs with respect to temperature for different values of coupling constants by plotting the \( \langle y \rangle \) with temperature by fixing the values of \( \beta = \frac{1}{k_b T}, a = 1.8 \text{ Å}^{-1} \) and force constant to be

\[ K = 2 \times 10^{-3} \text{ eV Å}^{-2}, 3 \times 10^{-3} \text{ eV Å}^{-2}, 4 \times 10^{-3} \text{ eV Å}^{-2}, \]  \hspace{1cm} (41)

where \( \langle y \rangle \) is given by

\[ \langle y \rangle = \int y \phi_1(y) dy. \]  \hspace{1cm} (42)

In the figure 1, \( \langle y \rangle \), is plotted with respect to temperature for the ground state wave function (36) with different values of coupling constant.

In the figure 2, \( \langle y \rangle \), is plotted with respect to temperature, for the first excited state wave function (38) with different values of coupling constant. For the first excited state, the K values that are used are \( K = 10 \times 10^{-3}, 11 \times 10^{-3} \) and \( 12 \times 10^{-3} \) and \( a = 0.8 \text{ Å}^{-1} \). It is clear from the equation (33) when \( i = 1 \) one gets the ground state and \( i = 2 \) corresponds to first excited state and so on. The mutation that occurs due to substitution generally happens when the sequence of DNA is altered. From the partition function (33), it is clear that if the value of \( i \) is altered from 1 to 2, one goes from the ground state to the first excited state. When the DNA changes from the ground state to the first excited state, the wave function changes, so does the potential. It is
clear from equations (26) and (27), the shape of potential in the Schrödinger equation (23) is unchanged and differs by a constant. In turn this does not change the Schrödinger equation (23). It is clear from equations (21) and (22) that the Coulomb and the Morse potentials are related by point canonical transformation. It is well known that the orbital structure of the atom is related to the eigenfunctions of the Coulomb potential [40]. A change in the eigenfunction leads to a change in the orbital structure. Similarly, the change in the eigenfunction of the Schrödinger equation (23) corresponds to altering the sequence in DNA, which in turn reflects in the chemical bonds. Thus it is inferred that this corresponds to a substitution mutation. Therefore, it is concluded that a mutation occurs when the DNA undergoes a transition from the ground state to the first excited state. Readers should note that the spherical symmetry is absent in our model.

3. Mutation by deletion

The deletion mutation occurs when one or more base pairs are lost and this is modeled using SUSY-QM without shape invariance. Here, one partner potential corresponds to the Laguerre polynomials and another partner potential corresponds to the exceptional Laguerre polynomials. Laguerre polynomials and exceptional Laguerre polynomials both form complete sets in the infinite dimensional Hilbert space but one state missing in the latter with respect to the former. The ground state is dropped as the Schrödinger equation (23) goes from Laguerre polynomials to the exceptional Laguerre polynomials. This corresponds to a loss of nucleotide or base pairs; hence this mutation corresponds to Deletion. On reparametrizing $y$ in the Schrödinger equation (23), also known as Liouville transformation [41],

$$z = \sqrt{2d} \exp(-2ay), \quad (43)$$

by introducing a dimensionless variable $\rho = \frac{z}{\sqrt{n}}$, such that the equation (23) reduces to the associated Laguerre differential equation given by

$$\rho F''(\rho) + [2s + 1 - \rho]F'(\rho) - \left(s + \frac{1 - \sqrt{2d}}{2}\right)F(\rho) = 0, \quad (44)$$
where \( F(\rho) = \phi_0(y(z(\rho))) \) and the solutions are Laguerre polynomials and are given by
\[
\phi_n(\rho) = N_n \rho^{-\frac{1}{2}} L_n^{2\lambda}(\rho),
\] (45)
where the eigenvalues are given in the equations (34) and (35), \( \nu = \sqrt{2d} \), and \( s = \frac{1}{2} \). In order to find the exceptional Laguerre polynomial as the solution to the Schrödinger equation (23) the following theorem is applied [21]: by adding an extra term \( V_e(\chi) \) to the Laguerre/Jacobi differential equation and demanding the solutions to be
\[
F(\rho) = \phi_n(\rho) + (n + V_e) \phi_n(\rho) = 0,
\] (46)
setting \( 2s = m \) and \( n = \lambda - 1 \) and by demanding the solution to the differential equation to be
\[
H(\rho) = \frac{\phi_n(\rho)}{\rho + m},
\] (47)
where \( H(\rho) \) satisfies the \( X_1 \) exceptional Laguerre differential equation,
\[
-xf''(\rho) + \left( \frac{\rho - m}{\rho + m} \right) \left[ (m + \rho + 1)f'(\rho) - f(\rho) \right] = (n - 1)f(\rho).
\] (48)
The eigenfunction is given by
\[
\phi_0^e(\zeta) = \left[ \frac{1}{(2d - 1)^{\frac{1}{2}}} \right] \left( \sqrt{2d} \right)^{\frac{1}{2}} \left( 2d - 1 \right)^{\frac{1}{2}} \exp\left( -d\nu \zeta \right) L_0(z),
\] (49)
where \( s = \sqrt{2d} \).
\[
\phi_0^e(\zeta) = \left( \sqrt{2d} \right)^{\frac{1}{2}} \left( 2d - 1 \right)^{\frac{1}{2}} \exp\left( -d\nu \zeta \right)
\times \exp\left[ - \left( d - \frac{1}{2} \right) \zeta \right] L(\gamma),
\] (50)
which determines \( V_e(\rho, m) \) to be
\[
V_e(\rho, m) = \frac{2m}{(\rho + m)^2} - \frac{1}{\rho + m}.
\] (51)
Substituting \( m = 2s \) the exceptional partner potential is obtained as
\[
V_e(\zeta, s) = \frac{4s}{(\zeta/n + 2s)^2} - \frac{1}{\zeta/n + 2s}.
\] (52)
We see that the potential depends on the quantum number \( n \) and thus the Morse potential is a conditionally or quasi exactly solvable model. Recently Quesne [42] has shown that Morse potential is a quasi exactly solvable model. In our model for DNA, the conditionally exactly solvable model makes sense as the new state of DNA that is, exceptional Laguerre polynomials...
Figure 3. Variation of $\langle y \rangle$ as a function of temperature for three values of coupling constant $K$.

has the signature of the old state, that is Laguerre polynomials. The free energy per site for the new state of DNA with exceptional potential is given by

$$f = -k_B T \left[ N \ln(2\pi m k_B T) + \frac{N}{2} \ln \left( \frac{2m k_B T}{K} \right) + \sum_{a=1}^{N} -\beta \epsilon_i \ln(\phi_i(z_a)) \right]. \quad (53)$$

Considering the ground state for the exceptional potential, that is $\phi_0^*(z)$ and free energy is given by

$$f = \epsilon \ln \left[ \frac{(\sqrt{2a})^{d-1}}{2d - 1 + \sqrt{2d} \exp(-2\alpha y)} \frac{(2d)^{d-\frac{1}{2}}}{\Gamma(2d-1)^{\frac{1}{2}}} \exp(-de^{-\sqrt{2}ay}) \right. 
\times \exp \left( -\left( d - \frac{1}{2} \right) \sqrt{2\alpha y} \right) \left( 1 - \sqrt{2d} \exp(-2\alpha y) \right) 
\left. - \frac{NK_B T}{\sqrt{\pi K}} \ln \left( \frac{2\pi m k_B T}{k_B T} \right) \right]. \quad (54)$$

The denaturation temperature is computed by plotting average stretching of base pairs with respect to temperature for different values of coupling constants $\langle y \rangle$,

$$\langle y \rangle = \int y \phi_0^*(y) dy, \quad (55)$$

with temperature by fixing the values of $\beta = \frac{1}{k_B T}, \quad a = 1.8 \ \AA^{-1}$ and force constant to be

$$K = 5 \times 10^{-3} \text{ eV } \AA^{-2}, \ 6 \times 10^{-3} \text{ eV } \AA^{-2}, \ 7 \times 10^{-3} \text{ eV } \AA^{-2}. \quad (56)$$

In the figure 3, $\langle y \rangle$ is plotted with respect to temperature for the exceptional potential ground state (50). In this case, it is noticed that the exceptional potential denaturation of DNA strands occurs at lower temperatures when compared to the standard potential.
Figure 3 shows $\langle y \rangle$ plotted against the temperatures for different values of $K$. From the above discussion it is concluded that when the solution for the DNA Hamiltonians are Laguerre polynomials and exceptional Laguerre polynomials respectively, a deletion mutation occurs when the DNA undergoes a transition from the ground state (36) to the ground state (50). In this case, the wave functions for both the Hamiltonians are known and one can construct the operator $\hat{A}$ from the following relation

$$\hat{A}H^+|\psi^+_{\nu}\rangle = E^+_{\nu}\hat{A}|\psi^+_{\nu}\rangle = H^-|\psi^-_{\nu+1}\rangle = E^-_{\nu+1}|\psi^-_{\nu+1}\rangle,$$

(57)

using the operator $\hat{O}$ [12, 15, 20], which connects the ordinary Laguerre polynomials to the exceptional Laguerre polynomials

$$\hat{O}L^{k-1}_{\nu}(x) = L^k_{\nu+1}(x),$$

(58)

where $\hat{O} = (x + k)(\frac{d}{dx} - 1) - 1$. It is also asserted that the addition mutation is the converse of the deletion mutation that is applying $\hat{O}^\dagger$ on exceptional Laguerre polynomials. As one can see that the new state is the ordinary Laguerre polynomials with an additional new state, hence an addition mutation.

4. Conclusion

In this paper, DNA denaturation through statistical mechanics has been investigated and shown that exceptional polynomials lead to DNA mutation. The DNA model with two chains connected by the Morse potential depict the H bonds. Then the partition function is calculated and converted it into a Schrödinger-like equation. By exploiting SUSY quantum mechanics techniques, a mathematical model for DNA mutations is developed. Then the evaluation of free energy and the denaturation temperature of DNA for each mutated state. A substitution mutation occurs when DNA undergoes a transition from the ground state to the first excited state has been demonstrated. The change in the eigenfunction of the Schrödinger equation (23) corresponds to altering the sequence in DNA, which in turn reflects in the chemical bonds. The deletion mutation occurs when the DNA undergoes a transition from the ground state (36) to the ground state (50), and it can be achieved through an operator $\hat{O}$ which connects the ordinary Laguerre polynomials to the exceptional Laguerre polynomials

$$\hat{O}L^{k-1}_{\nu}(x) = L^k_{\nu+1}(x),$$

(59)

where $\hat{O} = (x + k)(\frac{d}{dx} - 1) - 1$. An addition mutation occurs when the DNA undergoes a transition from the ground state (50) to the ground state (36). It can be achieved through an operator $\hat{O}^\dagger$ on exceptional Laguerre polynomials. The dependence of denaturation temperature on the inter-strand separation has been presented. The curve has a non-linear rise far before the rise occurred. The application of exceptional potential involves the dropping of the ground state of the DNA. Theoretically, there is a mutation of DNA involved in this process, wherein there is an alteration in the base units of DNA. The mean stretching of hydrogen bonds $\langle y \rangle$ of the ground state and the first excited state of the eigenfunction have been determined. The mean stretching of a new state has been calculated. It should be noted that it is not an excited state of the earlier state but it is a new state whose ground state is eliminated due to exceptional potential. The dependence of mean stretching of hydrogen bonds corresponding to a new state on temperature is plotted and found that the denaturation occurs only for higher coupling constant values. The role of exceptional polynomials is to delete the ground state of the function. Hence, we claim the occurrence of Mutation in the DNA.
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Data availability statement

No new data were created or analysed in this study.

ORCID iDs

K V S Shiv Chaitanya https://orcid.org/0000-0002-6447-2010

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