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A STUDY OF THE LINEAR FREE ENERGY MODEL FOR DNA STRUCTURES USING THE GENERALIZED HAMILTONIAN FORMALISM

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We generalize the results of Nesterenko [13, 14] and Gogilidze and Surovtsev [15] for DNA structures. Using the generalized Hamiltonian formalism, we investigate solutions of the equilibrium shape equations for the linear free energy model.

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1. INTRODUCTION

The elastic properties of DNA are very important in molecular physics. Hence, the elastic theories have been much used for studying the DNA structures in recent years. The elastic model of DNA represents the DNA molecule as a thin elastic rod. Scientists use DNA as a tool to study the theory of elasticity. Recently, our understanding of DNA structures has increased. It is now possible to measure the elastic properties of DNA with the modern experimental developments such as optical tweezer methods and atomic force microscopy [1–6].

The importance of the computation of free energy for DNA structures has been known in many researches. Using the geometrical properties of DNA, we are able to determine the exact form of its free energy function. Many biopolymer chains, such as DNA, are linear, i. e., the chain length is much larger than the width. Consequently, we can describe them by 1-dimensional smooth curves. Hence, the total free energy F_{total} for a biopolymer chain can be written on a smooth curve $x(s)$ in 3-dimensional flat space in the form

$$F_{total} = \int F\left[x(s)\right] ds, \tag{1}$$

where s is arc length of the biopolymer chain and F is the free energy function, which depends on $x(s)$. On the other hand, a smooth curve in Euclidean space has two local invariants, the curvature $k = k(s)$ and the torsion $\tau = \tau(s)$. The curvature and torsion, i. e., the principal curvatures, encode all geometric information of a curve. Hence, the shape of a biopolymer chain is usually characterized by its curvature and torsion. Therefore, the free energy can be expressed as the general form $F = F(k, \tau, k', \tau')$ that depends on the curvature, torsion, and their derivatives (with the prime standing for the derivative with respect to s). In this analysis, we use a natural parameterization of the curve $x(s)$ in Euclidean space $x^i(s)$, $i = 1, 2, 3$. In this parameterization, we have[1)]

$$\frac{dx_i}{ds}\frac{dx_i}{ds} = 1, \tag{2}$$

where summation over repeated indices is always understood. As is well known from differential geometry, the curvature and torsion are defined as [7–9]

$$k = \sqrt{\frac{d^2x_i}{ds^2}\frac{d^2x_i}{ds^2}}\,, \tag{3}$$

and

$$\tau = \frac{\sqrt{\det(d_{ij})}}{k^2}\,, \tag{4}$$

where $d_{ij} = x_k^{(i)} x_k^{(j)}$, with $x^{(i)} = d^i x/ds^i$ and $i, j, k = 1, 2, 3$.

A biopolymer chain can be identified with the equilibrium shape equations. Hence, these equations play a vital role in understanding the properties of biomolecules [10]. The equilibrium shape equations of

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1) In flat spacetime, we have $x^i = x_i$.

a biopolymer chain are obtained by taking the variation of the total free energy, i. e., $\delta F_{total} = 0$. The variation of this function can be written as

$$\int \frac{\partial F}{\partial k}\,\delta k\,ds + \int \frac{\partial F}{\partial \tau}\,\delta\tau\,ds + \int \frac{\partial F}{\partial k'}\,\delta k'\,ds + \\ + \int \frac{\partial F}{\partial \tau'}\,\delta\tau'\,ds + \int F\delta\,ds = 0. \quad (5)$$

Thamwattana et al. [11] obtained the equilibrium shape equations for the general $F = F(k, \tau, k', \tau')$ in the form

$$\frac{d^2}{ds^2}\left[\frac{\partial F}{\partial k} - \frac{d}{ds}\left(\frac{\partial F}{\partial k'}\right)\right] + \frac{2\tau}{k} \times \\ \times \frac{d^2}{ds^2}\left[\frac{\partial F}{\partial \tau} - \frac{d}{ds}\left(\frac{\partial F}{\partial \tau'}\right)\right] - \left(\frac{2k'\tau}{k^2} - \frac{\tau'}{k}\right) \times \\ \times \frac{d}{ds}\left[\frac{\partial F}{\partial \tau} - \frac{d}{ds}\left(\frac{\partial F}{\partial \tau'}\right)\right] + (k^2 - \tau^2)\left[\frac{\partial F}{\partial k} - \frac{d}{ds}\left(\frac{\partial F}{\partial k'}\right)\right] + \\ + 2k\tau\left[\frac{\partial F}{\partial \tau} - \frac{d}{ds}\left(\frac{\partial F}{\partial \tau'}\right)\right] + \\ + k\left(k'\frac{\partial F}{\partial k'} + \tau'\frac{\partial F}{\partial \tau'} - F\right) = 0, \quad (6)$$

and

$$-\frac{d^3}{ds^3}\left[\frac{\partial F}{\partial \tau} - \frac{d}{ds}\left(\frac{\partial F}{\partial \tau'}\right)\right] + \frac{2k'}{k} \times \\ \times \frac{d^2}{ds^2}\left[\frac{\partial F}{\partial \tau} - \frac{d}{ds}\left(\frac{\partial F}{\partial \tau'}\right)\right] + 2k\tau\frac{d}{ds}\left[\frac{\partial F}{\partial k} - \frac{d}{ds}\left(\frac{\partial F}{\partial k'}\right)\right] + \\ + \left[\frac{k''}{k} - 2\left(\frac{k'}{k}\right)^2 - k^2 + \tau^2\right]\frac{d}{ds}\left[\frac{\partial F}{\partial \tau} - \frac{d}{ds}\left(\frac{\partial F}{\partial \tau'}\right)\right] + \\ + k\tau'\left[\frac{\partial F}{\partial k} - \frac{d}{ds}\left(\frac{\partial F}{\partial k'}\right)\right] - \\ - kk'\left[\frac{\partial F}{\partial \tau} - \frac{d}{ds}\left(\frac{\partial F}{\partial \tau'}\right)\right] = 0. \quad (7)$$

These equations are the equilibrium shape equations of biopolymer chains.

Feoli et al. [12] studied the free energy function $F = F(k)$ that depends only on curvature and tried to answer the following question: "*Is it possible to determine the free energy function in such a way that the extremals of function* (1) *would be only helices*?" They showed that the answer is positive and the free energy should be a linear function of the curvature, $F(k) = a + bk(s)$, where a and b are constants.

Taking the linear nature of DNA into account, it seems that the linear free energy model of curvature and torsion can be a simple (but important) candidate for describing the DNA structure. This motivates our interest in investigating solutions of the equilibrium shape equations for a linear free energy model. We now discuss the free energy of a biopolymer chain within the general linear model as

$$F = m + \alpha k + \beta\tau, \quad (8)$$

where α, β, and m are arbitrary constants. This model has been studied previously in [11]. After some calculations, Eqs. (6) and (7) are transformed into

$$\alpha\tau^2 - \beta k\tau + mk = 0, \quad (9)$$

and

$$\alpha\tau' - \beta k' = 0. \quad (10)$$

By integrating the last equation, we can obtain

$$\tau = \frac{\beta}{\alpha}\,k + C, \quad (11)$$

where C is a constant of integration. The sign of this constant determines the chirality of the corresponding curves. It has been shown that there are only two equations, i. e., (9) and (11), which contain four unknown constants α, β, m, and C. Therefore, more relations among the variables are required. For this, the generalized Hamiltonian formalism is used in the next section.

2. CALCULATION OF THE FIRST CASIMIR INVARIANT IN THE GENERALIZED HAMILTONIAN FORMALISM

The generalized Hamiltonian formalism has been attracting interest in recent years. A considerable amount of work has been devoted to the study of this formalism.

Nesterenko [13,14] and Gogilidze and Surovtsev [15] separately studied the motion of a relativistic particle by using the generalized Hamiltonian formalism for a linear lagrangian model with $\mathcal{L} = c_1 k + c_2\tau + c_3$, where c_i are constants. They calculated the Casimir invariants by using a complete set of constraints in the phase space. In this section, we develop their results for the linear free energy model in (8). We recall that the free energy defined in such a way is analogous to the action in quantum field theory [12, 16].

Also, Golo and Kats [17] simulated a DNA molecule as an anisotropic elastic fiber. They showed that the system Hamiltonian of the DNA molecule consists of Kirchhoff's classical elastic energy and the energy of a quantum anisotropic chain of "spins" 1/2. First, we intend to give a short review of the generalized Hamiltonian formalism. This formalism has been shown to naturally arise from the Euler–Lagrange equations writ-

ten in terms of an arbitrary parameter. Hence, an arbitrary parameterization of the curve $x(\sigma)$ with an arbitrary parameter σ is employed. In this parametric representation, Eqs. (2)–(4) become

$$\frac{d}{ds} = \frac{1}{\sqrt{\dot{x}^2}}\,\frac{d}{d\sigma} \tag{12}$$

and

$$k = \sqrt{\frac{\dot{x}^2\ddot{x}^2 - (\dot{x}\ddot{x})^2}{(\dot{x}^2)^3}}\,, \tag{13}$$

$$\tau = \frac{\varepsilon_{ijk}\dot{x}_i\ddot{x}_j\dddot{x}_k}{\dot{x}^2\ddot{x}^2 - (\dot{x}\ddot{x})^2}\,, \tag{14}$$

where $\dot{x}^2 = \dot{x}_i\dot{x}_i$ while the dot over x denotes the derivative with respect to σ, and ε_{ijk} is a totally antisymmetric unit tensor, $\varepsilon_{123} = +1$. In this representation, the total free energy function (1) has the form

$$F_{total} = \int \sqrt{\dot{x}^2}\,F(k,\tau)\,d\sigma. \tag{15}$$

As a result, it can be shown that function (15) is invariant under translations of the curve coordinates by a constant vector [12, 18]. Using the Noether theorem [12, 16], we can show that the invariance of the total free energy function under these translations implies the conservation of the momentum vector under the motion along the curve $x(\sigma)$.

With Eqs. (8), (13), and (14), relation (15) can be written in the form

$$F_{total} = \alpha\int \frac{\sqrt{\dot{x}^2\ddot{x}^2 - (\dot{x}\ddot{x})^2}}{\dot{x}^2}\,d\sigma + \\ + \beta\int \sqrt{\dot{x}^2}\frac{\varepsilon_{ijk}\dot{x}_i\ddot{x}_j\dddot{x}_k}{\dot{x}^2\ddot{x}^2 - (\dot{x}\ddot{x})^2}\,d\sigma + m\int\sqrt{\dot{x}^2}\,d\sigma. \tag{16}$$

We see that this function depends on third-order derivatives of the coordinates. We construct the generalized Hamiltonian formalism for our model including the higher derivatives in accordance with the Ostrogradsky method [19–21]. The canonical variables are then defined as follows:

$$q_{1i} = x_i, \quad q_{2i} = \dot{x}_i, \quad q_{3i} = \ddot{x}, \tag{17}$$

$$p_{1i} := P_i = -\frac{\partial\left(\sqrt{\dot{x}^2}\,F\right)}{\partial\dot{x}_i} - \frac{dp_{2i}}{d\sigma}, \tag{18}$$

$$p_{2i} = -\frac{\partial\left(\sqrt{\dot{x}^2}\,F\right)}{\partial\ddot{x}_i} - \frac{dp_{3i}}{d\sigma}, \tag{19}$$

$$p_{3i} = -\frac{\partial\left(\sqrt{\dot{x}^2}\,F\right)}{\partial\dddot{x}_i}. \tag{20}$$

From the definition of the canonical momentum p_3, we have

$$p_{3i} = -\frac{\beta\sqrt{q_2^2}}{q_2^2q_3^2 - (q_2q_3)^2}\,\varepsilon_{ijk}q_{2j}q_{3k}, \tag{21}$$

where $q_2q_3 = q_{2i}q_{3i}$.

Nesterenko [14, 22] showed that function (16) is invariant under Poincaré transformations and under reparameterizations $\sigma \to f(\sigma)$ with an arbitrary function $f(\sigma)$. As a result, there should be the constraints in the phase space [22–24].

By projecting Eq. (21) onto q_2 and q_3, the following three primary constraints are easily obtained:

$$\Sigma_1^1 = p_3q_2 = 0, \tag{22}$$

$$\Sigma_2^1 = p_3q_3 = 0, \tag{23}$$

$$\Sigma_3^1 = \varepsilon_{ijk}p_{3i}q_{2j}q_{3k} - \beta\sqrt{q_2^2} = 0. \tag{24}$$

According to Ostrogradsky method, the canonical Hamiltonian has the form [13–15]

$$H_c = -p_1\dot{x} - p_2\ddot{x} - p_3\dddot{x} - \sqrt{\dot{x}^2}\,F = \\ = -p_1q_2 - p_2q_2 - m\sqrt{q_2^2} - \alpha\frac{\sqrt{q_2^2q_3^2 - (q_2q_3)^2}}{q_2^2}. \tag{25}$$

Next, the Dirac method for the time conservation of constraints is applied. A complete set of constraints can be obtained by this method [13–15]. In this method, the equations of motion in the phase space are written as

$$\frac{d\Sigma_i^1}{d\sigma} = \left\{\Sigma_i^1, H\right\} = 0, \tag{26}$$

where $H = H_c + e_i\Sigma_i^1$, e_i are the Lagrange multipliers, and the Poisson brackets are defined by

$$\{f,g\} = \frac{\partial f}{\partial p_{ij}}\,\frac{\partial g}{\partial q_{ij}} - \frac{\partial f}{\partial q_{ij}}\,\frac{\partial g}{\partial p_{ij}}, \tag{27}$$

where f and g are arbitrary functions. By imposing conservation condition (26) on constraints (22)–(24), we obtain the secondary constraints

$$\Sigma_1^2 = p_2q_2 = 0, \tag{28}$$

$$\Sigma_2^2 = p_2q_3 + \alpha\frac{\sqrt{q_2^2q_3^2 - (q_2q_3)^2}}{q_2^2} = 0, \tag{29}$$

$$\Sigma_3^2 = \varepsilon_{ijk}p_{2i}q_{2j}q_{3k} + \beta\frac{q_2q_3}{\sqrt{q_2^2}} = 0. \tag{30}$$

Using the conditions

$$\frac{d\Sigma_i^2}{d\sigma} = \left\{\Sigma_i^2, H\right\} = 0, \tag{31}$$

we obtain two constraints of the third generation:

$$\Sigma_1^3 = p_1 q_2 + m\sqrt{q_2^2} = 0, \tag{32}$$

$$\Sigma_2^3 = p_1 q_3 + m\frac{q_2 q_3}{\sqrt{q_2^2}} = 0. \tag{33}$$

Next, from the conservation condition $d\Sigma_2^3/d\sigma = \{\Sigma_2^3, H\} = 0$, the following constraint can be deduced:

$$p_1^2 - \alpha m k - \beta k\sqrt{m^2 - p_1^2} - m^2 = 0, \tag{34}$$

where we recall that

$$k = \frac{\sqrt{q_2^2 q_3^2 - (q_2 q_3)^2}}{(q_2^2)^{3/2}}.$$

Also, we can show that the condition $d\Sigma_1^3/d\sigma = 0$ is trivial. Finally, we solve Eq. (34) for p_1^2 to obtain

$$P^2 = m^2 - \frac{1}{4}\left[-\beta k + \varepsilon\sqrt{\beta^2 k^2 + 4\alpha m k}\right]^2, \tag{35}$$

where $\varepsilon = \pm 1$ and $P^2 = P_i P_i$. Furthermore, it can be shown that [13]

$$\frac{d}{d\sigma} P^2 = 0, \tag{36}$$

i. e., P^2 is a constant of motion.

On the other hand, we again calculate the first Casimir invariant using Feoli's method. This method has been formulated for the free energy in the form $F = F(k)$. In this case, shape equations (6) and (7) reduce to

$$\frac{d^2}{ds^2}\left(\frac{\partial F}{\partial k}\right) + (k^2 - \tau^2)\frac{\partial F}{\partial k} - kF = 0, \tag{37}$$

$$2\frac{d}{ds}\left(\tau\frac{\partial F}{\partial k}\right) - \tau'\frac{\partial F}{\partial k} = 0. \tag{38}$$

These equations have been derived similarly by Feoli et al. [12]. Nesterenko et al. [18] studied the motion of a relativistic particle with an arbitrary Lagrangian function $\mathcal{L}(k)$. They obtained the equations of motion in terms of the Lagrangian function exactly similar to Eqs. (37) and (38).

First, from Eqs. (8) and (11), we have

$$F = \frac{\alpha^2 + \beta^2}{\alpha} k + m + \beta C. \tag{39}$$

This shows that we can apply Feoli's method for the linear model. Also, with the help of Eqs. (37) and (38), Feoli et al. proved that the momentum vector has the form [12]

$$P_i = \frac{1}{k}\frac{\partial F}{\partial k}\frac{d^3 x_i}{ds^3} + \frac{k'}{k}\left(\frac{\partial^2 F}{\partial k^2} - \frac{1}{k}\frac{\partial F}{\partial k}\right)\frac{d^2 x_i}{ds^2} + \left(2k\frac{\partial F}{\partial k} - F\right)\frac{dx_i}{ds}. \tag{40}$$

Furthermore, using Eqs. (2) and (3), the following consequences are easily obtained:

$$\frac{dx_i}{ds}\frac{d^2 x_i}{ds^2} = 0, \tag{41}$$

$$\frac{dx_i}{ds}\frac{d^3 x_i}{ds^3} = -k^2, \tag{42}$$

$$\frac{d^2 x_i}{ds^2}\frac{d^3 x_i}{ds^3} = kk', \tag{43}$$

$$\frac{d^3 x_i}{ds^3}\frac{d^3 x_i}{ds^3} = (k')^2 + k^4 + k^2\tau^2. \tag{44}$$

By applying these identities, it can be shown that the square of Eq. (40) is of the form [12]

$$P^2 = \left(k'\frac{\partial^2 F}{\partial k^2}\right)^2 + (k^2 + \tau^2)\left(\frac{\partial F}{\partial k}\right)^2 - 2kF\frac{\partial F}{\partial k} + F^2. \tag{45}$$

If we substitute relation (39) in Eq. (45), we arrive at

$$P^2 = \frac{(\alpha^2 + \beta^2)^2(\beta k + \alpha C)^2}{\alpha^4} + (m + \beta C)^2. \tag{46}$$

Comparing Eqs. (35) and (46) yields

$$\left[\alpha^4(5\beta + 1) + 8\alpha^2\beta^3 + 4\beta^5\right]\beta k^2 + 4\left[\alpha^4(m + 2\beta C) + 2(2\alpha^2 + \beta^2)\beta^3 C\right]\alpha k + 2\varepsilon\alpha^4\beta k\sqrt{\beta k^2 + 4\alpha m k} + 4\left[\alpha^4 C + \alpha^2\beta(2m + 3\beta C) + \beta^4 C\right]\alpha^2 C = 0. \tag{47}$$

Consequently, within applying the generalized Hamiltonian formalism, another relation among the unknown constants α, β, m, and C is obtained. Hence, our presented method seems to be a useful way for determining the unknown parameters of the free energy function. In the next section, we determine numerical values of these parameters for DNA structures.

3. CALCULATION OF THE FREE ENERGY FOR DNA STRUCTURES

DNA is a coiled biopolymer chain inside the cell nucleus. DNA was first identified by Friedrich Miescher in

Fig. 1. Schematic representation of the DNA double helix

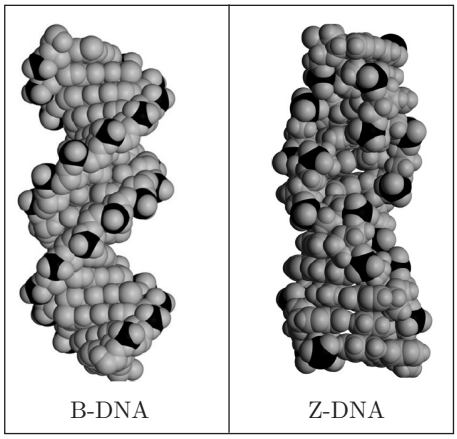

Fig. 2. Space-filling representation of B- and Z-DNA [29]

1869. The discovery of DNA provided new insights into the nature of living organisms. DNA does not usually exist as a single molecule. It has a double helix shape. The double helix structure of DNA was first discovered by Watson and Crick in 1953. DNA molecules have two long biopolymers made of repeating units called nucleotides [25–27] (displayed in Fig. 1).

The parametric equation of a double helix is usually described by

$$\mathbf{r}(s) = (r_0\cos(\omega s), r_0\sin(\omega s), h\omega s)\,, \qquad (48)$$

where the coiled pitch of the double helix is $p = 2\pi h$, r_0 is the radius of the double helix, and $\omega = 1/\sqrt{r_0^2+h^2}$. The curvature and torsion of a double helix are given by[2)] $k_0 = r_0\omega^2$ and $\tau_0 = h\omega^2$.

We now rewrite our results for DNA structures with parametric equation (48). Eliminating the term C from Eqs. (11) and (47), we obtain

$$4\alpha^4\tau_0^2 + 4\alpha^3 m k_0 + \alpha^2\beta \times$$
$$\times\left[(\beta{+}1)k_0^2{+}12\beta\tau_0^2{+}8m\tau_0{+}2\varepsilon k_0\sqrt{\beta k_0^2{+}4\alpha m k_0}\right] -$$
$$- 8\alpha\beta^2(m+\beta\tau_0)k_0 + 4\beta^4(k_0^2+\tau_0^2) = 0. \qquad (49)$$

Solving Eqs. (9) and (49), we obtain

$$\alpha = -\frac{\tau_0+\varepsilon\sqrt{2k_0^2+\tau_0^2}}{k_0}\,\beta, \qquad (50)$$

and

$$(3\beta+1)k_0^8 + 4(10\beta+1)k_0^6\tau_0^2 + 2(66\beta+1)k_0^4\tau_0^4 +$$
$$+\ 120\beta k_0^2\tau_0^6 + 64\beta\tau_0^8 + 2\varepsilon\tau_0 \times$$
$$\times\left[(4\beta{+}1)k_0^6{+}(30\beta{+}1)k_0^4\tau_0^2{+}44\beta k_0^2\tau_0^4{+}16\beta\tau_0^6\right] \times$$
$$\times\sqrt{2k_0^2+\tau_0^2} + 2\varepsilon k_0^3\sqrt{\beta}\ \times$$
$$\times\left[k_0^4 + 4k_0^2\tau_0^2 + 2\tau_0^4 + 2\tau_0(k_0^2+\tau_0^2)\sqrt{2k_0^2+\tau_0^2}\right] \times$$
$$\times\sqrt{k_0^2 - 4m\left(\tau_0+\varepsilon\sqrt{2k_0^2+\tau_0^2}\right)} = 0. \qquad (51)$$

It is obvious that the last equation is nonlinear and complicated. We next determine numerical values of α and β for B- and Z-DNA.

It is now known that DNA can exist in many possible conformations. But only the B- and Z-DNA have been directly observed in living organisms [27]. The most common DNA structure is known as B-DNA, first described by Watson and Crick [28,29]. In B-DNA, the double helix is right-handed. B-DNA is flexible and contains a major and a minor groove. B-DNA is more accessible for interactions with proteins. The shapes of the standard B- and Z-DNA are shown in Fig. 2.

Z-DNA is one of the possible structures of DNA. Z-DNA was first discovered by Alexander Rich and his associates in 1979 [30,31]. It is a left-handed double helix with a zig-zag (hence the name) pattern [29]. The Z-DNA conformation does not exist as a stable feature of a double helix. Scientists believe that Z-DNA plays an important biological role in the transcription of genes. The helical parameters of B- and Z-DNA are compared in Table.

[2)] The subscript "0" in k_0 and τ_0 refers to the constant curvature and torsion.

Table. Characteristics of B- and Z-DNA [29]

Characteristic	B-DNA	Z-DNA
Helix direction	Right-handed	Left-handed
Rotation	35.9°	60.2°
Helical twist	+16°	0°
Pitch, nm	3.32	4.46
Radius, nm	1	0.90

Using this Table, after some calculations, we obtain

$$\begin{aligned}\beta_{B\text{-}DNA} &= -0.0681 - 0.1379m - \\ &- \sqrt{0.0190m^2 + 0.0187m - 0.0019}, \quad \varepsilon = +1, \\ \beta_{B\text{-}DNA} &= -0.1071 + 0.2427m + \\ &+ \sqrt{0.0589m^2 - 0.0520m - 0.0126}, \quad \varepsilon = -1\end{aligned} \tag{52}$$

and

$$\begin{aligned}\beta_{Z\text{-}DNA} &= -0.0347 - 0.0396m - \\ &- \sqrt{0.0015m^2 + 0.0027m - 0.0002}, \quad \varepsilon = +1, \\ \beta_{Z\text{-}DNA} &= -0.0694 - 0.0674m + \\ &+ \sqrt{0.0045m^2 - 0.0093m - 0.0021}, \quad \varepsilon = -1.\end{aligned} \tag{53}$$

We note that Eq. (51) is very sensitive to changes in the position of decimal numbers. By substituting the last results in Eqs. (50) and (8), we finally conclude that

$$\begin{aligned}F_{B\text{-}DNA} &= -0.0803 + 1.1628m + \\ &+ \sqrt{0.0265m^2 + 0.0261m - 0.0027}, \quad \varepsilon = +1, \\ F_{B\text{-}DNA} &= -0.1264 + 1.2865m + \\ &+ \sqrt{0.0820m^2 - 0.0724m - 0.0176}, \quad \varepsilon = -1\end{aligned} \tag{54}$$

and

$$\begin{aligned}F_{Z\text{-}DNA} &= 0.0385 + 1.0439m + \\ &+ \sqrt{0.0019m^2 + 0.0033m - 0.0002}, \quad \varepsilon = +1, \\ F_{Z\text{-}DNA} &= -0.0770 + 1.0748m + \\ &+ \sqrt{0.0056m^2 - 0.0115m - 0.0026}, \quad \varepsilon = -1.\end{aligned} \tag{55}$$

Consequently, the linear free energy model, which contains four unknown constants α, m, and C, is reduced to Eqs. (54) and (55) with only one parameter m.

Finally, for the use in the next section, we need to calculate the minimum value of the quantity $\Delta F^{B\to Z}$, i. e., the free energy difference between B- and Z-DNA, in terms of the parameter m. In the case $\varepsilon = +1$, we have $\min(\Delta F^{B\to Z}) = 0.6669$ and in the case $\varepsilon = -1$, $\min(\Delta F^{B\to Z}) = 0.0664$. We recall that the unit of the free energy is kcal/mol.

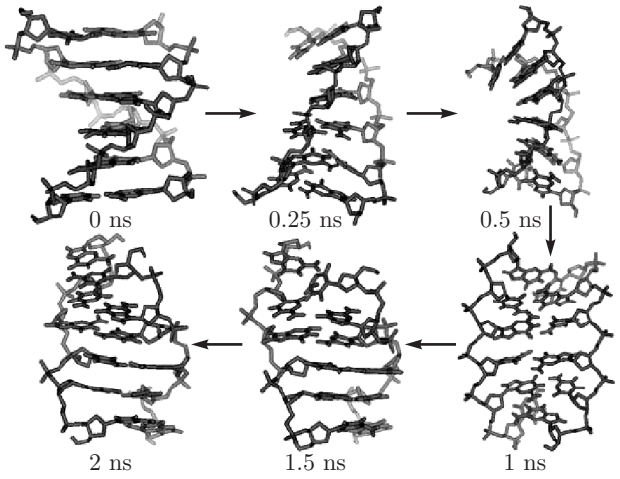

Fig. 3. Structure snapshots along the B- to Z-DNA transition pathway observed in the TMD simulation [32] (duration 2 ns)

4. B- TO Z-DNA TRANSITION

4.1. Introduction

The conformational change between B- and Z-DNA was first discovered in 1972 by Pohl and Jovin [33] (this transition is simulated in Fig. 3). It is usually referred to as the B- to Z-DNA transition in biophysics and biology. This transition occurs at the molecular level. This phenomenon provides an interesting test of the theories and models that are used in the study of DNA. The B to Z transitions could be involved in the control of the structural state of the chromosomes. The transition between B and Z conformations depends on several experimental parameters, such as temperature and salt concentration [34]. The experimental studies about this transition have been focused on the salt effects [33, 35] due to its biological relevance. The salt-induced transition is an important problem in molecular biology. Jovin et al. [34] reported the experimental data from the salt-induced transition. It is well known that the DNA base sequence determines the salt concentration in the transition between B- and Z-DNA. The experimental point at which both forms B and Z are equally probable is called the transition midpoint. The experimental range of the midpoint concentrations of added NaCl for the B to Z transition has been reported from 0.7 M to 5.4 M [36–38].

Pohl [35] accurately obtained the free energy of the transition in terms of the salt concentration via the experimental formula

$$\Delta F_{exp}^{B\to Z} = -0.3 \log\left(\frac{\mu}{2.25}\right) k_B T, \qquad (56)$$

where the free energy is given per DNA phosphate, μ is the NaCl molar concentration, 2.25 M is the transition midpoint, and $k_B = 0.00198$ kcal/mol·K and T are the Boltzmann constant and temperature. This relation was observed in [35] to be independent of the DNA length.

4.2. Some experimental observations

Chairest and Sturtevant [39] studied the thermodynamics of the B to Z transition for the poly(m^5dG-dC) plasmids [40]. In sodium phosphate buffer (pH 7.0) containing 50 mM NaCl and 1.0 mM $MgCl_2$, at a heating rate of 0.25 K/min, the reversible B–Z transition of the polymer is centered at $38.2 \pm 2.1\,^\circ$C and is characterized by $\Delta F_{exp}^{B\to Z} = 0.61 \pm 0.07$ kcal per mol of base pairs.

Peck and Wang [41] calculated the free energies of the B to Z transitions for the $d(pCpG)_{21}.d(pCpG)_{21}$ plasmids. For 0.1 M sodium at room temperature, they measured $\Delta F_{exp}^{B\to Z} = 0.65$ kcal per mol of base pairs. Also, the free energy difference between a d(pCpG.pCpG) unit in the left-handed Z and right-handed B helical structure is calculated to be 0.66 kcal, or 0.33 kcal per mol of base pairs.

O'Connor et al. [42] determined the B to Z transitions for the $(dT\text{-}dG)_{16}$ plasmids. At temperatures of 5, 10, 18, 22, 28, and 35 °C, they reported the $\Delta F_{exp}^{B\to Z}$ values ranging from 0.35 to 0.60 kcal/mol.

Ferreira and Sheardy [43] discussed the B to Z transitions for the $(dm^5C\text{-}dG)_4$ plasmids. In standard phosphate buffer with 115 mM Na^+ at 25 °C, they found that the B to Z transition is characterized by $\Delta F_{exp}^{B\to Z} = 0.70 \pm 0.04$ kcal/mol.

By comparing our results with these experimental data, we can conclude that our method is compatible with the standard experimental techniques in biophysics and biology. Anyhow, we have a very small deviation about 4.42 % from the last experiment.

5. CONCLUSION

In this paper, we have solved the equilibrium shape equations for the linear free energy model with the help of the generalized Hamiltonian formalism. By calculating the first Casimir invariant, we have shown that we can obtain an extra relation among the parameters of the considered model. This means a reduction in the number of parameters in our model. We also exactly determined the free energy functions for our solutions in terms of only one parameter. Finally, the free energy of B- to Z-DNA transition has been calculated for our solutions.

In a similar manner, the author of [44–46] obtained the solutions of the equilibrium shape equations for some specific free energy models for DNA structures using the second Casimir invariant. Hence, we hope that the techniques of quantum field theory may provide new insights into the study of DNA structures.

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