

Theory of sequence-dependent DNA elasticity

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The elastic properties of a molecule of duplex DNA are strongly dependent on nucleotide sequence. In the theory developed here the contribution ψ^n of the n th base-pair step to the elastic energy is assumed to be given by a function $\tilde{\psi}^n$ of six kinematical variables, called tilt, roll, twist, shift, slide, and rise, that describe the relative orientation and displacement of the n th and $(n+1)$ th base pairs. The sequence dependence of elastic properties is determined when one specifies the way $\tilde{\psi}^n$ depends on the nucleotides of the two base pairs of the n th step. Among the items discussed are the symmetry relations imposed on $\tilde{\psi}^n$ by the complementarity of bases, i.e., of A to T and C to G, the antiparallel nature of the DNA sugar-phosphate chains, and the requirement that $\tilde{\psi}^n$ be independent of the choice of the direction of increasing n . Variational equations of mechanical equilibrium are here derived without special assumptions about the form of the functions $\tilde{\psi}^n$, and numerical solutions of those equations are shown for illustrative cases in which $\tilde{\psi}^n$ is, for each n , a quadratic form and the DNA forms a closed, 150 base-pair, minicircle that can be called a DNA o-ring because it has a nearly circular stress-free configuration. Examples are given of noncircular equilibrium configurations of naked DNA o-rings and of cases in which the interaction with ligands induces changes in configuration that are markedly different from those undergone by a minicircle of intrinsically straight DNA. When a minicircle of intrinsically straight DNA interacts with an intercalating agent that upon binding to DNA causes a local reduction of intrinsic twist, the configuration that minimizes elastic energy depends on the number of intercalated molecules, but is independent of the spatial distribution of those molecules along the minicircle. In contrast, it is shown here that the configuration and elastic energy of a DNA o-ring can depend strongly on the spatial distribution of the intercalated molecules. As others have observed in calculations for Kirchhoff rods with intrinsic curvature, an o-ring that has its intrinsic twist reduced at a single base-pair step can undergo large deformations with localized untwisting and bending at remote steps, even when the amount α of twist reduction is less than the amount required to induce supercoiling in rings of intrinsically straight DNA. We here find that the presence in the functions $\tilde{\psi}^n$ of cross-terms coupling twist to roll can amplify the configurational changes induced by local untwisting to the point where there can be a value of α at which a first-order transition occurs between two distinct stable noncircular configurations with equal elastic energy. © 2003 American Institute of Physics. [DOI: 10.1063/1.1559690]

I. INTRODUCTION

Although there are cases in which one can treat a DNA molecule as an idealized homogeneous elastic rod that is straight when stress-free and has uniform elastic properties, it is known that the genetic information in DNA determines not only the amino acid sequences of encoded proteins and RNA but also the geometry and deformability of DNA at a local level, i.e., at the level of base-pair steps. Recent advances in structural biochemistry have yielded information about the dependence on base-pair sequence of the structure

and elastic response of DNA. In this paper we present a method of taking such information into account when one calculates and determines the stability of equilibrium configurations of DNA segments subject to preassigned end conditions.

In a stress-free state, the local bend, twist, and stretch of duplex (double helical) DNA varies from one base-pair step to another. Some steps are wedge shaped with inclination (i.e., bending) strongly dependent on nucleotide composition and occasionally as large as 5° . Moreover, there are steps that are sites of over- or undertwisting as large as 3.5° , and there are steps at which the barycenter of a base pair is displaced relative to that of its predecessor and gives rise to a

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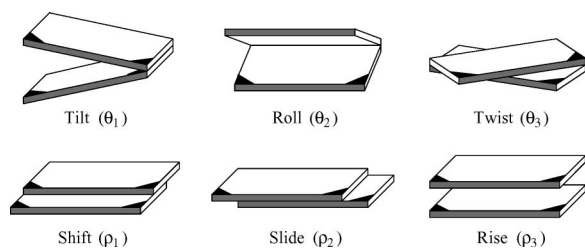


FIG. 1. Schematic representation of kinematical variables describing the relative orientation and displacement of successive base pairs. *Tilt* and *roll* measure local bending, *twist* measures rotation in the base-pair plane, *shift* and *slide* local shearing, and *rise* local stretch. For precise definitions, see Refs. 13, 14, and 17 and Eqs. (2.5a)–(2.7).

local shear that can be as large as 0.65 Å (or 20% of the elevation of a base pair relative to its predecessor).^{1–6}

The chemical architecture of DNA results also in mechanical couplings between kinematical variables (such as those of Fig. 1) that characterize the relative displacement and orientation of adjacent base pairs. Observed correlations in the values of the kinematical variables for crystals of DNA oligomers have led to the proposal that such couplings should appear as cross-terms in constitutive equations relating the elastic energy (or, equivalently, local forces and moments) to the kinematical variables.⁶

Recent research on the derivation of energy functions that govern the structure and deformation of individual base-pair steps in crystals of pure DNA and DNA–protein complexes^{5–7} makes it possible to develop models for DNA elasticity that take into account a strong dependence of intrinsic structure and elastic moduli on nucleotide sequence and have, of necessity, a discrete rather than a continuum nature with constitutive relations showing cross-terms that couple twisting to bending. In this paper we construct a theory of a general class of discrete models in which the elastic energy Ψ of a DNA segment is assumed to be the sum of the interaction energies of adjacent base pairs. For each n , ψ^n , the energy resulting from deformation of the n th (dimer) base-pair step, is assumed to be given by a function of $\tilde{\psi}^n$ of six independent kinematical variables that determine the relative orientation and displacement of the n th and $(n+1)$ th base pairs; these are the three angular variables (tilt, roll, twist) and the three displacement variables (shift, slide, rise) that are illustrated schematically in Fig. 1 and are defined precisely in Sec. II.

The underlying mathematical assumptions of the theory are stated in Sec. II along with the equations that govern configurations in mechanical equilibrium. Those equations are obtained by setting equal to zero the first variation of the total energy E , which we take to be a sum of the elastic energy $\Psi = \sum_n \psi^n$ and the potential energy P of external forces and moments. Our derivation of the equilibrium equations does not require special assumptions about the form of the functions $\tilde{\psi}^n$. The symmetry relations imposed on the $\tilde{\psi}^n$ by the complementarity of adenine to thymine and guanine to cytosine, the antiparallel nature of the DNA sugar–phosphate chains, and the requirement that those functions are independent of the choice of the direction of increasing n are presented at the same level of generality as our deriva-

tions of the equilibrium equations. Also shown in Sec. II are the forms that the symmetry relations take when $\tilde{\psi}^n$ is quadratic in appropriate kinematical variables. Details of derivations of the equations of equilibrium and of the symmetry relations for $\tilde{\psi}^n$ are given in Sec. III.

The principal results of the paper are those given in Secs. II and III, namely (i) the formulation of the theory, (ii) the analysis of the symmetry restrictions imposed on ψ^n by the structure of commonly found forms of duplex DNA including the B, A, and C forms, (iii) the derivation of the variational equations of equilibrium that requires the attainment of a computationally manageable expression for the matrix inverse of the gradient of the orthogonal matrix $[D_{ij}^n]$, relating bases embedded in the n th and $(n+1)$ th base pairs to the parameters tilt, roll, and twist [see Eq. (A1) and Eqs. (3.7), (3.9)–(3.11)], and (iv) the development of an efficient computational method [of order $O(N)$, with N the number of base pairs] for solving the equilibrium equations and determining the stability of computed solutions.

To illustrate the way in which the theory can be used to explore the influence of a nucleotide sequence on configurations of DNA subject to constraints such as ring closure and ligand-induced changes in local structure, we give, in Sec. IV, a few examples in which the theory is employed to calculate equilibrium configurations of closed minicircles, which, because they have nearly circular stress-free configurations, are called DNA o-rings.⁸ Discussions are given of ways in which equilibrium configurations of naked DNA and DNA that is interacting with ligands can, under appropriate circumstances, show a behavior markedly different from that predicted by the familiar idealized rod model.⁹ Among the new topics treated here is the influence of the cross-terms coupling twist to roll on the configurational changes induced by local untwisting.

II. CONSTITUTIVE RELATIONS AND VARIATIONAL EQUATIONS

In the present theory the base pairs are taken to be flat objects that are represented by rectangles. The configuration of a DNA segment with $N+1$ base pairs, and hence N base pair steps, is specified by giving, for each n , both the location \mathbf{x}^n of the center of the rectangle \mathfrak{B}^n that represents the n th base pair and a right-handed orthonormal triad $\mathbf{d}_1^n, \mathbf{d}_2^n, \mathbf{d}_3^n$ that is embedded in the base pair (see Fig. 2). The polygonal curve \mathcal{C} formed by the N line segments connecting the spatial points $\mathbf{x}^1, \dots, \mathbf{x}^{N+1}$ is called the *axial curve*.

Each DNA nucleotide in a base pair belongs to one of the two strands that make up the duplex molecule. In a strand, the nucleotide bases are laterally attached (through covalent bonds) to a sugar–phosphate chain. The chains of the two strands are antiparallel in the sense that increasing n corresponds to advance in the 5′–3′ direction on one strand and in the 3′–5′ direction on the other.¹⁰

We assume that the elastic energy Ψ of a configuration is the sum over n of the energy ψ^n of interaction of the n th and $(n+1)$ th base pairs, and that ψ^n is a function of the relative orientation and displacement of the two neighboring base pairs, i.e., of the components of the vectors \mathbf{d}_j^{n+1} and

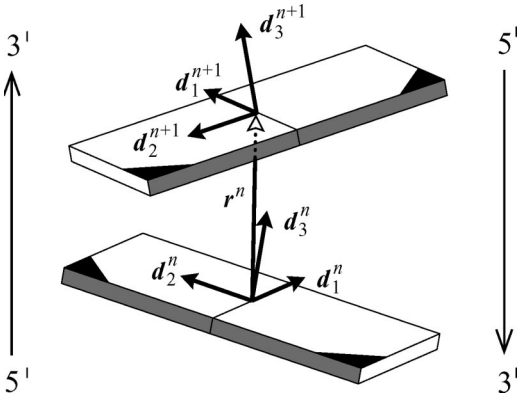


FIG. 2. Drawing of the model employed for a base-pair step showing the vectors \mathbf{r}^n , \mathbf{d}_i^n , \mathbf{d}_i^{n+1} . Each nucleotide base of a pair is covalently bonded (at its darkened corner) to one of the two sugar–phosphate chains. The arrows give the 5′–3′ directions of those chains. The gray-shaded long edges are in the minor groove of the DNA.

$\mathbf{r}^n = \mathbf{x}^{n+1} - \mathbf{x}^n$ with respect to the basis \mathbf{d}_i^n . As the 3×3 matrix $[D_{ij}^n]$ with entries $D_{ij}^n = \mathbf{d}_i^n \cdot \mathbf{d}_j^{n+1}$ is orthogonal, it can be parametrized by a triplet $(\theta_1^n, \theta_2^n, \theta_3^n)$ of angles, with θ_1^n the *tilt*, θ_2^n the *roll*, and θ_3^n the *twist* of \mathfrak{B}^{n+1} relative to \mathfrak{B}^n . Hence, in the formula

$$\Psi = \sum_{n=1}^N \psi^n, \quad (2.1)$$

the elastic energy ψ^n of the n th base-pair step is given by a constitutive relation of the type

$$\psi^n = \hat{\psi}^n(\theta_1^n, \theta_2^n, \theta_3^n, r_1^n, r_2^n, r_3^n), \quad r_i^n = \mathbf{d}_i^n \cdot \mathbf{r}^n. \quad (2.2)$$

It is often useful to write this relation in the form¹¹

$$\psi^n = \tilde{\psi}^n(\theta_1^n, \theta_2^n, \theta_3^n, \rho_1^n, \rho_2^n, \rho_3^n), \quad (2.3)$$

where the displacement variables $\rho_1^n, \rho_2^n, \rho_3^n$, called *shift*, *slide*, and *rise* are given by coordinate transformation functions, $\hat{\rho}_k$, that are independent of n :

$$\rho_k^n = \hat{\rho}_k(\theta_1^n, \theta_2^n, \theta_3^n, r_1^n, r_2^n, r_3^n). \quad (2.4)$$

As shown in Fig. 2, the vectors \mathbf{d}_i^n are defined so that \mathbf{d}_3^n is perpendicular to \mathfrak{B}^n with $\mathbf{d}_3^n \cdot \mathbf{r}^n > 0$; \mathbf{d}_2^n is parallel to the long edges of \mathfrak{B}^n and points toward the short edge containing the corner of \mathfrak{B}^n bonded to a deoxyribose group in the sugar–phosphate chain for which n increases in the 5′–3′ direction; \mathbf{d}_1^n is parallel to the short edges of \mathfrak{B}^n and points toward the major groove of the DNA, i.e., $\mathbf{d}_1^n = \mathbf{d}_2^n \times \mathbf{d}_3^n$.¹²

Each drawing in Fig. 1 illustrates one of the kinematical variables $\theta_1^n, \theta_2^n, \theta_3^n, \rho_1^n, \rho_2^n, \rho_3^n$ for a case in which that variable has a positive value and the others (with the exception of ρ_3^n) are set equal to zero. That figure is intended to be suggestive rather than precise. To give a precise definition of θ_i^n and ρ_i^n for cases in which several of these variables are not zero, we follow a procedure (introduced by Zhurkin, Lysov, and Ivanov¹³ and further developed by El Hassan and Calladine¹⁴) in which one employs the Euler-angle system $\zeta^n, \kappa^n, \eta^n$ for which¹⁵

$$D_{ij}^n = \mathbf{d}_i^n \cdot \mathbf{d}_j^{n+1} = Z_{ij}(\zeta^n) Y_{kl}(\kappa^n) Z_{lj}(\eta^n), \quad (2.5a)$$

$$[Y_{ij}(\alpha)] = \begin{bmatrix} \cos \alpha & 0 & \sin \alpha \\ 0 & 1 & 0 \\ -\sin \alpha & 0 & \cos \alpha \end{bmatrix}, \quad (2.5b)$$

$$[Z_{ij}(\alpha)] = \begin{bmatrix} \cos \alpha & -\sin \alpha & 0 \\ \sin \alpha & \cos \alpha & 0 \\ 0 & 0 & 1 \end{bmatrix}, \quad (2.5c)$$

and defines $\theta_1^n, \theta_2^n, \theta_3^n$ by the relations

$$\zeta^n = \frac{1}{2} \theta_3^n - \gamma^n, \quad \eta^n = \frac{1}{2} \theta_3^n + \gamma^n, \quad (2.6a)$$

$$\kappa^n = \sqrt{(\theta_1^n)^2 + (\theta_2^n)^2}, \quad \tan \gamma^n = \frac{\theta_1^n}{\theta_2^n}. \quad (2.6b)$$

As in Ref. 14, we here use Eqs. (2.5)–(2.6) to define ρ_i^n in terms of r_i^n and θ_i^n :

$$\rho_i^n = Z_{ij}(-\gamma^n) Y_{jk}(-\frac{1}{2} \kappa^n) Z_{kl}(-\zeta^n) r_i^n. \quad (2.7)$$

This last equation renders explicit the functions $\hat{\rho}_k$ in Eq. (2.4) and implies that the numbers ρ_i^n are the components of \mathbf{r}^n with respect to an orthonormal basis $\bar{\mathbf{d}}_i^n$, which is called the *mid-basis* for step n and is defined by the relation

$$\bar{\mathbf{d}}_i^n \cdot \bar{\mathbf{d}}_j^n = Z_{ik}(\zeta^n) Y_{kl}(\frac{1}{2} \kappa^n) Z_{lj}(\gamma^n). \quad (2.8)$$

In Sec. III [i.e., in the discussion containing Eqs. (3.4) and (3.8)] we render precise the following remark: The present definition of θ_i^n and ρ_i^n is such that, for each configuration of a DNA segment, a change in the choice of the direction of increasing n leaves $\theta_2, \theta_3, \rho_2, \rho_3$ invariant but changes the sign of θ_1 and ρ_1 .

Several computer programs have been developed to reduce atomic coordinate data (of the type available for DNA crystal structures in the Nucleic Acid Database¹⁶) to variables θ_i^n, ρ_i^n , which, like those just defined, are compatible with a convention¹⁷ known as the “Cambridge Accord of 1988.” For a survey see Ref. 18.

The function ψ^n of Eq. (2.3) depends on which nucleotide bases are in the n th and $(n+1)$ th base pairs. To discuss the restrictions imposed on $\tilde{\psi}^n$ by the complementarity of A to T and G to C, the antiparallel directions of the sugar–phosphate chains, and the assumption that $\tilde{\psi}^n$ is independent of the composition of base pairs other than the n th and $(n+1)$ th, let us write $\tilde{\psi}^{XY}$ for $\tilde{\psi}^n$, where XY, with X in the n th and Y in the $(n+1)$ th base pair, is a sequence of two nucleotide bases attached to the chain for which n increases in the 5′–3′ direction. In this notation, for the complement of the base X, one writes \bar{X} (i.e., $\bar{A} = T, \bar{G} = C$). The complement of a sequence of bases is the sequence of complementary bases in the reverse order: the complement of XY is $\bar{Y}\bar{X}$ (e.g., the complement of AC is GT), because \bar{X} and \bar{Y} are attached at the locations n and $n+1$ to the chain for which n decreases

in the $5'-3'$ direction. In Sec. III it is shown that when θ_i^n , ρ_i^n are defined as here, each function $\tilde{\psi}^{XY}$ determines its complementary function $\tilde{\psi}^{\bar{Y}\bar{X}}$ by the relation

$$\begin{aligned} &\tilde{\psi}^{XY}(\theta_1^n, \theta_2^n, \theta_3^n, \rho_1^n, \rho_2^n, \rho_3^n) \\ &= \tilde{\psi}^{\bar{Y}\bar{X}}(-\theta_1^n, \theta_2^n, \theta_3^n, -\rho_1^n, \rho_2^n, \rho_3^n). \end{aligned} \quad (2.9)$$

It follows that, if XY is self-complementary, i.e., if $XY = \bar{Y}\bar{X}$, then $\tilde{\psi}^{XY}$ is an even function of the pair (θ_1^n, ρ_1^n) for each fixed value of the quadruple $(\theta_2^n, \theta_3^n, \rho_2^n, \rho_3^n)$.

We define an equilibrium configuration to be one for which the first variation of the total energy, i.e.,

$$E = \Psi + P, \quad (2.10)$$

vanishes for all variations in configuration that are admissible in the sense that they are compatible with the imposed constraints. (Here P is the potential energy of external forces and moments.) The resulting variational equations, which are derived in Sec. III, can be written as

$$\mathbf{f}^n - \mathbf{f}^{n-1} = \boldsymbol{\varphi}^n, \quad \mathbf{m}^n - \mathbf{m}^{n-1} = \mathbf{f}^n \times \mathbf{r}^n + \boldsymbol{\mu}^n \quad (2 \leq n \leq N), \quad (2.11)$$

where, for each n , \mathbf{f}^n and \mathbf{m}^n are the force and moment that the $(n+1)$ th base pair exerts on the n th base pair and $\boldsymbol{\varphi}^n$ and $\boldsymbol{\mu}^n$ are the external force and moment acting on the n th base pair.¹⁹ The vectors \mathbf{f}^n and \mathbf{m}^n are the analogs of the vectors $\mathbf{f}(s^*)$ and $\mathbf{m}(s^*)$ that, in Kirchhoff's theory of elastic rods, are interpreted as the resultant force and moment of the contact forces (i.e., Piola stresses) exerted on the cross section with the arc-length coordinate s^* by the material with arc-length coordinates $s > s^*$. The components of \mathbf{f}^n and \mathbf{m}^n with respect to the local basis \mathbf{d}_i^n are given by the relations

$$f_i^n = \frac{\partial \hat{\psi}^n}{\partial r_i^n}, \quad m_i^n = \Gamma_{ij}^n \frac{\partial \hat{\psi}^n}{\partial \theta_j^n}. \quad (2.12)$$

The numbers Γ_{ij}^n form a 3×3 matrix $[\Gamma_{ij}^n] = [\hat{\Gamma}_{ij}^n(\theta_1^n, \theta_2^n, \theta_3^n)]$ that depends on the definitions employed for the kinematical variables θ_i^n . When those variables are as in Eqs. (2.5)–(2.6), $[\Gamma_{ij}^n]$ is given by Eq. (A1). The chain rule permits us to write Eqs. (2.12) in the forms

$$f_i^n = \frac{\partial \tilde{\psi}^n}{\partial \rho_j^n} \frac{\partial \hat{\rho}_j}{\partial r_i^n}, \quad m_i^n = \Gamma_{ij}^n \left(\frac{\partial \tilde{\psi}^n}{\partial \theta_j^n} + \frac{\partial \tilde{\psi}^n}{\partial \rho_k^n} \frac{\partial \hat{\rho}_k}{\partial \theta_j^n} \right), \quad (2.13)$$

in which $\tilde{\psi}^n$ and $\hat{\rho}_k$ are as in Eqs. (2.3) and (2.4). When θ_i^n and ρ_i^n are defined by Eqs. (2.5)–(2.8), for $\partial \hat{\rho}_j / \partial r_i^n$ and $\partial \hat{\rho}_k / \partial \theta_j^n$, we have

$$\frac{\partial \hat{\rho}_j}{\partial r_i^n} = Z_{jk}(-\gamma^n) Y_{kl} \left(-\frac{1}{2} \kappa^n \right) Z_{li}(-\zeta^n), \quad (2.14)$$

$$\frac{\partial \hat{\rho}_k}{\partial \theta_j^n} = {}_j \Lambda_{kl}^n \rho_l^n, \quad (2.15)$$

with ${}_j \Lambda_{kl}^n$ as in Eqs. (A2)–(A4).

If a DNA segment with $N+1$ base pairs is subject to strong anchoring end conditions at both ends, then $(\mathbf{x}^1, \mathbf{d}_1^1)$ and $(\mathbf{x}^{N+1}, \mathbf{d}_1^{N+1})$ have preassigned values. A closed (or ‘‘circularized’’) DNA segment of N base pairs (bp) can be considered an $N+1$ bp segment that is subject to the constraint that its terminal base pairs coincide, i.e., have the same location and orientation, and hence

$$\mathbf{x}^1 = \mathbf{x}^{N+1}, \quad \mathbf{d}_i^1 = \mathbf{d}_i^{N+1} \quad (i=1,2,3). \quad (2.16)$$

A necessary condition for an equilibrium configuration to be stable is that there be no admissible variation in configuration for which $\delta^2 E$, the second variation of E , is negative. As a configuration is described in the present theory by giving a finite number of variables, namely the $6N$ numbers, $\theta_1^n, \theta_2^n, \theta_3^n, \rho_1^n, \rho_2^n, \rho_3^n$, we can say that a sufficient condition for stability is that $\delta^2 E$ be positive for all admissible variations. A configuration that is stable but does not give a global minimum to E can be called metastable.

For calculations of the type reported in Sec. IV, $\boldsymbol{\varphi}^n = \boldsymbol{\mu}^n = \mathbf{0}$, i.e., P is set equal to zero.²⁰ The Eqs. (2.11) with \mathbf{f}^n and \mathbf{m}^n given by Eqs. (2.12) then are a system \mathcal{E} of $6N - 6$ nonlinear algebraic equations for the unknown coordinates $\theta_1^n, \theta_2^n, \theta_3^n, \rho_1^n, \rho_2^n, \rho_3^n$. That system is weakly coupled in the sense that for each n , $2 \leq n \leq N$, Eqs. (2.11) are a set of six equations that are solved numerically using a Newton–Raphson procedure to obtain (θ_i^n, ρ_i^n) for given $(\theta_i^{n-1}, \rho_i^{n-1})$. This allows one to solve \mathcal{E} efficiently [using $O(N)$ computational steps] by a recursive algorithm in which, for each n , (θ_i^n, ρ_i^n) is obtained as a function of (θ_i^1, ρ_i^1) . Equilibrium configurations of segments subject to specified end conditions are calculated using an iterative scheme in which (θ_i^1, ρ_i^1) is repeatedly adjusted until the appropriate relations, e.g., Eq. (2.16), hold.

The case in which ψ^n is given by a quadratic form

To describe quadratic energy functions of the type employed for calculations presented in Sec. III, we write $\bar{\theta}_i^n$ and $\bar{\rho}_i^n$ for the values of θ_i^n and ρ_i^n in a stress-free state with $\psi^n = 0$, and put

$$\Delta \theta_i^n = \theta_i^n - \bar{\theta}_i^n, \quad \Delta \rho_i^n = \rho_i^n - \bar{\rho}_i^n. \quad (2.17)$$

When $|\Delta \theta_i^n|$ and $|\Delta \rho_i^n|$ are small, the assumption that $\tilde{\psi}^n$ is three-times differentiable implies that, to within an error $O(\delta^3)$ with

$$\delta = \max_{i=1,2,3} \{|\Delta \theta_i^n|, |\Delta \rho_i^n|\}, \quad (2.18)$$

$\tilde{\psi}^n$ can be taken to be a quadratic function,

$$\begin{aligned} \psi^n = & \frac{1}{2} F_{ij}^n (\Delta \theta_i^n) (\Delta \theta_j^n) + G_{ij}^n (\Delta \theta_i^n) (\Delta \rho_j^n) \\ & + \frac{1}{2} H_{ij}^n (\Delta \rho_i^n) (\Delta \rho_j^n), \end{aligned} \quad (2.19)$$

in which F_{ij}^n , G_{ij}^n , and H_{ij}^n are constants with $F_{ij}^n = F_{ji}^n$, $H_{ij}^n = H_{ji}^n$, $(i, j=1,2,3)$.²¹ If one wishes, one may write the right-hand side of Eq. (2.19) as a quadratic form in $(\Delta \theta_1^n, \Delta \theta_2^n, \Delta \theta_3^n, \nu_1^n, \nu_2^n, \nu_3^n)$, where the dimensionless numbers,

$$\nu_i^n = \Delta \rho_i^n / \bar{\rho}_3^n, \quad (2.20)$$

are such that ν_3^n can be interpreted as a stretching strain and ν_1^n and ν_2^n as shearing strains.

It follows from Eq. (2.9) that if we replace F_{ij}^n by F_{ij}^{XY} , etc., and let Z stand for F , G , or H , then in Eq. (2.19),

$$\bar{\theta}_i^{XY} = Q_{ij} \bar{\theta}_j^{\bar{Y}\bar{X}}, \quad \bar{\rho}_i^{XY} = Q_{ij} \bar{\rho}_j^{\bar{Y}\bar{X}}, \quad (2.21a)$$

$$Z_{ij}^{XY} = Q_{ik} Z_{kl}^{\bar{Y}\bar{X}} Q_{lj}, \quad (2.21b)$$

where

$$-Q_{11} = Q_{22} = Q_{33} = 1, \quad Q_{ij} = 0, \quad \text{when } i \neq j. \quad (2.22)$$

Equations (2.21) imply that, when $XY = AT, GC, TA, \text{ or } CG$,²²

$$F_{12}^{XY} = F_{13}^{XY} = 0, \quad H_{12}^{XY} = H_{13}^{XY} = 0, \quad (2.23a)$$

$$G_{12}^{XY} = G_{13}^{XY} = G_{21}^{XY} = G_{31}^{XY} = 0, \quad \bar{\theta}_1^{XY} = \bar{\rho}_1^{XY} = 0. \quad (2.23b)$$

Estimates from x-ray crystal structure data of values of the elastic moduli F_{ij}^{XY} , G_{ij}^{XY} , H_{ij}^{XY} and the intrinsic parameters $\bar{\theta}_i^{XY}$, $\bar{\rho}_i^{XY}$ for each distinct combination of a base pair and its successor^{5,6} confirm that these moduli and intrinsic parameters are strongly dependent on the nucleotide composition. If we focus attention on the angular variables θ_i^{XY} , we can give as follows a rough summary of the nature of the sequence dependence of moduli and intrinsic parameters of the B form of DNA.²³ It follows from Eqs. (2.21) that the intrinsic tilt $\bar{\theta}_1^{XY}$ obeys the relation $\bar{\theta}_1^{XY} = -\bar{\theta}_1^{\bar{Y}\bar{X}}$, and the available data indicate that its largest value is $\sim 1.5^\circ$. The data indicate that the intrinsic roll $\bar{\theta}_2^{XY}$ is positive with its largest value $\sim 5^\circ$ and thus more than three times the largest value of $\bar{\theta}_1^{XY}$. The smallest value of $\bar{\theta}_2^{XY}$ is $\sim 0.5^\circ$. The ratio of the tilt modulus F_{11}^{XY} to the roll modulus F_{22}^{XY} varies in the range ~ 1 to ~ 5 , and the ratio of the twist modulus F_{33}^{XY} to the harmonic mean $A^{XY} = 2[(1/F_{11}^{XY}) + (1/F_{22}^{XY})]$ of the tilt and roll moduli varies in the range ~ 0.5 to ~ 1.8 . The twist-roll coupling modulus F_{23} , in units of kT/deg^2 , varies in the range ~ 0.00 to ~ 0.03 .

In Ref. 24, Gonzales and Maddocks develop a theory that relates the moduli $F_{ij}^n, G_{ij}^n, H_{ij}^n$ and the intrinsic parameters $\bar{\theta}_i^n, \bar{\rho}_i^n$ to statistical averages and correlations between θ_i^n and ρ_i^n for ensembles of configurations obtainable from all-atom molecular dynamics simulations.

III. DERIVATION OF THE PRINCIPAL RESULTS

A. Symmetry relations

The underlying assumption behind Eq. (2.2) is that ψ^n in Eq. (2.1) is given by a function $\check{\psi}^n$ of \mathbf{r}^n and the two right-handed orthonormal triads $\mathbf{d}_1^n, \mathbf{d}_2^n, \mathbf{d}_3^n$ and $\mathbf{d}_1^{n+1}, \mathbf{d}_2^{n+1}, \mathbf{d}_3^{n+1}$; thus

$$\psi^n = \check{\psi}^n(\mathbf{d}_i^n, \mathbf{d}_j^{n+1}, \mathbf{r}^n) \quad (i, j = 1, 2, 3). \quad (3.1)$$

The principle of material frame indifference requires that $\check{\psi}^n$ obey, for each proper orthogonal second-order tensor \mathbf{J} , the relation

$$\check{\psi}^n(\mathbf{d}_i^n, \mathbf{d}_j^{n+1}, \mathbf{r}^n) = \check{\psi}^n(\mathbf{J}\mathbf{d}_i^n, \mathbf{J}\mathbf{d}_j^{n+1}, \mathbf{J}\mathbf{r}^n), \quad (3.2)$$

as an identity. It follows from this last relation and Cauchy's representation theorem for scalar-valued isotropic functions of lists of vectors that there is a function such that²⁵

$$\psi^n = \bar{\psi}^n(D_{ij}^n, r_i^n); \quad (3.3)$$

this relation is equivalent to Eq. (2.2).

Now, the functions $\check{\psi}^n$ and $\bar{\psi}^n$ are assumed to be determined by the (ordered) pair XY of nucleotide bases located at the n th and $(n+1)$ th positions on the sugar-phosphate chain for which n increases in the $5' - 3'$ direction. Hence, for $\check{\psi}^n$ and $\bar{\psi}^n$ we may write $\check{\psi}^{XY}$ and $\bar{\psi}^{XY}$. To derive restrictions that the antiparallel arrangement of the oriented sugar-phosphate chains of duplex DNA impose on these functions, we note that, as the complements of A and G are $\bar{A} = T$ and $\bar{G} = C$, the 16 ordered pairs XY separate into two classes. One class contains the four self-complementary pairs $\{AT, GC, TA, CG\}$, each of which, because it has $Y = \bar{X}$, obeys the relation $XY = \bar{Y}\bar{X}$. The remaining class of twelve is made up of six sets of complementary pairs (i.e., pairs $\{X_1 Y_1, X_2 Y_2\}$ with $X_2 Y_2 = \bar{Y}_1 \bar{X}_1$), namely, $\{AA, TT\}$, $\{AG, CT\}$, $\{AC, GT\}$, $\{GA, TC\}$, $\{GG, CC\}$, $\{TG, CA\}$.

We consider now the (unique) transformation that changes the direction of increasing n while leaving invariant the orientation and spatial position of base pairs. Under such a transformation $\mathbf{d}_i^n, \mathbf{d}_j^{n+1}, \mathbf{r}^n$ is taken into ${}^* \mathbf{d}_i^m, {}^* \mathbf{d}_j^{m+1}, {}^* \mathbf{r}^m$, where $m = N - n + 1$ and

$${}^* \mathbf{d}_1^m = \mathbf{d}_1^{n+1}, \quad {}^* \mathbf{d}_1^{m+1} = \mathbf{d}_1^n, \quad (3.4a)$$

$${}^* \mathbf{d}_2^m = -\mathbf{d}_2^{n+1}, \quad {}^* \mathbf{d}_2^{m+1} = -\mathbf{d}_2^n, \quad (3.4b)$$

$${}^* \mathbf{d}_3^m = -\mathbf{d}_3^{n+1}, \quad {}^* \mathbf{d}_3^{m+1} = -\mathbf{d}_3^n, \quad (3.4c)$$

$${}^* \mathbf{r}^m = -\mathbf{r}^n, \quad (3.4d)$$

ψ^n remains unchanged, i.e., ${}^* \psi^m = \psi^n$, because the rectangles \mathfrak{B}^n , although they are renumbered in reverse order, keep their previous spatial positions and orientations. The transformation takes the vectors $\mathbf{d}_2^n, \mathbf{d}_2^{n+1}$, into vectors ${}^* \mathbf{d}_2^m, {}^* \mathbf{d}_2^{m+1}$, that again point toward the short edges that have corners attached to the chain for which n increases in the $5' - 3'$ direction (which is the one for which n decreased in that direction before the transformation). As the transformation replaces XY with its complement $\bar{Y}\bar{X}$ while leaving ψ^n invariant, the functions $\check{\psi}^{XY}$ and $\check{\psi}^{\bar{Y}\bar{X}}$ must obey the relation, $\check{\psi}^{XY}(\mathbf{d}_i^n, \mathbf{d}_j^{n+1}, \mathbf{r}^n) = \check{\psi}^{\bar{Y}\bar{X}}({}^* \mathbf{d}_i^m, {}^* \mathbf{d}_j^{m+1}, {}^* \mathbf{r}^m)$, i.e.,

$$\begin{aligned} & \check{\psi}^{XY}(\mathbf{d}_1^n, \mathbf{d}_2^n, \mathbf{d}_3^n, \mathbf{d}_1^{n+1}, \mathbf{d}_2^{n+1}, \mathbf{d}_3^{n+1}, \mathbf{r}^n) \\ &= \check{\psi}^{\bar{Y}\bar{X}}(\mathbf{d}_1^{n+1}, -\mathbf{d}_2^{n+1}, -\mathbf{d}_3^{n+1}, \mathbf{d}_1^n, -\mathbf{d}_2^n, -\mathbf{d}_3^n, -\mathbf{r}^n), \end{aligned} \quad (3.5)$$

or, equivalently,

$$\bar{\psi}^{XY}(D_{ij}^n, r_i^n) = \bar{\psi}^{\bar{Y}\bar{X}}(Q_{ik}D_{lk}^n Q_{jl}, Q_{il}D_{kl}^n r_i^n), \quad (3.6)$$

where Q_{ij} is as in Eq. (2.22). If the pair XY is self-complementary, i.e., is AT, GC, TA, or CG, then $\bar{Y}\bar{X} = XY$, and Eq. (3.5) becomes an identity for the function $\bar{\psi}^{XY}$.

As the tangent spaces to the manifold \mathfrak{M} of proper orthogonal 3×3 matrices are of dimension 3, each point of \mathfrak{M} has a neighborhood in which \mathfrak{M} has a smooth three-coordinate parametrization of the type discussed in Sec. II, and we can write

$$D_{ij}^n = \hat{D}_{ij}(\theta_1^n, \theta_2^n, \theta_3^n), \quad (3.7)$$

where the functions \hat{D}_{ij} are independent of n and locally one-to-one with continuously differentiable inverses. In terms of the kinematical variables θ_i^n and ρ_i^n defined in Eqs. (2.5)–(2.7), the Eqs. (3.4) take the form

$$\begin{aligned} & (*\theta_1^n, *\theta_2^n, *\theta_3^n, *\rho_1^n, *\rho_2^n, *\rho_3^n) \\ &= (-\theta_1^n, \theta_2^n, \theta_3^n, -\rho_1^n, \rho_2^n, \rho_3^n), \end{aligned} \quad (3.8)$$

and hence Eq. (3.5) is equivalent to the symmetry relation Eq. (2.9).

For use below, we note that because the three matrices $[{}_l V_{ij}^n]$, ($l=1,2,3$), with components

$${}_l V_{ij}^n = \hat{D}_{jk} \frac{\partial \hat{D}_{ik}}{\partial \theta_l^n}, \quad (3.9)$$

are skew in the sense that ${}_l V_{ij}^n = -{}_l V_{ji}^n$ for all i, j , there are numbers Ξ_{kl}^n ($k, l=1,2,3$), such that²⁶

$$*V_{ij}^n = \epsilon_{ijk} \Xi_{kl}^n. \quad (3.10)$$

The local invertibility of the function $[\hat{D}_{ij}]$ implies that the columns of the matrix $[\Xi_{kl}^n]$ form a (not necessarily orthogonal) basis for the tangent space of \mathfrak{M} at the point with coordinates $\theta_1^n, \theta_2^n, \theta_3^n$, and hence $[\Xi_{kl}^n]$ has a matrix inverse $[\Xi_{kl}^n]^{-1}$. For the transpose of $[\Xi_{kl}^n]^{-1}$ we write $[\Gamma_{kl}^n]$:

$$\Gamma_{ki}^n \Xi_{kj}^n = \delta_{ij}. \quad (3.11)$$

B. Equations of equilibrium

A configuration \mathcal{Z} of a DNA segment with $N+1$ base pairs is specified by giving the $(N+1)$ -tuple $\{(\mathbf{d}_1^n, \mathbf{d}_2^n, \mathbf{d}_3^n, \mathbf{x}^n)\}_{n=1}^{N+1}$, of ordered sets $(\mathbf{d}_1^n, \mathbf{d}_2^n, \mathbf{d}_3^n, \mathbf{x}^n)$ in which $\mathbf{d}_1^n, \mathbf{d}_2^n, \mathbf{d}_3^n$ is a right-handed orthonormal basis and \mathbf{x}^n a point in space. The total energy E of the segment is given by Eq. (2.10), in which $P = P(\mathcal{Z})$ is the potential energy of the external forces and moments acting on the segment. A configuration $\mathcal{Z}^\#$ is said to be *in equilibrium* if for each one-parameter family,

$$s \mapsto \mathcal{Z}(s), \quad \mathcal{Z}(0) = \mathcal{Z}^\#, \quad -\epsilon < s < \epsilon, \quad (3.12)$$

of configurations compatible with the imposed constraints [e.g., the strong anchoring end conditions or the closure conditions of Eq. (2.16)] there holds $E'(0) = 0$, i.e., in view of Eqs. (2.1) and (2.10),

$$\sum_{n=1}^N (\psi^n)'(0) + P'(0) = 0; \quad (3.13)$$

here primes indicate derivatives with respect to s .

To derive the variational equations implied by this definition, we employ Eq. (2.2), which yields

$$(\psi^n)' = \frac{\partial \hat{\psi}^n}{\partial \theta_i^n} (\theta_i^n)' + \frac{\partial \hat{\psi}^n}{\partial r_i^n} (r_i^n)', \quad (3.14)$$

where

$$(r_i^n)' = (\mathbf{d}_i^n \cdot \mathbf{r}^n)', \quad (3.15)$$

and, in view of Eq. (3.7), $(\theta_i^n)'$ obeys the relation

$$\frac{\partial \hat{D}_{ik}}{\partial \theta_l^n} (\theta_l^n)' = (D_{ij}^n)' = (\mathbf{d}_i^n \cdot \mathbf{d}_j^{n+1})'. \quad (3.16)$$

As the vectors $\mathbf{d}_1^n, \mathbf{d}_2^n, \mathbf{d}_3^n$ are orthonormal, there is a vector \mathbf{w}^n such that

$$(\mathbf{d}_i^n)' = \mathbf{w}^n \times \mathbf{d}_i^n. \quad (3.17)$$

By Eqs. (3.9)–(3.11), (3.15), and (3.17),

$$(r_i^n)' = \mathbf{d}_i^n \cdot [(\mathbf{r}^n)' - \mathbf{w}^n \times \mathbf{r}^n], \quad (3.18a)$$

$$(\theta_i^n)' = \Gamma_{ji}^n \mathbf{d}_j^n \cdot (\mathbf{w}^{n+1} - \mathbf{w}^n), \quad (3.18b)$$

$$P' = \sum_{n=1}^N \left[\left(\mathbf{d}_i^n \times \frac{\partial P}{\partial \mathbf{d}_i^n} \right) \cdot \mathbf{w}^n + \frac{\partial P}{\partial \mathbf{x}^n} \cdot (\mathbf{x}^n)' \right], \quad (3.18c)$$

and, if we put

$$\mathbf{f}^n = f_i^n \mathbf{d}_i^n, \quad f_i^n = \frac{\partial \hat{\psi}^n}{\partial r_i^n}, \quad (3.19a)$$

$$\mathbf{m}^n = m_i^n \mathbf{d}_i^n, \quad m_i^n = \Gamma_{ij}^n \frac{\partial \hat{\psi}^n}{\partial \theta_j^n}, \quad (3.19b)$$

$$\boldsymbol{\varphi}^n = \frac{\partial P}{\partial \mathbf{x}^n}, \quad (3.19c)$$

$$\boldsymbol{\mu}^n = \mathbf{d}_i^n \times \frac{\partial P}{\partial \mathbf{d}_i^n}, \quad (3.19d)$$

and write $\mathbf{v}^n = (\mathbf{x}^n)'$, then Eqs. (3.14) and (3.18c), respectively, can be cast into the forms

$$(\psi^n)' = \mathbf{m}^n \cdot (\mathbf{w}^{n+1} - \mathbf{w}^n) + \mathbf{f}^n \cdot (\mathbf{v}^{n+1} - \mathbf{v}^n - \mathbf{w}^n \times \mathbf{r}^n), \quad (3.20)$$

$$P' = \sum_{n=1}^N (\boldsymbol{\mu}^n \cdot \mathbf{w}^n + \boldsymbol{\varphi}^n \cdot \mathbf{v}^n). \quad (3.21)$$

In the last two equations, although end conditions affect the choice of the vectors \mathbf{w}^1 , \mathbf{v}^1 , \mathbf{w}^{N+1} , and \mathbf{v}^{N+1} , the vectors \mathbf{w}^n and \mathbf{v}^n can be selected arbitrarily for $n=2, \dots, N$. Hence, the relation (3.13) holds for the configuration $\mathcal{Z}^\#$ if and only if that configuration obeys the following *variational equations*:

$$\mathbf{f}^n - \mathbf{f}^{n-1} = \boldsymbol{\varphi}^n, \quad \mathbf{m}^n - \mathbf{m}^{n-1} = \mathbf{f}^n \times \mathbf{r}^n + \boldsymbol{\mu}^n \quad (2 \leq n \leq N), \quad (3.22)$$

and *natural end conditions*,

$$(\mathbf{m}^1 - \mathbf{f}^1 \times \mathbf{r}^1 - \boldsymbol{\mu}^1) \cdot \mathbf{w}^1 - (\mathbf{m}^N + \boldsymbol{\mu}^{N+1}) \cdot \mathbf{w}^{N+1} + (\mathbf{f}^1 - \boldsymbol{\varphi}^1) \cdot \mathbf{v}^1 - (\mathbf{f}^N + \boldsymbol{\varphi}^{N+1}) \cdot \mathbf{v}^{N+1} = 0. \quad (3.23)$$

The relations (3.22) are the analogs in the present theory of the equations of balance of moments and forces in Kirchhoff's (continuum) theory of elastic rods²⁷⁻³⁰ and several recent generalization of that theory (*vid.*, e.g., the treatise of Antman,³¹ Sec. VIII).

An equilibrium configuration $\mathcal{Z}^\#$ is stable if, for each one-parameter family of configurations that obeys (3.12) and is compatible with the imposed constraints, there holds, in addition to Eq. (3.13),

$$0 < E''(0) = \sum_{n=1}^N (\psi^n)''(0) + P''(0). \quad (3.24)$$

In practice, to verify stability we employ Eqs. (3.13)–(3.18) to express $E''(0)$ as a quadratic form Q on the $6(N+1)$ -dimensional space of the components of $\mathbf{w}^1, \mathbf{v}^1, \dots, \mathbf{w}^{N+1}, \mathbf{v}^{N+1}$ with respect to one fixed basis, e.g., $\mathbf{d}_1^1, \mathbf{d}_2^1, \mathbf{d}_3^1$. If λ , the smallest proper number of Q , is less than zero, the configuration $\mathcal{Z}^\#$ is unstable. If $\lambda > 0$, $\mathcal{Z}^\#$ is stable. This test was used to verify statements made in Sec. IV about the stability of calculated configurations.

IV. EXAMPLES OF EQUILIBRIUM CONFIGURATIONS

Much of the research on DNA elasticity employs an idealized elastic rod model, based on the assumption that a duplex DNA molecule is an intrinsically straight, homogeneous, elastic rod obeying the special case of Kirchhoff's general theory in which there are just two elastic constants: a twisting modulus and a bending modulus. Several recent studies (e.g., Refs. 32–40) of the influence of intrinsic curvature on the elastic response of DNA are based on Kirchhoff's general theory⁴¹ in which a rod has two bending moduli and, in addition, the possible presence of intrinsic curvature and torsion is taken into account. The constitutive relation for the elastic energy of a rod obeying that theory does not contain cross-terms directly coupling the twisting moment to the local curvature. It is known that in a materially homogeneous region of a rod with intrinsic curvature the density of excess twist is, in general, not uniform in equilibrium. In Ref. 33 it is shown that the equations of equilibrium appropriate to Kirchhoff's theory imply that when intrinsic curvature is present the derivative of twist with respect to distance along the rod axis is a function of local curvature. See also the papers of Bauer, Lund, and White^{32,35,37} and

Garrivier and Fourcade⁴⁰ and the calculations therein of the effect of intrinsic curvature on the shape and twist density profile of o-rings^{32,35,37} and plectonemic loops.⁴⁰

Here we give examples of calculated equilibrium configurations of DNA minicircles obeying the theory presented in Sec. II. In order to obtain insight into the implication of our theory, we deliberately treat cases in which known results for intrinsically curved rods obeying Kirchhoff's theory can yield physical intuition as to what to expect. We therefore treat minicircles that may be called "DNA o-rings" because they are intrinsically bent in such a way that in stress-free configurations their axial curves are nearly circular. The helical nature of DNA makes it impossible to form a stress-free o-ring with the intrinsic kinematical variables the same at each base-pair step, for if they were the same, the bendings occurring in the two halves of each helical repeat length, being then of equal magnitudes, but in opposite directions would cancel. For this reason, the minicircles we treat are composed of 10 bp helical repeat units in which 5 bp form an intrinsically straight segment and the remaining 5 bp form an intrinsically curved segment.⁴² (The highly curved sequences found in the kinetoplast DNA from the Trypanosomatidae *Crithidia fasciculata* and *Leishmania tarentolae* have on one strand stretches of four to six adenine bases that are separated by stretches of comparable length rich in guanine and cytosine bases⁴³⁻⁴⁶).

In analogy with the familiar assumptions in the continuum theories of DNA elasticity, in our examples $\tilde{\psi}^n$ is taken to be a quadratic function of the kinematical variables. Results are presented for two types of DNA minicircles: For those of type I, the matrix of the quadratic form characterizing $\tilde{\psi}^n$ is diagonal for each n . For those of type II, each helical repeat length contains five base-pair steps for which the off-diagonal modulus associated with coupling between roll and twist is not zero and hence the minicircle is expected to show chiral phenomena not predicted by Kirchhoff's classical theory of rods. The configurations shown were obtained by a solution of the equations of mechanical equilibrium.

The minicircles we consider have $N=150$ bp and are composed of 15 repetitions of a 10 bp unit in which the first 5 bp have

$$(\bar{\theta}_1^n, \bar{\theta}_2^n, \bar{\theta}_3^n) = (0, 0, 36^\circ), \quad (\bar{\rho}_1^n, \bar{\rho}_2^n, \bar{\rho}_3^n) = (0, 0, 3.4 \text{ \AA}), \quad (4.1)$$

and hence form an ideal Watson–Crick DNA segment while the remaining 5 bp have⁴⁷

$$(\bar{\theta}_1^n, \bar{\theta}_2^n, \bar{\theta}_3^n) = (0, 7.413^\circ, 35.568^\circ), \quad (4.2)$$

$$(\bar{\rho}_1^n, \bar{\rho}_2^n, \bar{\rho}_3^n) = (0, 0, 3.4 \text{ \AA}),$$

and hence form an intrinsically curved segment. [For the calculations we report, the kinematical variables $\theta_1^n, \theta_2^n, \theta_3^n, \rho_1^n, \rho_2^n, \rho_3^n$ that are schematically illustrated in Fig. 1 are taken to be those defined in Ref. 14 and Eqs. (2.5)–(2.7).] A minicircle with this choice of N and the indicated parameters $\bar{\theta}_i^n, \bar{\rho}_i^n$ has a linking number \mathcal{L} of 15, and in its stress-free configuration its axial curve \mathcal{C} has the appearance

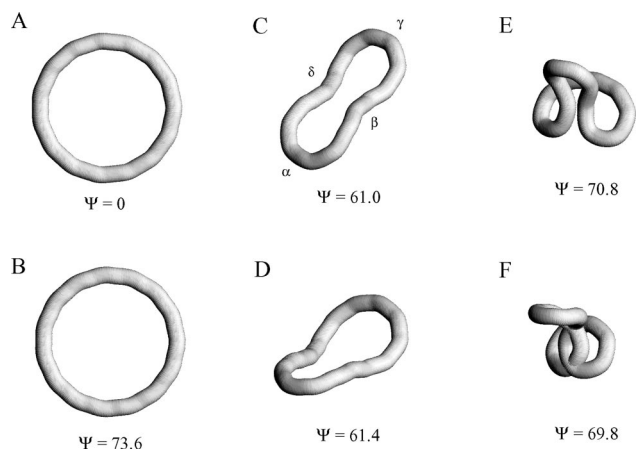


FIG. 3. Equilibrium configurations of the 150 bp o-ring, Minicircle I, for the case $\omega=0.7$. Shown are the stress-free configuration A that gives a global minimum to Ψ , the unstable everted ring configuration B, the metastable chair configuration, and the unstable configurations D and E; F is an unstable solution of the equilibrium equations that is incompatible with the assumed impenetrability of DNA. Configuration D lies at a saddle point in the energy landscape for configurations of the o-ring. Here, as in Figs. 5, 7, 9, and 11, configurations are drawn as tubes of diameter 20 Å. The elastic energy Ψ is given in units of kT .

of a polygon of 15 sides with rounded vertices that is sufficiently close to a circle to permit us to refer to the minicircle as an o-ring. For both I and II, the moduli G_{ij}^n and H_{ij}^n are here taken to be independent of n with $G_{ij}=0$ for all i, j , with $H_{ij}=0$ for $i \neq j$, and with H_{11}, H_{22}, H_{33} large enough to suppress deformations that change the displacement variables ρ_i^n . The two minicircles differ in the value of the coupling coefficients F_{ij}^n , $i \neq j$; for both, F_{11}, F_{22}, F_{33} are independent of n and such that $F_{11}=F_{22}=4.27 \times 10^{-2} kT/\text{deg}^2$; the ratio

$$\omega = F_{33}/F_{11}, \quad (4.3)$$

was set equal to 0.7 for certain calculations and 1.4 for others.⁴⁸

A. Minicircle I

Minicircle I is such that, for $i \neq j$ and $n = 1, \dots, 150$,

$$F_{ij}^n = 0, \quad (4.4)$$

and hence Eq. (2.19) does not contain off-diagonal terms coupling the kinematical variables.

Even when this minicircle is kept free of bound proteins and other chemical agents, it has multiple equilibrium configurations, several of which (each with $\mathcal{L}=15$) are shown in Fig. 3, where $\omega=0.7$. In that figure, A is the stress-free, nearly circular, minimum energy configuration. The “everted ring” configuration B has the axial curve close to a circle (as does A) and may be described, to a good approximation, as a configuration obtained from A by rotating each base pair in its plane by one half-turn (as in the motion called the “smoke-ring rotation”). It has been known for a long time⁴⁹ that everted ring configurations of o-rings are unstable. The “chair” configuration C is familiar from experience with elastic rings and was treated by Charitat and Fourcade³⁶ us-

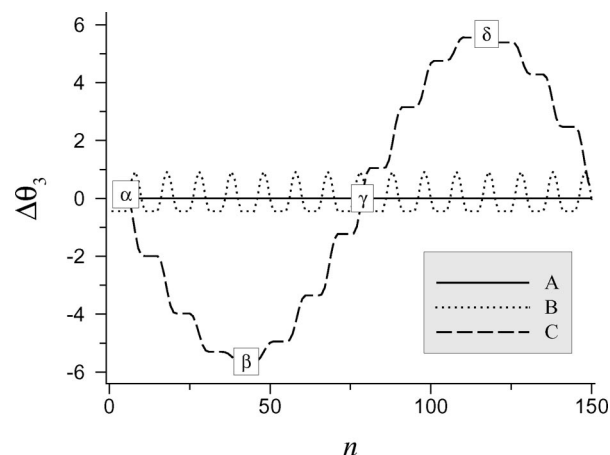


FIG. 4. The excess twist $\Delta\theta_3^n$ (in degrees) as a function of n for selected configurations of Fig. 3. The points on the graph for the chair configuration C that are labeled $\alpha, \beta, \gamma, \delta$ have the geometric locations indicated in Fig. 3 and correspond to the apexes (α, γ) of the chair and the midpoints (β, δ) of its sides.

ing Kirchhoff’s theory. The stability of chair configurations depends on ω . We find that (i) when $\omega < 1$, as it is in the present example, the configuration C is metastable; (ii) C is unstable when $\omega > 1$; and (iii) when $\omega = 1$, there is a one-parameter family of distinct chair configurations of equal energies.⁵⁰ The configurations D and E, which to our knowledge have not been discussed before, have less symmetry than C and are unstable; in the present example, D lies at a mountain pass for a transition path from C to the globally stable configuration A. The item labeled F, although it corresponds to a solution of Eqs. (2.11), (2.12), and (2.17), is not a physically admissible configuration, because it does not obey the condition of impenetrability of base pairs.

Figure 4 contains graphs of excess twist $\Delta\theta_3^n$ versus n for selected configurations of Fig. 3 and shows that although $\Delta\theta_3^n$ is zero for the globally stable circular configuration A and approximately zero for the unstable circular configuration B, such is not the case for the chair configuration C. For that configuration, $|\Delta\theta_3^n|$ vanishes near the two “apexes” of the chair (labeled α and γ), and attains its (remarkably large) maximum near the centers of the “sides” of the chair (β and δ). In Fig. 4 (and also in Figs. 6, 8, and 10) it can be seen that the excess twist $\Delta\theta_3^n$ is constant within each of the intrinsically straight segments in which Eq. (4.1) holds. This local constancy is a consequence of the fact that in the intrinsically straight segments of Minicircle I the quadratic constitutive functions ψ^n are free of cross-terms coupling twist to other kinematical variables. In the intrinsically curved segments obeying Eq. (4.2), regardless of whether cross-terms are present in ψ^n , $\Delta\theta_3^n$ is generally nonmonotone, and is constant only if the o-ring is stress-free. Arguments of the type that led to Eq. (28) of Ref. 33 can be employed here to show that if $\Delta\theta_1^n$ in an intrinsically curved segment changes sign between n and $n+1$, then $\Delta\theta_3^n$ has an extremum at n or $n+1$.

It has been known for a long time that one can induce negative supercoiling in closed DNA by reacting it with an intercalating agent, such as ethidium bromide (EtBr), that

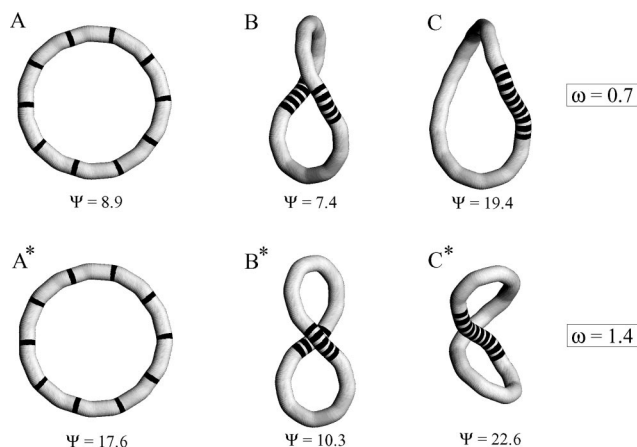


FIG. 5. Influence of the spatial distribution of intercalated molecules on the minimum elastic energy configuration of Minicircle I. Shown are calculated results for cases in which ten molecules are intercalated into the minicircle with each inducing the local change $\bar{\theta}_3^n \rightarrow \bar{\theta}_3^n - 30^\circ$, $\bar{\rho}_3^n \rightarrow \bar{\rho}_3^n + 3.4 \text{ \AA} = 6.8 \text{ \AA}$. The sites of binding are shown as dark bands. In configurations A and A*, these sites are equally spaced along the axial curve; in B and B* they occupy every other base-pair step in two antipodally placed 11 bp subsegments of the minicircle; in C and C* they occupy every other base-pair step in a single 21 bp subsegment. As indicated, $\omega = 0.7$ for A, B, C, and $\omega = 1.4$ for A*, B*, C*.

binds to DNA between base pairs and causes a local reduction of the intrinsic twist of the double helix.⁵¹ If, while maintaining the other assumptions we have made about Minicircle I, we were to assume that Eqs. (4.1) hold for $1 \leq n \leq 150$, which would make the minicircle not only homogeneous in n but also one that was formed from intrinsically straight DNA (with $\bar{\theta}_1^n \equiv \bar{\theta}_2^n \equiv 0$),⁵² then the equilibrium shape and elastic energy of the minicircle would depend on the number of molecules of EtBr intercalated in it but would be essentially independent of their distribution along \mathcal{C} .⁵³ We have found, however, that, because Minicircle I is an o-ring formed from DNA that is intrinsically curved in accord with Eqs. (4.1) and (4.2), its equilibrium shape and elastic energy are strongly dependent on both the number and the distribution along \mathcal{C} of the bound molecules.⁵⁴

Figure 5 contains results of calculations in which ten identical molecules are assumed to be intercalated at specified base-pair steps of Minicircle I, with each such molecule reducing the intrinsic twist $\bar{\theta}_3^n$ by 30° and doubling the intrinsic rise $\bar{\rho}_3^n$ at the step at which it is intercalated, as is the case for EtBr.⁵⁵ In the discussion that follows we assume that the intercalating agent obeys the principle of nearest neighbor exclusion, requiring that two bound molecules be separated by at least one base-pair step. (There is evidence to the effect that this exclusion principle does hold for small intercalating ligands.^{56,57}) If at any given instant the distribution of the ten intercalated molecules is spatially uniform, Minicircle I retains its circular configuration. When those molecules are distributed in such a way that they occupy every other base pair step within two antipodally placed subsegments of equal length, the o-ring folds into one of the “figure-8” configurations B and B*. When the bound molecules are concentrated in a short subsegment (but yet obey the principle of nearest neighbor exclusion), the o-ring again

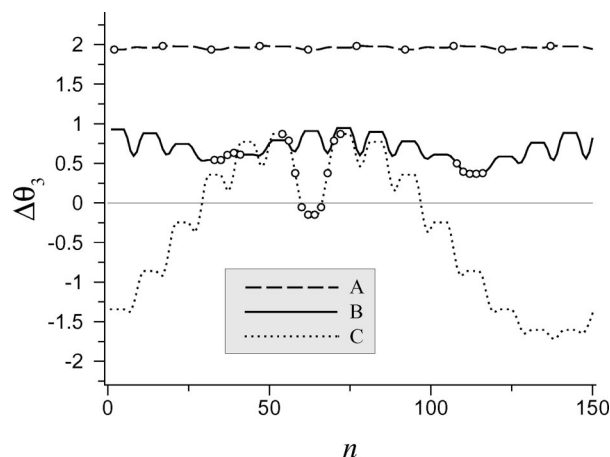


FIG. 6. $\Delta\theta_3^n$ as a function of n for the configurations of Fig. 5 for which $\omega = 0.7$. The symbols \circ mark the sites at which the intercalating agent is bound.

deforms out of plane and, in the case of $\omega = 1.4$, folds into a configuration of the “clamshell” type, here labeled C*. In the present case we obtain the result that, for both values of ω the distribution into two equal and antipodally placed subsegments, seen in B and B*, is the distribution that minimizes Ψ over all distributions of ten intercalated molecules.⁵⁸

The values of Ψ given in Fig. 5 tell us that, if we assume that EtBr binding is independent of nucleotide composition, in the case of dynamical equilibrium the most probable spatial distribution of bound molecules will be close to that seen in B and B*. Of course, the number of bound molecules is a fluctuating quantity that depends on the concentration of EtBr and DNA in solution. A complete analysis of curvature-induced binding cooperativity of EtBr molecules leading to the prediction of Scatchard plots of EtBr binding activity would be a computationally intensive task that has not yet been undertaken. However, the preliminary results shown here do suggest that, for DNA subject to appropriate end conditions, such as those of the Eqs. (2.16) that characterize ring closure, the spatial distribution of EtBr can be expected to be sensitive to assumed intrinsic curvature.

Under the present assumptions about the o-ring and the intercalating agent, although $\Delta\theta_3^n$ is positive for all n when the intercalating molecules are equally spaced along the length of the minicircle, if those molecules are concentrated into a short enough subsegment \mathcal{S} , as they are in the minimum energy configurations C and C*, $\Delta\theta_3^n$ becomes negative in a neighborhood of the antipode of the midpoint \mathcal{S} (see Fig. 6).

To investigate the effect of the localization of changes in the intrinsic twist, we have calculated configurations for cases in which a single molecule of an agent is bound to an o-ring at one base-pair step, say that with $n = 1$, and reduces the intrinsic twist of the DNA at that site by a large positive amount α , i.e., induces the transformation $\bar{\theta}_3^1 \rightarrow \bar{\theta}_3^1 - \alpha$ while leaving other intrinsic variables unchanged. In a study of the effect of intrinsic curvature on configurations of DNA minicircles obeying Kirchhoff’s theory (in which, as is the case for Minicircle I, the constitutive relations do not contain

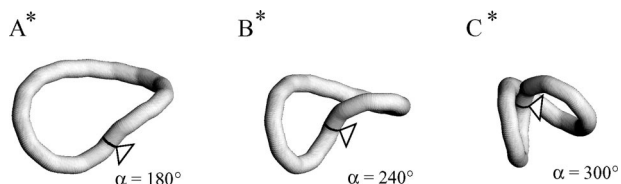


FIG. 7. Configurations of Minicircle I that minimize Ψ when the minicircle is bound to an untwisting agent supposed capable of lowering $\bar{\theta}_3^1$ by 180° in the case of A^* , 240° in the case of B^* , and 300° (which is equivalent to the total untwisting induced by the intercalation of ten molecules of EtBr) in the case of C^* . The binding site for the agent is indicated by a triangle. Here, as in all subsequent figures, $\omega=1.4$.

cross-terms coupling curvature to the twisting moment). Bauer, Lund, and White^{32,35,37} found that a reduction of the excess link by cutting at a single cross-section (which is roughly equivalent to an increase in intrinsic twist at a single base pair step) can lead to remarkably large deformations even when the magnitude of that reduction is less than 1 (i.e., $|\alpha| < 360^\circ$) and hence less than the amount required to induce supercoiling in intrinsically straight rods.⁵⁹ Results for Minicircle I with ω equal to 1.4 and for rather extreme values of α are shown in Figs. 7 and 8.⁶⁰ As seen in Fig. 7, as α increases the o-ring folds up, with the folding becoming appreciable for α near 180° , and at sufficiently high α the o-ring attains a clamshell configuration. When, as here, the change of intrinsic twist is confined to one base-pair step, configurations (but not their energies) are approximately independent of ω . In Fig. 8 one sees that, as expected from the results shown in Fig. 6, the excess twist is negative in a neighborhood of the antipode to the binding site.⁶¹ As the constitutive equation for the energy of Minicircle I does not contain off-diagonal terms directly coupling roll or tilt to twist, if the twisting agent were one that raises $\bar{\theta}_3^1$ (i.e., that has $\alpha < 0$), the resulting configurations would be essentially mirror images of those shown in Fig. 7. See, however, Fig. 11 and comments made below about Minicircle II.

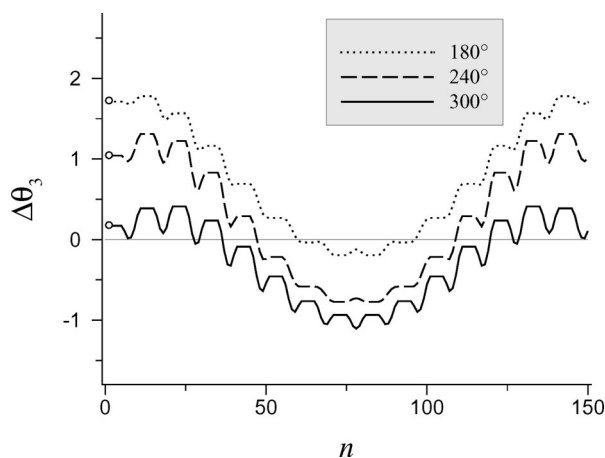


FIG. 8. Graphs of $\Delta\theta_3^n$ vs n for the configurations of Fig. 7. The untwisting agent is bound at the base-pair step marked by \circ for which $n=1$.

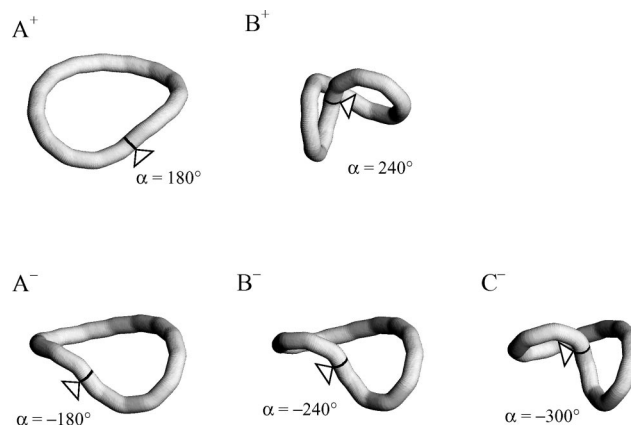


FIG. 9. The configurations of Minicircle II that minimize Ψ when $\bar{\theta}_3^1$ is changed to $\bar{\theta}_3^1 - \alpha$ with α at the indicated values.

B. Minicircle II, an o-ring with off-diagonal terms coupling twist to roll

In the case of Minicircle II, for those values of n at which Eq. (4.1) holds,

$$(F_{12}^n, F_{23}^n, F_{13}^n) = (0, 0, 0), \quad (4.5)$$

and, for the n at which Eq. (4.2) holds,

$$(F_{12}^n, F_{23}^n, F_{13}^n) = (0, \frac{4}{5} F_{22}^n, 0). \quad (4.6)$$

Thus, in each repeated 10 bp unit, the first 5 bp form an intrinsically straight segment and do not show coupling between kinematical variables, while the remaining 5 bp form an intrinsically curved segment and are such that the twist-roll coupling modulus F_{23}^n is positive and hence raising the roll tends to lower the twist, i.e., an increase in θ_2^n results in a twisting moment that tends to decrease θ_3^n . (The positivity of F_{23}^n is compatible with the coupling of parameters observed in high-resolution DNA crystal structures.^{4,6}) The calculations shown here for Minicircle II (Figs. 9–12) were done with $\omega=1.4$.

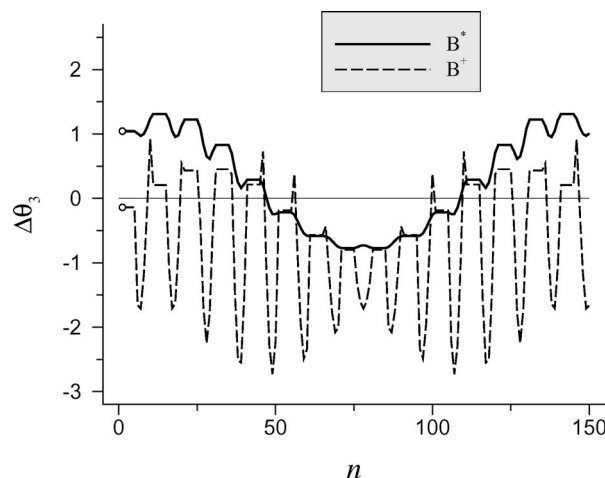


FIG. 10. Graphs of $\Delta\theta_3^n$ vs n for the configuration B^* of Minicircle I (see Fig. 7) and the configuration B^+ of Minicircle II (see Fig. 9). The untwisting agent is bound at the base-pair step marked by \circ , for which $n=1$.

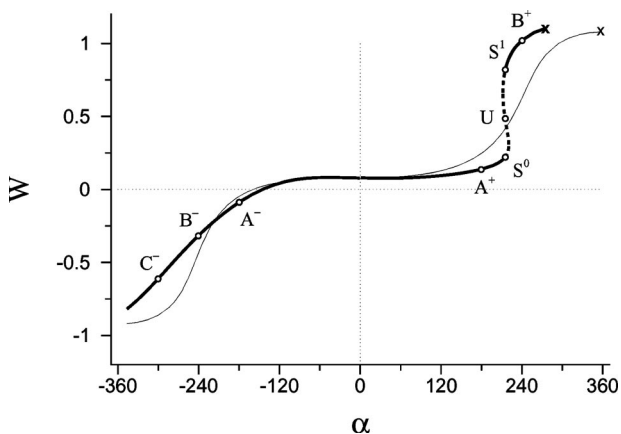


FIG. 11. Graphs of the writhe W vs α for minimum energy configurations of Minicircle I (light curve) and Minicircle II (heavy curve) bound to a twisting agent. (In both cases $\omega=1.4$.) The points A^+ , B^+ , A^- , B^- , C^- correspond to the configurations of Fig. 9, and the points S^0 , S^1 , U to the configurations of Fig. 12. The configurations at which Ψ has its global minimum for the specified α lie in the regions drawn as solid curves (light or heavy); there are configurations on the heavy dashed curve that are not even local minimizers of Ψ (see Figs. 12 and 13). The \times marks the largest α for which the minimum energy configuration of each minicircle is free from self-contact.

Although Minicircles I and II both have minimum energy configurations that are stress-free and nearly circular, the effect of a twisting agent on II is dependent on whether the agent reduces or increases the intrinsic twist of DNA. If, subject to the transformation $\bar{\theta}_3^1 \rightarrow \bar{\theta}_3^1 - \alpha$, Minicircle II (like I) shows appreciable folding when $|\alpha|$ exceeds 180° . However, as one sees in Fig. 9, in contrast to what the theory yields for I, the minimum energy configurations of II for α and $-\alpha$ are *not* mirror images. The graphs of $\Delta\theta_3^n$ versus n in Fig. 10 for the configurations of Minicircles I and II with $\alpha=240^\circ$ tell us that in the 5 bp subsegments of II in which coupling is present $\Delta\theta_3^n$ is much lower than it is in the corresponding subsegments of I, which is a consequence of the fact that in those subsegments θ_2^n (i.e., roll) is larger than its stress-free value. The presence of coupling here induces untwisting by as much as 2.7° , with the most untwisting attained at the base-pair steps with $n=49$ and 106, which are located roughly 1/3 of the circumference away from the binding site of the untwisting agent.

The graphs of Fig. 11 showing the dependence on α of the writhe W , which is a measure of the folding of the o-ring,^{62,63} illustrate well the difference in the response of the two minicircles to the binding of a twisting agent. While the response of I is nearly antisymmetric, in the sense that the configurations corresponding to α and $-\alpha$ are close to mirror

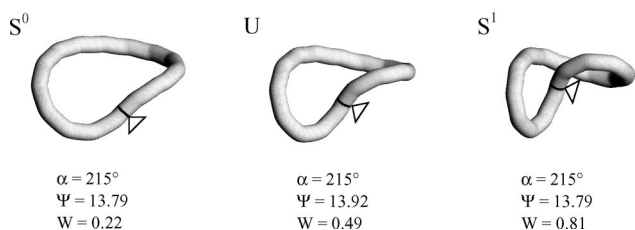


FIG. 12. The stable configurations S^0 , S^1 and the unstable configuration U of Minicircle II of Fig. 11 with $\alpha=215.0^\circ$.

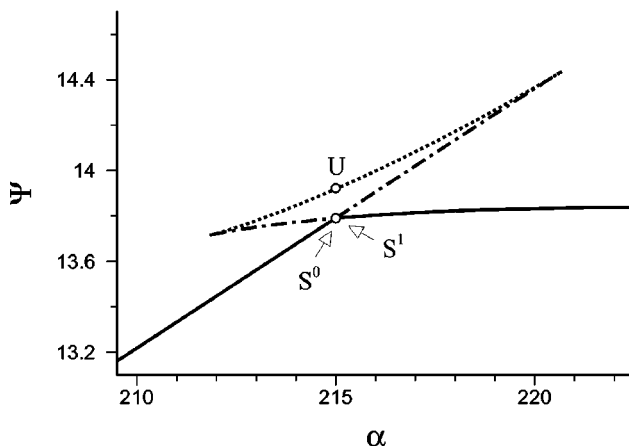
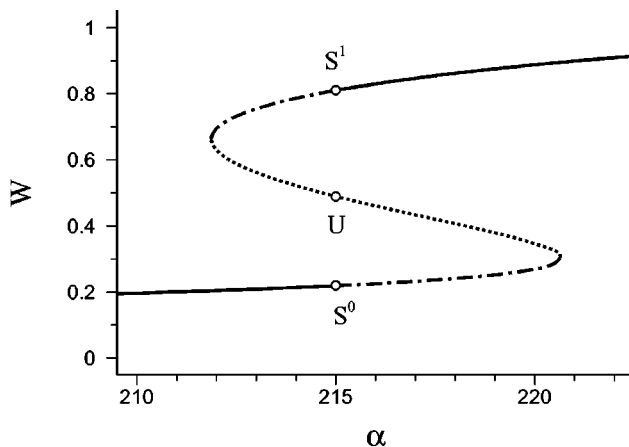


FIG. 13. Graphs of W vs α and Ψ vs α for equilibrium configurations of Minicircle II with α in a neighborhood of 215.0° . S^0 and S^1 are points of exchange of global stability, U determines the energy barrier for the transition $S^0 \rightarrow S^1$. Stability of configurations is indicated as follows: (—) globally stable, (---) locally stable, (···) unstable.

images and hence $W(-\alpha) \cong 2W(0) - W(\alpha)$, the response of II is chiral and such that, for negative α (i.e., for an increase in intrinsic twist), W changes monotonically with α , but for each (positive) α in the interval $211.9^\circ < \alpha < 220.7^\circ$ there are three equilibrium configurations, with two stable and one unstable. When $\alpha=215.0^\circ$, the two stable configurations (labeled S^0, S^1) have equal elastic energy (Fig. 12). As seen in Fig. 13, the configurations with preassigned $\alpha \leq \alpha(S^0)$ that give a global minimum to Ψ form a continuous one-parameter family of configurations that terminates at S^0 and is not connected to the family of minimum energy configurations with $\alpha \geq \alpha(S^1)$. At $\alpha=215.0^\circ$ infinitesimal changes in α result in first-order transitions between the stable equilibrium states S^0 and S^1 . The unstable configuration U with $\alpha(U) = \alpha(S^0) = \alpha(S^1)$ lies at a mountain pass for these transitions. The graph of Ψ versus α seen in Fig. 13 tells us that there is an essentially negligible energy barrier, namely $0.13 kT$, for the transitions $S^0 \rightarrow S^1$ and $S^1 \rightarrow S^0$ between the “open” configuration S^0 and the “partially folded” configurations S^1 , both of which give to Ψ its global minimum in the class of all configurations that are accessible without changes in α .

ACKNOWLEDGMENTS

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APPENDIX: EXPLICIT EXPRESSIONS FOR MATRICES IN EQS. (2.12)–(2.15)

For the matrix $[\Gamma_{ij}^n]$ of Eq. (2.12), the Eqs. (2.5)–(2.6) and (3.9)–(3.11) yield

$$[\Gamma_{ij}^n] = \begin{bmatrix} -\frac{\theta_1^n \sin \zeta^n + \frac{\theta_2^n \cos \zeta^n}{2 \tan\left(\frac{1}{2} \kappa^n\right)}}{\kappa^n} & -\frac{\theta_2^n \sin \zeta^n - \frac{\theta_1^n \cos \zeta^n}{2 \tan\left(\frac{1}{2} \kappa^n\right)}}{\kappa^n} & \tan\left(\frac{1}{2} \kappa^n\right) \cos \zeta^n \\ \frac{\theta_1^n \cos \zeta^n + \frac{\theta_2^n \sin \zeta^n}{2 \tan\left(\frac{1}{2} \kappa^n\right)}}{\kappa^n} & \frac{\theta_2^n \cos \zeta^n - \frac{\theta_1^n \sin \zeta^n}{2 \tan\left(\frac{1}{2} \kappa^n\right)}}{\kappa^n} & \tan\left(\frac{1}{2} \kappa^n\right) \sin \zeta^n \\ & -\frac{\theta_2^n}{2} & \frac{\theta_1^n}{2} & 1 \end{bmatrix}. \quad (\text{A1})$$

For each j , the numbers ${}_j\Lambda_{kl}^n$ of Eq. (2.15) are the components of a skew matrix $[_j\Lambda_{kl}^n]$. When $j = 1$,

$$\begin{aligned} {}_1\Lambda_{12}^n &= \frac{\theta_2^n \left(1 - \cos\left(\frac{1}{2} \kappa^n\right)\right)}{(\kappa^n)^2}, \\ {}_1\Lambda_{13}^n &= \frac{\theta_1^n \theta_2^n \left(2 \sin\left(\frac{1}{2} \kappa^n\right) - \kappa^n\right)}{2(\kappa^n)^3}, \\ {}_1\Lambda_{23}^n &= \frac{1}{2} + \left(\frac{\theta_2^n}{\kappa^n}\right)^2 \frac{2 \sin\left(\frac{1}{2} \kappa^n\right) - \kappa^n}{2 \kappa^n}. \end{aligned} \quad (\text{A2})$$

When $j = 2$,

$$\begin{aligned} {}_2\Lambda_{12}^n &= \frac{\theta_1^n \left(\cos\left(\frac{1}{2} \kappa^n\right) - 1\right)}{(\kappa^n)^2}, \\ {}_2\Lambda_{13}^n &= \left(\frac{\theta_1^n}{\kappa^n}\right)^2 \frac{\kappa^n - 2 \sin\left(\frac{1}{2} \kappa^n\right)}{2 \kappa^n} - \frac{1}{2}, \\ {}_2\Lambda_{23}^n &= \frac{\theta_1^n \theta_2^n \left(\kappa^n - 2 \sin\left(\frac{1}{2} \kappa^n\right)\right)}{2(\kappa^n)^3}. \end{aligned} \quad (\text{A3})$$

When $j = 3$,

$$\begin{aligned} {}_3\Lambda_{12}^n &= \frac{1}{2} \cos\left(\frac{1}{2} \kappa^n\right), \quad {}_3\Lambda_{13}^n = -\frac{\theta_1^n}{2 \kappa^n} \sin\left(\frac{1}{2} \kappa^n\right), \\ {}_3\Lambda_{23}^n &= -\frac{\theta_2^n}{2 \kappa^n} \sin\left(\frac{1}{2} \kappa^n\right). \end{aligned} \quad (\text{A4})$$

¹C. R. Calladine and H. R. Drew, *J. Mol. Biol.* **178**, 773 (1984).

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⁸In engineering practice the term "o-ring" is commonly used for elastic rings that are circular when stress-free.

⁹See also the discussion given in Refs. 32–40.

¹⁰In our numbering of base pairs the choice of the direction of increasing n is arbitrary. Although it is common to number the base pairs so that increasing n corresponds to advance in the 5'–3' direction of the strand that (in discussions of transcription) is called the sequence strand, we do not impose such a convention here. Because we study the implications of the requirement that the energy ψ^n be independent of the choice of the direction of increasing n , it is necessary for us to consider transformations that change that direction while leaving invariant the orientation and spatial position of the base pairs.

¹¹The superposed symbols, \sim , $\hat{\cdot}$, etc., here serve to emphasize the distinction between a value of a quantity and a function relating the quantity to other quantities.

¹²In general, \mathbf{x}^n , the center of the *rectangle* \mathfrak{B}^n , is not the barycenter (center of mass) of the corresponding *base pair*. Here, as in Ref. 64, \mathbf{x}^n , \mathbf{d}_1^n , and \mathbf{d}_3^n are obtained by the following construction: Let l_2 be the straight line connecting the C1' atoms of the deoxyribose groups corresponding to the n th pair base, and let l_1 be the line that passes at a right angle through the midpoint of l_2 and intersects the straight line containing the C8 atom of the purine base and the C6 atom of the complementary pyrimidine base. The point \mathbf{x}^n is taken to lie at the intersection of l_1 and l_2 ; the vector \mathbf{d}_1^n

- is parallel to l_1 and points in the direction of the major groove; \mathbf{d}_3^n is perpendicular to both l_1 and l_2 with $\mathbf{d}_3^n \cdot \mathbf{r}^n > 0$.
- ¹³ V. B. Zhurkin, Y. P. Lysov, and V. I. Ivanov, *Nucleic Acids Res.* **6**, 1081 (1979).
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- ¹⁹ Such an external force and moment can arise when the n th base pair is in contact with a protein or with a base pair sequentially distant from it. When electrostatic forces are taken into explicit account, P in Eq. (2.10) will include the potential energy of the interaction of charged residues.
- ²⁰ The configurations discussed in Sec. IV may be considered appropriate to cases in which the ionic strength of the solution is sufficiently high (≥ 1 M) that the Debye length is significantly less than the distance between charged sites and the employed values of elastic moduli and intrinsic kinematical parameters have been adjusted to account for the electrostatic interaction of adjacent base pairs.
- ²¹ Packer, Dauncy, and Hunter (Ref. 65) have used a computational model to calculate the potential energy surface for base-pair steps as a function of two principal degrees of freedom, slide, and shift, and obtained results that suggest that the presence of close local minima of energy (of the type observed in crystal structures of DNA oligomers in Ref. 5) can limit the range of applicability of quadratic approximations for ψ^n . Their calculations for tetramer steps (Ref. 66) further suggest that one should not blandly assume that interactions of nonadjacent base pairs need not be taken into account. However, there are not as yet a sufficient number of high-resolution crystallographic structures available to treat all 136 tetramer steps in the analysis of the sequence-dependent properties of DNA and to answer the question, posed in Ref. 67, of whether the base-pair neighbors adjacent to a dimer step have a strong influence on its elastic properties.
- ²² O'Hern *et al.* (Ref. 68) developed a model of DNA elasticity in which base pairs are assumed to be rigid plates separated by a homogeneous isotropic elastic material, and showed that their model implies that, for each n , ψ^n is a quadratic function obeying the relations seen in Eqs. (2.23). We here show that the Eqs. (2.23) hold in our more general model when $XY = \bar{Y}\bar{X}$. The available experimental data (Refs. 5 and 6) strongly indicate that Eqs. (2.23) hold when and *only* when $XY = \bar{Y}\bar{X}$. A DNA sequence for which $XY = \bar{Y}\bar{X}$ at every base-pair step must be either of the type $\cdots ATATAT \cdots$ or $\cdots GCGCGC \cdots$.
- ²³ The values and ranges we give for the moduli and parameters are based on data reported in Ref. 6.
- ²⁴ O. Gonzales and J. H. Maddocks, *Theor. Chem. Acc.* **106**, 76 (2001).
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- ⁴¹ For a statement and a discussion of the assumptions behind Kirchhoff's theory of rods (Refs. 27 and 28) see Ref. 29.
- ⁴² Base-pair level modes of DNA deformability constructed to account for results of measurements of cyclization kinetics and gel electrophoretic mobility of short DNA segments suggest that highly curved DNA is made up of two types of duplex structure within each helical repeat length: the canonical B-type duplex and a perturbed form in which the base pairs are inclined with respect to the duplex axis (Refs. 69 and 70) as they are in an A-type or C-type duplex.
- ⁴³ J. C. Marini, S. D. Levene, D. M. Crothers, and P. T. Englund, *Proc. Natl. Acad. Sci. U.S.A.* **79**, 7664 (1982).
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- ⁴⁵ T. E. Haran, J. D. Kahn, and D. M. Crothers, *J. Mol. Biol.* **244**, 135 (1994).
- ⁴⁶ Electron micrographs of a 219 bp segment with such a sequence found in *C. fasciculata* indicate that the segment has the form of a complete circle (Ref. 71) and DNA segments with higher intrinsic curvature have been synthesized. Koo *et al.* (Ref. 72) have given strong evidence, based on a study of cyclization kinetics, to the effect that a 210 bp DNA segment with the sequence (AAAAAACGGCAAAAAACGGGC)_n can form a complete circle when stress-free. Previously, Ulanovsky *et al.* (Ref. 73) had showed that DNA segments with sequences (AAAAAATATATAAAATCTCT)_n can be closed to form minicircles with 105, 126, 147, and 168 bp, i.e., with $n = 5, 6, 7, 8$. They found that the maximum value of the ratio of concentrations at equilibrium of circular and noncircular products occurred when the sequence length was either 126 or 147 bp, and they suggested that such an observation indicates that it may be possible to obtain stress-free minicircles with as few as 137 bp. See also the review of Crothers *et al.* (Ref. 74).
- ⁴⁷ So as to obtain an o-ring of small size, i.e., with $N = 150$ bp, while making the simplifying assumption that the intrinsic shears $\bar{\rho}_1^n$ and $\bar{\rho}_2^n$ are everywhere zero, we chose $\bar{\theta}_3^n$ in Eq. (4.2) to be larger than the available estimates of the upper bound for stress-free values of the roll.
- ⁴⁸ The values of F_{11} and F_{22} were chosen so that the bending rigidity $2[(1/F_{11}) + (1/F_{22})]$ of each minicircle equals that of naturally straight DNA with a persistence length of 500 Å. The choice $\omega = 0.7$ is then compatible with measurements of fluorescence anisotropy of dyes intercalated in open segments of DNA (see Ref. 75). Measurements of topoisomer distributions for miniplasmids (Ref. 76) suggest that ω should be close to 1.4. [See also Bouchiat and Mezard (Ref. 77), who state that single molecule stretching experiments (Ref. 78) yield a value of 1.6 for ω .]
- ⁴⁹ See, e.g., the treatise of Thomson and Tait (Ref. 79). A modern discussion containing exact solutions of the nonlinear dynamical equations governing the oscillatory motion of an inextensible elastic rod (obeying Kirchhoff's theory) with uniformly distributed intrinsic curvature and torsion is given in Ref. 34.
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- ⁵³ We say "essentially independent," for the intercalative binding of EtBr changes not only the twist $\bar{\theta}_3^n$ but also the rise $\bar{\rho}_3^n$ (Ref. 51).
- ⁵⁴ The present theory is not intended to provide an interpretation of an observed preference of EtBr for binding to pyrimidine-purine base-pair steps (Ref. 82).
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- ⁵⁸ As the o-ring we are considering here is composed of periodically repeating units of length 10 bp, the minimum energy configuration for a given distribution of sites of intercalation would not be affected if each such site were shifted by 10 bp in the direction of increasing n . Although a shift in the distribution by less than 10 bp can affect the minimum energy configuration, our calculations show that for Minicircle I the corresponding change in Ψ does not exceed 0.15 kT .
- ⁵⁹ It follows from the theory of ideal elastic rods that if the minicircle were formed by closing naturally straight DNA, i.e., if Eq. (4.2) were replaced by Eq. (4.1), then the untwisting at a single base-pair step by an angle of

- magnitude less than 360° , as it corresponds to a change in excess link less than 1, would not affect the shape of the minicircle, i.e., the axial curve would remain circular.
- ⁶⁰There are protein structures that can induce a comparable change in the magnitude of twist, but the changes they induce are generally distributed over several base-pair steps. See, e.g., Ref. 83 reporting a case in which an 8 bp long region is untwisted by 147° in a crystal structure of the human TFIIB-TBP protein complex bound to duplex DNA.
- ⁶¹See also Ref. 32.
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