Superhelices in steady-state configurations of molecules of the DNA type

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Steady-state configurations of molecules of the DNA type are analyzed. The elastic anisotropy of the molecules is taken into account, as are the existence of spontaneously deformed states, external factors, and the interactions of various types of deformations. Depending on the values of the parameters characterizing these effects, various types of steady-state structures are found: ordered and slightly deformed helices, superhelices which form "windings" of an original helix on surfaces of some sort, closed and periodic or quasiperiodic configurations, disordered balls, and structures with intermittent ordered and disordered regions. © *1994 American Institute of Physics.*

1. The DNA molecule is an extremely complicated entity which stores biological information in living organisms. Under normal conditions, the DNA molecule is a linear elastic chain containing 10^7 elements in a strictly fixed order. These elements form a helicoidal structure with a period ~ 36 Å . The linear molecule as a whole, on the other hand, is characterized by a persistent length on the order of 500 Å . Since there are two very different length scales for twisting and bending deformations of a DNA molecule, there are some extremely complicated steady-state configurations. Marko and Siggia[1,2] have recently studied configurations with constant curvature and twisting. They demonstrated that the interaction of bending and rotational deformations plays an important role.

In the present letter we analyze elastic properties of a DNA molecule in a general form, incorporating an anisotropy, spontaneous deformations, external agents, and cross terms in the elastic energy, which describe the interactions of different types of deformations.

The properties and structure of a DNA molecule are governed by more than its elastic energy; important roles are also played by the entropy, external conditions, etc. Nevertheless, any realistic model of DNA must include, as a first step, a study of the elastic energy of the molecule and an analysis of steady-state and equilibrium structures. Even more incentive to study steady states of an elastically anisotropic, spontaneously deformed filament arises from the circumstance that even in such a simple model it is possible to find some extremely nontrivial configurations, which have not been discussed

previously in the scientific literature, to the best of our knowledge.

2. Following Refs. 1 and 2, we treat the axis around which the double helix of a molecule of the DNA type is wound, with a pitch on the order of 36 Å , as an elastic filament or rod. To describe deformations of the thin elastic rod (or filament) used to model the DNA molecule, we use the vector $\boldsymbol{\omega}$, which describes the rotation of the coordinate axes as we move along the filament. For this purpose we introduce a local coordinate system $\mathbf{v}_1$, $\mathbf{v}_2$, $\mathbf{v}_3$, where the vector $\mathbf{v}_1$ is tangent to the $\mathbf{r}(t)$ curve, which specifies the configuration of the axis of the molecule (t is the coordinate along the curve). The vectors $\mathbf{v}_2$ and $\mathbf{v}_3$ are directed along the axes of the principal deformations of the elastic rod,[3] in such a manner that we have

$$\mathbf{v}_1 = \frac{d}{dt}\mathbf{r}, \quad \mathbf{v}_i \times \mathbf{v}_j = \delta_{ij}. \tag{1}$$

The change in the local coordinate system along the filament or rod is described by the equation[3]

$$\frac{d}{dt}\mathbf{v}_j = \boldsymbol{\omega} \times \mathbf{v}_j \quad j = 1,2,3. \tag{2}$$

The elastic energy of an anisotropic rod can be written as a series expansion in $\boldsymbol{\omega}$ (Ref. 3). The leading terms of this expansion are

$$E = \sum_{i,j=1}^{3} \frac{1}{2} a_{ij}\omega_i\omega_j + \sum_{i=1}^{3} b_i\omega_i. \tag{3}$$

The matrix a_{ik} is the symmetric matrix of elastic moduli of the rod; the vector $\mathbf{b}$ describes spontaneous deformation of the steady-state configuration of the molecule. The physical cause of a spontaneous deformation might be, for example, the adsorption of the DNA molecule on nucleosomes (which are usually modeled by a cylindrical surface).

A symmetry analysis carried out in Ref. 1 showed that only the components a_{11}, a_{22}, a_{33}, and a_{13} are nonvanishing in the case of the DNA molecule. The energy in (3) under consideration here makes it possible to describe some situations, of interest from the physical standpoint, involving adsorption of DNA and the behavior of molecules in external fields. That approach furthermore has the technical advantage that we can formulate an equation which describes the change in the local coordinate system in (2) as a chiral-field theory (see Chap. 8 in Ref. 4), as we have done in the case of membranes.[5]

We introduce the matrix

$$X_{ij} = (\mathbf{v}_j)_i. \tag{4}$$

The chiral current constructed from this matrix is

$$J = \frac{d}{dt} XX^{-1}. \tag{5}$$

To satisfy kinematic condition (1), the matrix J must have the structure

$$J_{kj} = -\sum_{i=1}^{3} \omega_i \epsilon_{ikj}, \tag{6}$$

where ϵ_{kij} if the Levi–Civita density.

An arbitrary infinitesimal variation of the coordinate system is specified by the transformation

$$X \to RX, \quad R = I + \delta\phi,$$

where

$$(\delta\phi)_{ij} = \sum_{i=1}^{3} \delta\phi_k \epsilon_{ijk},$$

and $\delta\phi$ is the matrix of an infinitely small rotation, specified by the vector $\boldsymbol{\delta\phi}$. Correspondingly, in accordance with (5), we write

$$\delta J = \frac{d}{dt}\,\delta\phi - [J, \delta\phi] = \nabla\,\delta\phi, \tag{7}$$

where $-[,]$ is a commutator, and ∇ is the covariant derivative (cf. the corresponding procedure for membranes in Ref. 5).

Using (5) and (6), we can express the variation $\delta\boldsymbol{\omega}$ in terms of the covariant derivative $\delta\boldsymbol{\phi}$,

$$\delta\boldsymbol{\omega} = \nabla\,\delta\boldsymbol{\phi},$$

and we can write an Euler–Lagrange equation for the energy functional $\mathcal{E} = \int dt E$ in the form

$$\nabla\left(\frac{\partial E}{\partial \omega_i}\right) = 0.$$

At this point, it is convenient to introduce the moment **M,** which is the conjugate of the vector $\boldsymbol{\omega}$:

$$M_j = \frac{\partial E}{\partial \omega_j} = \sum_{i=1}^{3} a_{ji}\omega_i + b_j. \tag{8}$$

By virtue of the definition of the covariant derivative, (7), the equation describing a steady-state solution for the moment **M** is

$$\frac{d}{dt}\,\mathbf{M} - \boldsymbol{\omega} \times \mathbf{M} = 0. \tag{9}$$

Determining the equilibrium configuration of a thin, elastically anisotropic rod thus reduces to solving two problems. First, we need to solve system of equations (8), (9), which is a purely mechanical and (see the discussion below) Hamiltonian system. As a result, we find a steady-state distribution of the coordinate system $\mathbf{v}_i$. In the second step

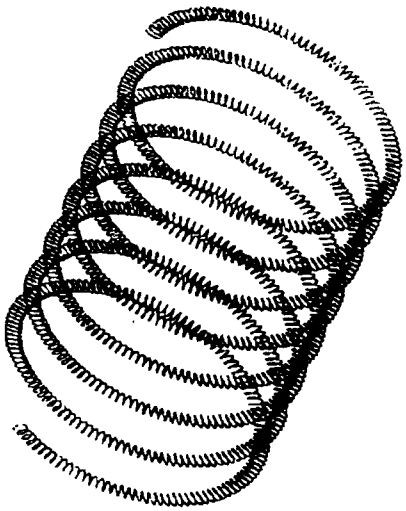

FIG. 1.

we can then reconstruct the curve itself, using the definition of the tangent vector [see (1)]. Before we present the results found in this manner, we need to make two comments.

• Using the definition of the moment in (8), we can rewrite the energy density in terms of **M**:

$$E=\frac{1}{2}\sum_{i,j=1}^{3}(a^{-1})_{ij}(M_iM_j-b_ib_j).$$

At the same time, it is easy to see that if we wish to obtain the correct "equation of motion" for **M** by the Poisson-brackets method, the Hamiltonian of the system must be of the form

$$H=\frac{1}{2}\sum_{i,j=1}^{3}(a^{-1})_{ij}(M_i-b_i)(M_j-b_j).$$

The energy density E and the Hamiltonian H are not the same (!). The difference stems from the existence of linear terms in energy expansion (3). Those terms describe spontaneous deformations of the DNA molecule. It should be kept in mind that H is an integral of the equations describing the steady-state configurations of the rod. The problem formulated in this manner is a completely integrable Hamiltonian system with Poisson brackets for the components of **M** and $\mathbf{v}_j$, $i=1,2,3$, specified by the equations

$$\{M_i,M_j\}=-\epsilon_{ijk}M_k,\quad \{M_i,(\mathbf{v}_i)_j\}=-\epsilon_{ijk}(\mathbf{v}_i)_k,$$

and with Kirchhoff integrals

$$H,\quad M^2,\quad \mathbf{M}\times\mathbf{v}_i,\quad i=1,2,3. \tag{10}$$

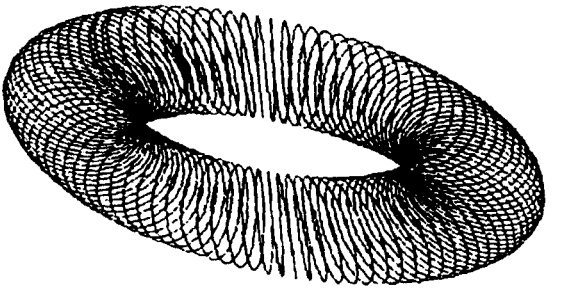

FIG. 2.

• The matrix a_{ik} is symmetric, so it can obviously be put in diagonal form. However, the physical state of the molecule fixes the spontaneous deformation [i.e., the vector **b** and the initial value $\mathbf{M}(t=0)$]. It is thus convenient to specify the vectors **b** and **M** (0); in this case the matrix a_{ik} has off-diagonal elements. The comment above seems quite natural in a geometric sense, since a steady-state configuration of the molecule is unambiguously determined by the intersection of the "sphere" $M^2=\text{const}$ and the elastic ellipsoid $H=\text{const}$, with a center displaced by a vector **b**. It was shown in Refs. 1 and 2 that only the off-diagonal element a_{12} is nonzero for a DNA molecule under normal conditions. This is the case which we are looking at in the present letter.

We have solved system of equations (8), (9) by means of a fourth-order Adams algorithm. The accuracy of the calculations was monitored on the basis of the values of the Kirchhoff integrals mentioned above. The error is 10^{-6} for a computation duration of several thousand steps for regular configurations of the rod, while it is 10^{-3} for helix–ball transitions (more on this below). We studied the behavior of the steady states of the rod as a function of various configurations of the matrix a_{ik} and of the vector **b** (Figs. 1–5). Postponing a detailed description of these structures to a separate paper, we simply list a few illustrative examples.

1. Ordered or weakly deformed helices are found in the case of a diagonal matrix a_{ik} and a zero vector **b**.
2. If we introduce even a small value of a_{12}, we find a large-scale nonuniformity: a superhelix [Fig. 1 shows the steady-state configuration of the axis of a DNA molecule in the case $\mathbf{b}=0$; $a_{12}=0.1a_{11}$; $\mathbf{M}=(0.1,0,0.7)$]. The superhelix is characterized by two pitches, large and small ones, L_1 and L_2. Each is considerably larger than the pitch of the double helix of the DNA molecule, ~ 36 Å.

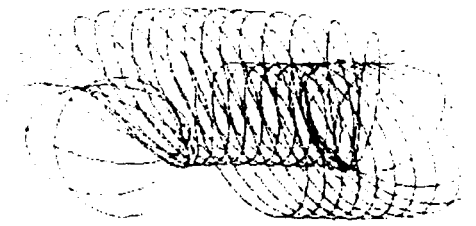

FIG. 3.

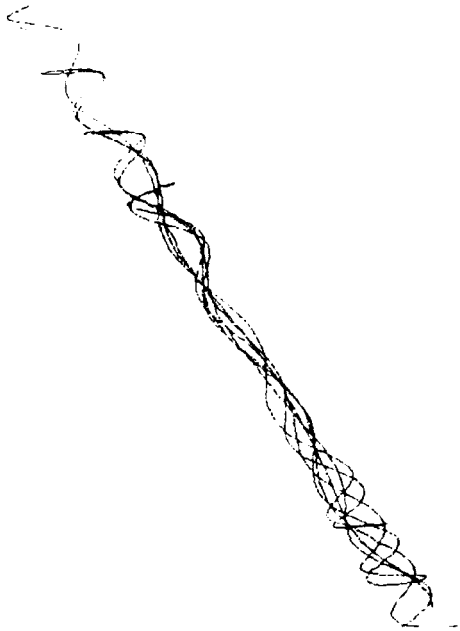

FIG. 4.

3. The steady-state configuration of the molecule can be characterized as a "winding" of a line around a closed surface. Figure 2 shows an example of such a winding on a torus, $\mathbf{b}=(0.1,0,0)$.
4. When an elastic anisotropy is introduced, structures of the type in (2) and (3) exhibit alternating regions with an ordered or slightly deformed helix. Figure 3 shows an example of such a structure. Finally, at values of the off-diagonal element a_{12}, which are not small, or at values of b, which are large, there is a helix–ball transition, and disordered structures are found (Fig. 4).
5. A closed configuration is shown in Fig. 5.

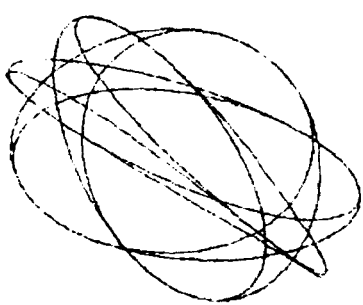

FIG. 5.

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