On the mechanical analogue of DNA

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Abstract The creation of mechanical analogues of biological systems is known as a useful instrument that helps to understand better the dynamical mechanisms of the functioning of living organisms. Mechanical analogues of biomolecules are usually constructed for imitation of their internal mobility, which is one of the most important properties of the molecules. Among the different types of internal motions, angular oscillations of nitrous bases are of special interest because they make a substantial contribution to the base pairs opening that in turn is an important element of the process of the DNA–protein recognition. In this paper, we investigate the possibility to construct a mechanical analogue for imitation of angular oscillations of nitrous bases in inhomogeneous DNA. It is shown that the analogue has the form of a mechanical chain of non-identical pendulums that oscillate in the gravitational field of the Earth and coupled by identical springs. The masses and lengths of pendulums, as well as the distances between neighboring pendulums and the rigidity of springs are calculated. To illustrate the approach, we present the result of construction of the mechanical analogue of the fragment of the sequence of bacteriophage T7D.

Keywords DNA dynamics · Oscillations of nitrous bases · Bacteriophage T7D · Chain of non-identical pendulums · Modified sine-Gordon equation

1 Introduction

Mechanical analogues of biological systems are known as a useful instrument that helps to understand better the dynamical mechanisms of the functioning of living organisms. The mechanical analogues of biomolecules, in particular of DNA molecules, are usually constructed for imitation of their internal mobility, which is one of the most important properties of the molecules. Two main approaches are used to study the mobility [1]. One of them deals with a precise starting DNA geometry (set of atomic coordinates) and with the methods of all-atom molecular dynamics

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(MD) simulations [2–5]. The other approach deals with the simplified DNA structural models that consider the motions of the atomic groups: bases, sugars, and phosphates, as a whole [6–8]. Just this approach is mostly used when constructing mechanical analogues.

In this paper, we consider the possibility to construct a mechanical analogue that imitates angular oscillations of nitrous bases. Among other internal motions, these oscillations are of special interest because they make a substantial contribution to the process of the base pair opening, which in turn is a necessary element of the process of the DNA–protein recognition.

Homogeneous versions of the mechanical analogue are well known and studied. One of them constructed, for example, by Scott [9], consists of identical nails, suspended on thin, taut, horizontal thread and coupled by a steel spring (Fig. 1a). Applying different initial and boundary conditions, Scott observed different dynamical regimes that were possible in the chain. Usually, theoreticians draw the model in a more simple way, as shown in Fig. 1b. Further, we shall use this way of presentation. Here φ_n is the angular displacement of the n -th pendulum in the plane perpendicular to the thread, m and r are the mass and the length of the pendulum, respectively, a is the distance between neighboring pendulums, and k is the rigidity of springs. The model of Scott as well as its more recent modifications [10, 11] are widely used in numerous applications [12–15]. The application to DNA has been proposed by Englander and co-authors [16] and developed in many works [17–26] where homogeneous and inhomogeneous DNA models were considered.

However, the direct application of the model of Scott to DNA is not quite correct because the model does not take into account the heterogeneity of the DNA molecule, which contains four types of nitrous bases: adenine (A), thymine (T), guanine (G), and cytosine (C), forming the sequence unique for any living organism (Fig. 2a). Besides that, the model of Scott does not take into account the presence of two types of interactions between nitrous bases in pairs (two hydrogen bonds in the case of an AT pair and three hydrogen bonds in the case of a GC pair). The aim of our work is to improve the mechanical analogue to have a possibility to take into account these properties of heterogeneous DNA.

Here we suggest that angular oscillations of nitrous bases in one of the two polynucleotide chains can be modeled by a mechanical chain of coupled non-identical pendulums oscillating

Fig. 1 Original model of Scott (a) and simplified presentation of the model (b)

Fig. 2 Schematic picture of the DNA double chain. Sugars are shown with *pentagons*, phosphate groups with *circles*, and nitrous bases (A, T, G, and C) with *colored polygons*. Weak hydrogen bonds between nitrous bases are shown by *dotted horizontal lines*. K is the rigidity of the sugar-phosphate chains, b is the distance between the neighboring base pairs

in the gravitation field of the Earth. It is also assumed that the mechanical chain contains four types of pendulums (A-, T-, G-, and C-pendulums) arranged in the same order as the bases: adenines (A), thymines (T), guanines (G), and cytosines (C), in the sequence of DNA.

In the next section, we give a mathematical description of the mechanical chain consisting of N -coupled non-identical pendulums. In the third section, we present the system of $2N$ -coupled equations imitating angular oscillations of nitrous bases in the DNA double chain, and reduce the equations to the form similar to that described in the previous section. This similarity gives us a possibility to find the relations between the parameters of DNA and the parameters of the mechanical analogue. The algorithm of calculation of pendulum masses and lengths, as well as the distances between neighboring pendulums and the rigidity of springs, is presented in the fourth section. The algorithm is applied for construction of the mechanical analogue of the fragment of the sequence of bacteriophage T7D.

2 Modeling angular oscillations of coupled non-identical pendulums in mechanics

Let us consider a mechanical chain containing four types of pendulums (A-, T-, G-, and C-pendulums) arranged in the same order as nitrous bases of four types (adenines (A),

thymines (T), guanines (G), and cytosines (C)) in a sequence of DNA. The dynamical equations, which imitate angular oscillations of pendulums, can be written in the following way:

$$m_n r_n^2 \frac{d^2 \varphi_n}{dt^2} - k r_n a^2 \frac{(r_{n+1} \varphi_{n+1} - 2 r_n \varphi_n + r_{n-1} \varphi_{n-1})}{a^2} + m_n g r_n \sin \varphi_n = 0, \quad n = 1, 2, \dots, N. \quad (1)$$

Here, φ_n is the angular displacement of the n -th pendulum, m_n is the mass of the n -th pendulum, r_n is the length of the n -th pendulum, a is the distance between the neighboring pendulums, k is the rigidity of the springs connecting pendulums, and g is the gravitational constant.

In the linear approximation, Eq. (1) takes the form:

$$m_n \frac{d^2 \varphi_n}{dt^2} - \frac{k a^2}{r_n} \frac{(r_{n+1} \varphi_{n+1} - 2 r_n \varphi_n + r_{n-1} \varphi_{n-1})}{a^2} + \frac{m_n g}{r_n} \varphi_{1,n} = 0, \quad n = 1, 2, \dots, N. \quad (2)$$

In the continuum approximation, Eq. (2) is reduced to one particular differential equation:

$$m_1(z) \frac{\partial^2 \varphi(z, t)}{\partial t^2} - \frac{k a^2}{r_1(z)} \frac{\partial^2 (r_1(z) \varphi(z, t))}{\partial z^2} + \frac{m_1 g}{r_1} \varphi_{1,n} = 0. \quad (3)$$

In the homogeneous case, when the chain consists, for example, of only A-pendulums, Eq. (3) transforms to:

$$m_A \frac{\partial^2 \varphi(z, t)}{\partial t^2} - k a^2 \frac{\partial^2 \varphi(z, t)}{\partial z^2} + \frac{m_A g}{r_A} \varphi(z, t) = 0. \quad (4)$$

Until this moment, the values of the parameters of Eq. (4) were arbitrary. Now we can choose the values that are convenient for visualization. One of the possible sets of parameters is shown in Table 1. Note that this set has been chosen for the chain containing only A-pendulums. The sets of the parameters for the chains containing other types of pendulums will be calculated in the next sections.

3 Modeling angular oscillations of nitrous bases in DNA science

Let us consider a system of $2N$ -coupled differential equations that imitate angular oscillations of nitrous bases in both polynucleotide chains [27] and accurately take into account the heterogeneity of the DNA molecule [28, 29]:

$$I_{1,n} \frac{d^2 \phi_{n,1}(t)}{dt^2} - K R_{1,n} [R_{1,n+1} \phi_{n+1,1}(t) - 2 R_{1,n} \phi_{n,1}(t) + R_{1,n-1} \phi_{n-1,1}(t)] + k_{1-2,n} R_{1,n} (R_{1,n} + R_{2,n}) \sin \phi_{n,1}(t) - k_{1-2,n} R_{1,n} R_{2,n} \sin [\phi_{n,1}(t) - \phi_{n,2}(t)] = 0, \quad (5)$$

$$I_{2,n} \frac{d^2 \phi_{n,2}(t)}{dt^2} - K R_{2,n} [R_{2,n+1} \phi_{n+1,2}(t) - 2 R_{2,n} \phi_{n,2}(t) + R_{2,n-1} \phi_{n-1,2}(t)] + k_{1-2,n} R_{2,n} (R_{1,n} + R_{2,n}) \sin \phi_{n,2}(t) - k_{1-2,n} R_{1,n} R_{2,n} \sin [\phi_{n,2}(t) - \phi_{n,1}(t)] = 0. \quad (6)$$

Here, $\phi_{n,i}(t)$ denotes the angular displacement of the n -th base of the i -th polynucleotide chain, $I_{i,n} = M_{i,n} R_{i,n}^2$ is the moment of inertia of the n -th base of the i -th polynucleotide chain.

Table 1 Parameters of the mechanical chain of coupled identical A-pendulums

Type of pendulum	m_A (kg)	r_A (m)	a (m)	k (N/m)	g (m/s ²)
A	0.1	0.1	0.03	111.111	9.8

otide chain, $M_{n,j}$ is the mass of the n -th base of the i -th polynucleotide chain, $R_{n,j}$ is the distance from the center of mass of the n -th base of the i -th polynucleotide chain to the sugar-phosphate chain, K is the rigidity of the sugar-phosphate chain, $k_{1-2,n}$ is the coefficient that characterizes interaction between two complementary bases which form the n -th pair of bases, $i = 1, 2$; $n = 1, 2, \dots, N$.

Let us take into account that the interactions between the bases inside pairs (hydrogen bonds) are much weaker than the interactions between the bases that are the nearest along the chain (covalent interactions). To the first approximation, which is often called the approximation of the average field, the influence of the mobility of the nitrous bases of one polynucleotide chain on the mobility of the nitrous bases of the other polynucleotide chain can be neglected. Then, Eqs. (5)–(6) can be transformed to the following form [27]:

$$I_{1,n} \frac{d^2 \phi_{n,1}(t)}{dt^2} - KR_{1,n} b^2 \frac{[R_{1,n+1} \phi_{n+1,1}(t) - 2R_{1,n} \phi_{n,1}(t) + R_{1,n-1} \phi_{n-1,1}(t)]}{b^2} + V_{1,n} \sin \phi_{n,1}(t) = 0, \quad (7)$$

$$I_{2,n} \frac{d^2 \phi_{n,2}(t)}{dt^2} - KR_{2,n} b^2 \frac{[R_{2,n+1} \phi_{n+1,2}(t) - 2R_{2,n} \phi_{n,2}(t) + R_{2,n-1} \phi_{n-1,2}(t)]}{b^2} + V_{2,n} \sin \phi_{n,2}(t) = 0, \quad (8)$$

where $V_{1,n} = k_{1-2,n}(R_{1,n})^2$, $V_{2,n} = k_{1-2,n}(R_{2,n})^2$. Equations (7)–(8) are independent. Each of the equations describes angular oscillations of nitrous bases in one of the two polynucleotide chains in the average field, which is induced by the other chain. Below, we shall consider Eq. (7). Equation (8) could be considered in the same way. The parameters of Eqs. (7)–(8) are shown in Table 2.

The values of I_n , R_n , and V_n presented in Table 2 have been taken from the work [27]. The parameter b was suggested to be 3.4×10^{-10} m. The coefficient K was estimated from the data on the sound velocity in DNA [30].

In the linear approximation Eq. (7) takes the following form:

$$M_{1,n}(R_{1,n})^2 \frac{d^2 \phi_{n,1}(t)}{dt^2} - KR_{1,n} b^2 \frac{[R_{1,n+1} \phi_{n+1,1}(t) - 2R_{1,n} \phi_{n,1}(t) + R_{1,n-1} \phi_{n-1,1}(t)]}{b^2} + k_{1-2,n}(R_{1,n})^2 \phi_{n,1}(t) = 0. \quad (9)$$

In the continuum approximation, Eq. (9) transforms to:

$$M_1(z) \frac{\partial^2 \phi_1(z, t)}{\partial t^2} - \frac{K b^2}{R_1(z)} \frac{\partial^2 (R_1(z) \phi_1(z, t))}{\partial z^2} + k_{1-2}(z) (R_1(z))^2 \phi_1(z, t) = 0. \quad (10)$$

Table 2 DNA parameters

Type of base	$I_n \times 10^{-44}$ (m ² kg)	$V_n \times 10^{-20}$ (J)	K (Jm ⁻²)	$R_n \times 10^{-10}$ (m)	$b \times 10^{-10}$ (m)
A	7.61	2.09	6.99	5.8	3.4
T	4.86	1.43	6.99	4.8	3.4
G	8.22	3.12	6.99	5.7	3.4
C	4.12	2.12	6.99	4.7	3.4

In the homogeneous case where the considered polynucleotide chain contains only identical nitrous bases (for example, adenines) with mass M_A and length R_A , Eq. (10) transforms to the form:

$$M_A \frac{\partial^2 \phi(z, t)}{\partial t^2} - Kb^2 \frac{\partial^2 \phi(z, t)}{\partial z^2} + k_{A-T} \phi(z, t) = 0, \quad (11)$$

which is very similar to Eq. (4).

4 Relations between the parameters of DNA and mechanical chain

Let us begin with two homogeneous systems: the mechanical chain consisting of only A-pendulums and homogeneous DNA sequence (*poly-A*). Parameters of *poly-A* are known and fixed (first line in Table 2). Parameters of the mechanical chain consisting of only A-pendulums have been chosen for convenience of visualization (Table 1). To find the relations between these two systems, let us introduce new variables

$$\tau = \beta t, \xi = \eta z, \quad (12)$$

and find the coefficients β and η .

4.1 Calculations of the coefficients β and η

To find the coefficients, let us insert (12) into Eq. (11), giving

$$M_A \beta^2 \frac{\partial^2 \phi(z, t)}{\partial \tau^2} - Kb^2 \eta^2 \frac{\partial^2 \phi(z, t)}{\partial \xi^2} + k_{A-T} \phi(z, t) = 0. \quad (13)$$

After several simple transformations, Eq. (13) takes the form

$$m_A \frac{\partial^2 \phi(z, t)}{\partial \tau^2} - \left(\frac{m_A}{M_A \beta^2} \frac{Kb^2 \eta^2}{ka^2} \right) ka^2 \frac{\partial^2 \phi(z, t)}{\partial \xi^2} + \left(\frac{m_A}{M_A \beta^2} \frac{k_{A-T}}{m_A g r_A} \right) m_A g r_A \phi(z, t) = 0. \quad (14)$$

Let us require:

$$\frac{m_A}{M_A \beta^2} \frac{Kb^2 \eta^2}{ka^2} = 1, \quad \frac{m_A}{M_A \beta^2} \frac{k_{A-T}}{m_A g r_A} = 1. \quad (15)$$

Then, Eq. (14) transforms to a form that is similar to (4):

$$m_A \frac{\partial^2 \phi(z, t)}{\partial \tau^2} - k a^2 \frac{\partial^2 \phi(z, t)}{\partial \xi^2} + m_A g r_A \phi(z, t) = 0. \quad (16)$$

Coefficients of transformation, found from (15), are equal to:

$$\eta^2 = \frac{k a^2}{K b^2} \frac{k_{A-T}}{m_A g r_A}, \quad \beta^2 = \frac{k_{A-T}}{M_A g r_A}. \quad (17)$$

After inserting the data from Tables 1 and 2 into (17) and taking into account that $M_A = \frac{L_A}{R_A} = 0.226 \cdot 10^{-24}$ kg, we obtain $\beta = 5.294 \cdot 10^{11}$, $\eta = 2.851 \cdot 10^8$.

4.2 Mass and length of T-pendulums

To obtain the parameters m_T and r_T , let us take the model equation written for polynucleotide chain containing only thymines:

$$M_T \frac{\partial^2 \phi(z, t)}{\partial t^2} - K b^2 \frac{\partial^2 \phi(z, t)}{\partial z^2} + k_{A-T} \phi(z, t) = 0, \quad (18)$$

Then we insert transformation (12) into Eq. (18)

$$M_T \beta^2 \frac{\partial^2 \phi(z, t)}{\partial \tau^2} - K b^2 \eta^2 \frac{\partial^2 \phi(z, t)}{\partial \xi^2} + k_{A-T} \phi(z, t) = 0. \quad (19)$$

After that we obtain:

$$\left(\frac{m_A M_T}{m_T M_A} \right) m_T \frac{\partial^2 \phi(z, t)}{\partial \tau^2} - \left(\frac{m_A}{M_A \beta^2} \frac{K b^2 \eta^2}{k a^2} \right) k a^2 \frac{\partial^2 \phi(z, t)}{\partial \xi^2} + \left(\frac{m_A}{M_A \beta^2} \frac{k_{A-T}}{m_T g r_T} \right) m_T g r_T \phi(z, t) = 0 \quad (20)$$

Next, we require:

$$\frac{m_A M_T}{m_T M_A} = 1, \quad \frac{m_A}{M_A \beta^2} \frac{K b^2 \eta^2}{k a^2} = 1, \quad \frac{m_A}{M_A \beta^2} \frac{k_{A-T}}{m_T g r_T} = 1. \quad (21)$$

Then Eq. (20) takes the form:

$$m_T \frac{\partial^2 \phi(z, t)}{\partial \tau^2} - k a^2 \frac{\partial^2 \phi(z, t)}{\partial \xi^2} + m_T g r_T \phi(z, t) = 0. \quad (22)$$

From the requirements (22), we obtain

$$m_T = m_A \frac{M_T}{M_A}, \quad r_T = r_A \frac{m_A}{m_T}. \quad (23)$$

Finally, inserting the data from Tables 1 and 2 into (23) and taking into account that $M_T = \frac{L_T}{R_T} = 0.211 \cdot 10^{-24}$ kg, we obtain $m_T = 0.093$ kg, $r_T = 0.107$ m.

Table 3 Analytical formulas for parameters of pendulums

Type of pendulum	Mass	Length
A	m_A	r_A
T	$m_T = m_A \frac{M_T}{M_A}$	$r_T = r_A \frac{M_A}{M_T}$
G	$m_G = m_A \frac{M_G}{M_A}$	$r_G = r_A \frac{k_{G-C} M_A}{k_{A-T} M_G}$
C	$m_C = m_A \frac{M_C}{M_A}$	$r_C = r_A \frac{k_{G-C} M_A}{k_{A-T} M_C}$

4.3 Mass and length of G- and C-pendulums

Acting in the same way as in the previous section, we find the mass and length of G-pendulums

$$m_G = m_A \frac{M_G}{M_A}, \quad r_G = r_A \frac{k_{G-C} M_A}{k_{A-T} M_G}, \quad (24)$$

and the mass and length of C-pendulums

$$m_C = m_A \frac{M_C}{M_A}, \quad r_C = r_A \frac{k_{G-C} M_A}{k_{A-T} M_C}. \quad (25)$$

After inserting the data from Tables 1 and 2, we obtain $m_G = 0.112$ kg, $r_G = 0.138$ m, $m_C = 0.082$ kg, $r_C = 0.188$ m.

Analytical results obtained in Sections 4.2 and 4.3 are summarized in Table 3. Comparing formulas gathered in the table, we notice that pendulum masses are proportional to the masses of bases. The coefficient of proportionality is equal to $\frac{m_A}{M_A}$.

Concerning pendulum lengths, the situation here is different. If we could neglect the difference between the coefficients k_{G-C} and k_{A-T} , the pendulums lengths should become inversely proportional to the masses of bases with the coefficient of proportionality $r_A M_A$, but according to the data of Table 2, the coefficients are

$$k_{A-T} = \frac{V_A}{(R_A)^2} = \frac{V_T}{(R_T)^2} \cong 0.062 \text{ J/m}^2 \text{ and } k_{G-C} = \frac{V_G}{(R_G)^2} = \frac{V_C}{(R_C)^2} \cong 0.096 \text{ J/m}^2.$$

So, as a result, we have: $k_{G-C} \neq k_{A-T}$

Estimated parameters of the mechanical model are gathered in Table 4.

Table 4 Parameters of the mechanical analogue

Type of pendulum	m_A (kg)	r_A (m)	a (m)	k (N/m)	g (m/s ²)
A	0.100	0.100	0.03	111.111	9.8
T	0.093	0.107	0.03	111.111	9.8
G	0.112	0.138	0.03	111.111	9.8
C	0.082	0.188	0.03	111.111	9.8

Fig. 3 **a** Mechanical analogue of a small fragment of bacteriophage T7D in the state of rest. **b** One of the possible dynamical regimes (kink), which can be expected by the analogy with the kink solution obtained numerically in the inhomogeneous DNA model [29]

4.4 Modeling promoter sequence of bacteriophage T7D

Let us consider, as an example, the sequence of bacteriophage T7D. The total length of the sequence is rather large (39937 base pairs). So, to construct a mechanical model of the whole sequence, we should be ready to deal with a mechanical chain consisting of 39,937 pendulums and with a total length equal to 1198.11 m. Below we illustrate a short

Fig. 4 Distribution of pendulum masses (m) in the mechanical analogue (**a**) and of nitrous base masses (M) in the fragment of the sequence of bacteriophage T7D (**b**). n denotes the number of pendulum bases

Fig. 5 Distribution of pendulum lengths (r) in the mechanical analogue (a) and of distances between the centers of mass of nitrous bases and the sugar-phosphate chain (R) in the fragment of the sequence of bacteriophage T7D (b). n denotes the number of pendulum bases

fragment of the mechanical chain that corresponds to a small fragment of the DNA sequence having the length equal to 21 base pairs:

$$\text{TTTAGGTGTA GGCTTTAGGT G} \quad (26)$$

which in turn is a part of promoter region [31]:

$$\begin{array}{cccc} -70 & -60 & -50 & -40 \\ \text{GGTCTGGTCT} & \text{TTATGTTTAA} & \text{ACTTTAAGAT} & \text{AGGCGTTGAC} \\ -30 & -20 & -10 & +1 \\ \text{TTGATGGGTC} & \text{TTTAGGTGTA} & \text{GGCTTTAGGT} & \text{G} \end{array} \quad (27)$$

To construct the fragment of the mechanical chain, the following components are required:

- 1) three A-pendulums with mass m_A and length r_A ,
- 2) nine T-pendulums with mass m_T and length,
- 3) eight G-pendulums with mass m_G and length r_G ,
- 4) one C-pendulum with mass m_C and length r_C .

Fig. 6 Electronic analogue of the model of Scott [9]

Then it is necessary to hang the pendulums on a thin, taut, horizontal thread and to connect them with each other by steel springs with rigidity k . The distances between the neighboring pendulums should be equal to a , and the sequence of pendulums should be the same as the sequence of nitrous bases in (26).

In Fig. 3 we present schematically the resulting chain. A-pendulums are colored blue, T-pendulums are colored yellow, G-pendulums are colored gray, and the C-pendulum is colored crimson. After mechanical analogue has been constructed, it can be used for visual demonstration and for the study of different dynamical regimes possible in DNA by specifying different initial and boundary conditions.

5 Conclusions

In this paper, we investigated the possibility to construct a mechanical analogue of inhomogeneous DNA. We showed that the analogue has the form of the chain of non-identical pendulums coupled by identical springs. We obtained formulas for calculation of pendulum masses and lengths, as well as the distances between neighboring pendulums and the rigidity of springs.

To illustrate the obtained results, we estimated parameters of the mechanical analogue of a small fragment of the sequence of bacteriophage T7D. We noted that the distribution of pendulums masses (m) in the mechanical chain is similar to the distribution of nitrous base masses (M) in the DNA sequence (Fig. 4). At the same time, the distribution of pendulums lengths (r) in the mechanical chain substantially differs from the distribution of the distances (R) between the centers of mass of nitrous bases and the sugar-phosphate chain in the DNA sequence (Fig. 5). This is explained by formulas from Table 3 and the inequality $k_{G-C} \neq k_{A-T}$ which is valid because of the law of Chargaff according to which adenines and thymines are coupled in A-T base pairs by two hydrogen bonds, and guanines and cytosines are coupled in G-C base pairs by three hydrogen bonds.

The advantage of the approach is that different dynamical events that occur in DNA can be reproduced visually. For example, it is possible to reproduce a situation that happens when RNA polymerase binds with the DNA promoter. To do this, it is enough to “put” a soliton-like perturbation on the fragment that corresponds to the promoter region and to fix the ends of the chain, which is suggested to be much longer than the promoter region.

It should be noted, however, that all results on the mechanical analogue have been obtained for a rather simple model of DNA, which included into consideration only angular displacements of nitrous bases. Other degrees of freedom such as transverse and longitudinal displacements of nucleotides were not taken into account. Moreover, we did not take into account the effects of dissipation and the effects of the helicity of the DNA structure.

One more disadvantage of the approach is that the length of the mechanical chain imitating the whole DNA sequence is too large. We think, however, that in the future this disadvantage will be overcome by constructing an electronic analogue of the mechanical chain. Indeed, it is known that the electronic analogue of the chain of identical pendulums exists (Fig. 6) [9]. So, one can expect that the electronic analogue of the chain of non-identical pendulums can also be constructed as a generalization of the electronic scheme shown in Fig. 6. It is obvious that the electronic analogue of that type may have significant future usefulness, as it could reproduce different dynamical regimes in DNA sequences of any length.

Summarizing the advantages and disadvantages of the approach, we can conclude that the mechanical analogue constructed above is of special interest because it gives the

possibility to see visually various dynamical regimes that may exist in a heterogeneous DNA. Simplicity and clarity of the mechanical analogue will stimulate researchers to reproduce the model and to use it in the investigations of the dynamical properties of different DNA sequences. Finally, the mechanical analogue can be regarded as a first important step towards the construction of an electronic DNA model.

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Compliance with ethical standards

Conflict of interest The author declares that she has no conflicts of interest.

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