Mechanical models of the double DNA

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Abstract: In this paper, we review different mechanical models of double DNA (polymer models, elastic rod model, network model, torsional springs model, soliton-existence supporting models) emphasising specifities of each model. We especially considered the DNA model of Kovaleva and Manevich (2005), and Kovaleva et al. (2007). On a basis of this model, we made double DNA helical models with ideally elastic, visco-elastic, hereditary properties and fractional order model and named them multi-pendulum/multi-chain models. For each of these models, we made systems of corresponding differential equations or integro-differential equations or differential fractional order equations. Our results point to existence of independent eigen multi-frequency signals in double DNA chains with subsets of the eigen frequencies as well as set of one eigen frequency normal modes. For some of these multi-pendulum models, we calculate transfer of energy trough the double DNA chains. We consider multi-pendulum models appropriate for experimental testing of visco-elastic properties of DNA.

Keywords: DNA models; elasticity; visco-elasticity; mechanical hereditary elements; signals; eigen modes; energy transfer.

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1 Introduction

1.1 DNA-structure and function

DNA is a biological polymer which basic function in the cell is to encode the genetic material. For using that information to make proteins, DNA molecule has to interact with other molecules in the cell. DNA molecules can be considered to be a mechanical structure on the nanolevel. There are different approaches to studding the mechanical properties of the DNA molecule (experimental, theoretical modelling). The mechanical

properties of DNA are closely related to its molecular structure and sequence, particularly the weakness of hydrogen bonds and electronic interactions that hold strands of DNA together compared to the strength of bonds within each strand. Every process which binds or reads DNA is able to use or modify the mechanical properties of DNA for purposes of recognition, packaging and modification. Binding of proteins and other ligands induces a strong deformation of the DNA structure (Bryant et al., 2003). Single-molecule biomechanics of DNA extension, bending and twisting; protein domain motion, deformation and unfolding; and the generation of mechanical forces and motions by bimolecular motors is another approach to explain the biological function of DNA in the cell (Bao, 2002). Knowledge of the elastic properties of DNA is required to understand the structural dynamics of cellular processes such as replication and transcription.

1.2 Mechanical properties of DNA achieved experimentally

Knowledge of DNA's stretching and twisting properties were obtained through physical techniques such as optical tweezers and atomic force microscopy and single-molecule technique (Bustamante et al., 2000; Shroff et al., 2008) or by dielectrophoresis technique (Dalir et al., 2009). Experimental evidence suggests that DNA mechanical properties, in particular intrinsic curvature and flexibility, have a role in many relevant biological processes. For small distortions, DNA overwinds under tension (Gore et al., 2006). Lowering of the temperature increases the DNA curvature (Tsai and Luo, 2000). The DNA double helix is much more resistant to twisting deformations than bending deformations; almost all of the supercoiling pressure is normally relieved by writhing (Arsuaga et al., 2002). The twist angle of the helix has been shown to depend on sequence when the molecule is in solution, both by the effects on supercoiling parameters when short segments of known sequence are inserted into closed circular DNA (Peck and Wang, 1981; Tung and Harvey, 1984). The force required to unbind a short DNA strand is highly stochastic and strongly dependent on the pulling rate and duration of experiment (Strunz et al., 1999, 2000). Double-stranded DNA (dsDNA) expresses sequence-dependent flexibility on the sub-microsecond timescale. Pyrimidine-purine type steps are the most flexible, purine-purine steps are about average, and purine-pyrimidine steps are the most inflexible (Okonogi et al., 2002).

Under low tension, DNA behaves like an isotropic flexible rod. At higher tensions, the behaviour of over- and under-wound molecules is different. In each case, DNA undergoes a structural change before the twist density necessary for buckling is reached (Dalir et al., 2009). DNA molecule is extremely negatively charged. Metal ions like Mg2+, Na+ and K+, and different ionic force may modulate intrinsic properties of DNA (Brukner et al., 1994; Heddi et al., 2007; Frontali et al., 1979). Fraction of bent molecules seen by electronic microscope (EM) or scanning force microscope (SFM) was higher in the presence of cationic metals. The mechanical stability of the DNA double helix may be investigated by using a modified atomic force microscope (AFM). The forces inside short, strained loops composed of both dsDNA and single-stranded DNA (ssDNA) is possible to measure by force sensors with optical readout (Shroff et al., 2008).

Theoretical and experimental DNA curvature and flexibility data are correspondent only in some cases and under specific conditions – depending on experimental technique used (Anselmi et al., 2005). dsDNA is a rather stiff molecule than ssDNA or RNA. It

means that a short dsDNA behaves like a rod rather than a flexible string. If positively charged molecules such as polyamines are added, coiled DNA becomes dramatically compacted (Ikai, 2008).

2 DNA mechanical models

A number of mechanical models of the DNA double helix have been proposed so far. Different models are focusing on different aspects of the DNA molecule (biological, physical and chemical processes in which DNA is involved). A number of models have been constructed to describe different kinds of movements in a DNA molecule: asymmetric and symmetric motion; movements of long and short segments; twisting and stretching of dsDNA, twist-opening conditions. Some models have, for example, been made for circular double-stranded DNA molecules in viral capsids. We are discussing here *polymer models, elastic rod models, network models, torsional springs models, soliton-existence supporting models*. dsDNA and its mechanical properties may be also modelled through: Poland_Scheraga model, Peyrard_Bishop model, Semi-microscopic model, Lattice models (Kumar and Li, 2010). Ivancevic and Jain (2010) explore Hamiltonian chaos and thermodynamical phase transitions related to Hamiltonian DNA dynamics using modified Peyrard-Bishop model. They have shown that second-order phase transitions have topological origin, rooted in the geometry of the DNA configuration. The DNA molecule is considered as a discrete system consisting of many atoms having a quasi-one-dimensional structure. dsDNA may be modelled at four levels of three-dimensional structure: at the all-atom level, the base-pair level, the mesoscopic level, and the scale of several thousand nucleotides, with the duplex described as an ideal elastic rod. Some DNA models can predict the sequence-dependent bending and twisting of the double helix, as well as solvent- and force-induced and over-stretching conformational transitions (Harris, 2006). To mimic nano-manipulation experiments (‘destruction test’ duplex DNA in silicon) Harris et al. (2005) developed computer simulation method that is verified by comparison with single molecule stretching experiments that measure the force required to unbind the two DNA strands. The model is then extended to investigate the thermodynamics of DNA bending and twisting.

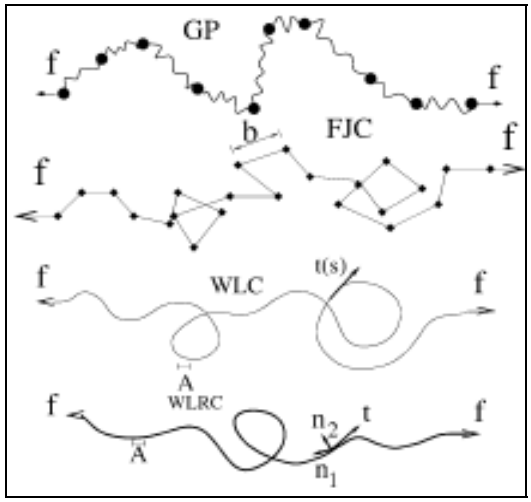
2.1 Polymer models

In polymer models DNA molecule is considered to be a polymer and calculations are done as for other polymers. There are several DNA polymer models (Cocco et al., 2002) (see Figure 1).

Double strained DNA differs from simple polymers because it exhibits torsional and bending stiffness and under tension DNA supercoiles. There several tipes of polimer models: Gaussian polymer (GP) model, freely jointed chains (FJC) model, worm-like chain (WLC) model, worm-like rod chain (WLRC) model. WLRC model is described by a rotating three-dimensional coordinate system, with local triedron (t, n_1, n_2) along the curvilinear coordinate s. These models are used to interpret single-molecule force-extension experiments on ssDNA and dsDNA. They show how combining the elasticity of two single-nucleic acid strands with a description of the base-pairing interactions between them explains much of the phenomenology and kinetics of RNA and DNA ‘unzipping’ experiments (Cocco et al., 2002; Zhou and Lai, 2001). Other

authors used WLC model to explain mechanical behaviour of the DNA (Shroff et al., 2008; Rouzina and Bloomfield, 2001; Mazur, 2006). To explain the elasticity and relaxation of shorter DNA segments stretched in thin slits in electrophoresis (Stigter, 2002) use the FJC model. Stick et al. (2000) gave a nice review of polymer models that explains experiments of twisting and stretching single DNA molecules "A limitation of the initial WLC model was the assumption of intrinsically straight homogeneous polymers whose thermal fluctuations are quantified as deviations from the straight line. DNA almost always contains curved regions, which can strongly affect the persistence length" (Anselmi et al., 2005).

Figure 1 Polimer models



Notes: GP = Gaussian polymer; FJP = freely jointed chain; WLC = worm-like chain; WLRC = worm-like rod chain

Source: Cocco et al. (2002)

For better fitting the experimental data into the WLC polymer model (Seol et al., 2007) develop finite worm-like chain (*FWLC*) model. FWLC models are suitable for both short (a few hundred nanometres in contour length) and very long (microns in contour length) molecule (Seol et al., 2007).

In the *bead-spring model*, the DNA chain is modelled as a bead-rod system with the first-order effective bead-spring integration scheme. The proposed effective bead-spring model may help simulate the dynamic behaviours of many types of polymer chains with different chain elasticity via an efficient unified integration scheme with large time steps. Combining with angular springs, this model can also be used to simulate the bending behaviours of semi-flexible polymers (Liu et al., 2008).

2.2 Elastic rod models

DNA can be modelled as an ideally elastic rod, or as an anisotropic rod.

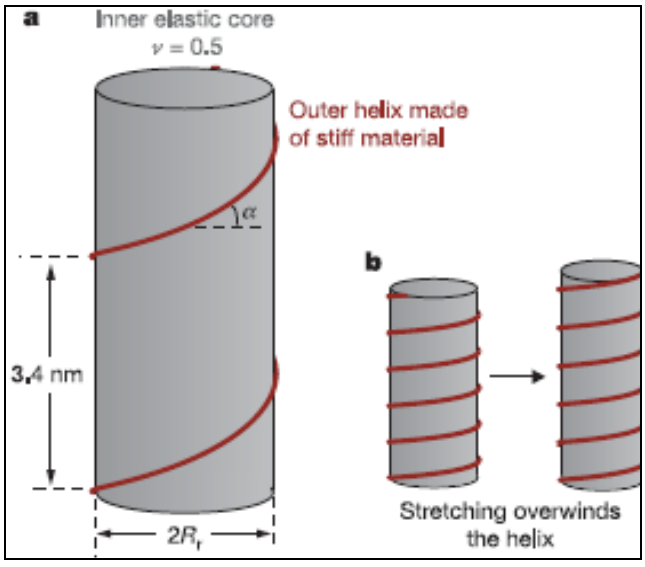
In simple elastic rod models, rod is ideally elastic which means that it will return to its original shape after deformation; one can compute the energy necessary for bending, stretching or torsional deformation. The model is not sequence dependent (i.e., all

segments are equal) and the model is equally bendable (deformable) in all directions. The phenomena that can be described using such simplified elastic model include gross shape changes in DNA, such as supercoiling, the response of plasmids to stress, etc. A technique of finite element analysis has been applied successfully for small DNA deformations. Model is suitable for DNA in plasmids (Munteanu et al., 1998). If DNA is modelled as a homogeneous and isotropic elastic rod, the DNA chain is characterised by three parameters: The bending rigidity, the torsional rigidity, and the DNA effective diameter (Maxim and Kamenetskii, 1997).

In *sequence-dependent anisotropic elastic model* DNA is considered to be an initially straight, segmented, elastic rod, in which the flexibility of each segment is greater towards the major groove than it is in other directions. This model can predict local bending phenomena and explains phenomena as the affinity of protein binding and kinking (Munteanu et al., 1998). Goyal and Perkins (2008) extend a computational rod model that captures the non-linear dynamics of hyperleastic, isotropic rods to accommodate large and discontinuous variations in bending and torsional stiffness.

Modelling DNA, as an isotropic rod can not explain some mechanical properties of DNA molecule achieved experimentally (twist-stretch coupling in single DNA measured by rotor bead tracking technique) like over-winding of DNA molecule under tensions. DNA molecule reaches the maximum twist level at a tension of 30 pN, as tension is increased above this critical value, the DNA begins to unwind. Elastic rod model is shown in Figure 2, which can explain these unusual mechanical properties.

Figure 2 Elastic rod model (see online version for colours)



Notes: DNA is modelled as an elastic rod (grey) wrapped helically by a stiff wire (red)

Source: Gore et al. (2006)

DNA is modelled as an elastic rod wrapped helically by a stiff wire. The inner core of radius R is assumed to have a Poisson's ratio v = 0.5. "The outer wire is affixed to the inner rod helically with a pitch of 3.4 nm, and contributes to the overall mechanical properties because it resists stretching and compression. The outer helix increases the

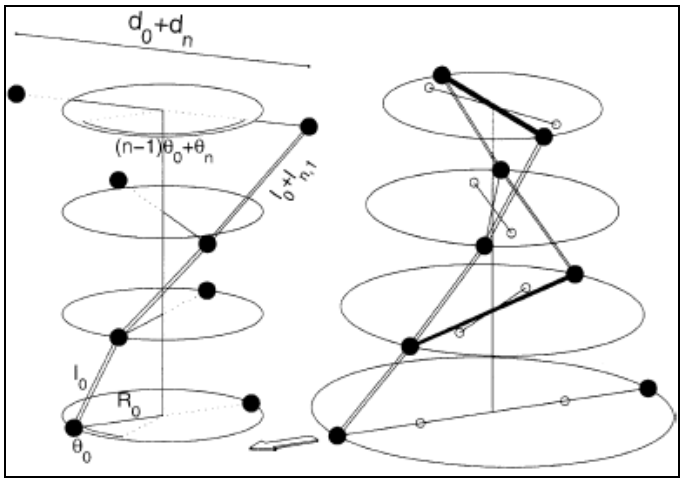
torsional rigidity and yields a twist – stretch coupling that depends upon the helix angle. Stretching generates an over-winding of the helix because the inner rod decreases in diameter as it is stretched. The outer helix is then able to wrap a larger number of times over the length of the molecule…" "These results have implications for the action of DNA-binding proteins that must stretch and twist DNA to compensate for variability in the lengths of their binding sites" (Gore et al., 2006). Linear isotropic rod model has some limitations in predicting DNA supercoiling of long molecules under applied tension and twist. There is coupling between bending and stretching (Smith and Healey, 2008). Bend-twist coupling is important in predicting the stability boundary. Eslami-Mossallam and Ejtehadi (2009) proposed the asymmetric elastic rod model for DNA.

Model of Lebrun and Lavery (1996) show how the double helix can be extended to twice its normal length before its base pairs break. Results correlate well with nanomanipulation experiments.

2.3 The network model

Double-stranded DNA is treated as a network of coupled oscillators incorporating essential microscopic degrees of freedom of DNA and the inherent interactions between them. The constituents of the oscillator network model represent the nucleotides, which are regarded as single non-deformable entities (see Figure 3).

Figure 3 Network model of DNA



Notes: Left geometry of the twisted dsDNA model showing the variables
Right: DNA molecule at the end of the pulling process with exaggerate distortions

Source: Hennig and Archilla (2004)

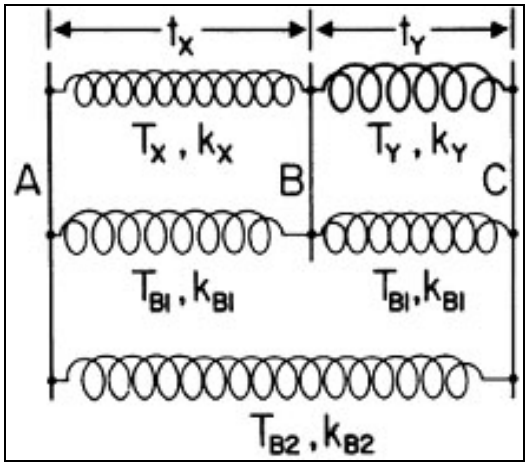
No inner dynamical degrees of freedom of the nucleotides are taken into account that is justified by the time scale separation between the small-amplitude and fast vibrational motions of the individual atoms and the slower and relatively large-amplitude motions of the atom groups constituting the nucleotides. The nucleotides are considered as identical objects of fixed mass all of four types of bases are treated as equal. The network model can explain the mechanical stability and elasticity properties of dsDNA molecules. This

model is suitable for studying the opening-closing dynamics of dsDNA molecules that are forced into non-equilibrium conformations, which are relevant for bimolecular processes. Hennig and Archilla (2004) show that the attainment of a quasi-equilibrium regime proceeds faster in the case of the twisted DNA form, than for its thus less flexible ladder counterpart.

2.4 Torsional spring model

In torsional springs model, Tung and Harvey (1984) made a distinction between purine bases (adenine and guanine) and also between pyrimidines, (cytosine and thymine), using the atomic resolution of conformational energy calculations (see Figure 4).

Figure 4 Torsional spring model



Notes: Torsional spring model for helix twist angles of a trimer. Note that distances in this figure correspond to angels not to lengths.

Source: Tung and Harvey (1984)

The model predicts a macroscopic torsional stiffness and a longitudinal compressibility (Young's modulus) that are both in good agreement with experiment. They use conformational energy calculations to determine the parameters of the model, and can quantitatively predict helix twist angles (Tung and Harvey, 1984).

2.5 Soliton-existence supporting models

One of the first of this kind was Yakushevich model (Y model) of DNA and models based on it (Gaeta, 1992; González and Martín-Landrove, 1994). Dynamics of topological solitons describing open states in the DNA double helix are studied in the framework of a model that takes into account asymmetry of the helix. Yakushevich et al. (2002) investigated interaction between the solitons, their interactions with the chain inhomogeneities and stability of the solitons with respect to thermal oscillations and have shown that three types of topological solitons can occur in the DNA double chain. *The composite model for DNA* is also based on Y model. The sugar-phosphate group and the base are described by separate degrees of freedom. The composite model fits

experimental data better than the simple Y model. DNA nucleotides are represented as two distinct discs, one still centred about the backbone axis and representing the sugar-phosphate group and the second rigidly rotating about a fixed point of the former. The composite model supports solitonic solutions, qualitatively and quantitatively very similar to the Yakushevich solitons (De Leo and Demelio, 2008; Cadoni et al., 2008). The results of numerical investigations show that the solitons are stable with respect to thermal oscillations (Muto et al., 1990; Bogolubska and Bogolubsky, 1994). It is found that a significant number of solitons is generated at physiological temperature (Balanovski and Beaconsfield, 1982).

Dynamic plane-base rotator model is suitable for study the non-linear dynamics of the inhomogeneous dsDNA especially angular rotation of bases in a plane normal to the helical axis (Daniel and Vasumathi, 2007). This model is also used to study the effect of phonon interaction on base pair opening in the dsDNA. The velocity of the soliton increases or decreases or remains uniform or even the soliton stops depending on the values of the coupling strengths. There is no change in the topological character of the soliton in the asymptotic region (Vasumathi and Daniel, 2008).

Other soliton-existence supporting models are: symmetric twist-opening model of DNA (Tabi et al., 2009), *non-linear Volkov-Kosevich DNA model*. Zdravković and Satarić (2009) used the Peyrard-Bishop-Dauxois (PBD) model for the DNA dynamics to study some intervals for parameters that describe longitudinal and helicoidal interactions between nucleotides.

2.5.1 DNA model by N. Kovaleva and L. Manevich

In this model, three beads represent each nucleotide with interaction sites corresponding to phosphate group, group of sugar ring and the base (Kovaleva et al., 2007) (see Figure 5). It is soliton-supporting model.

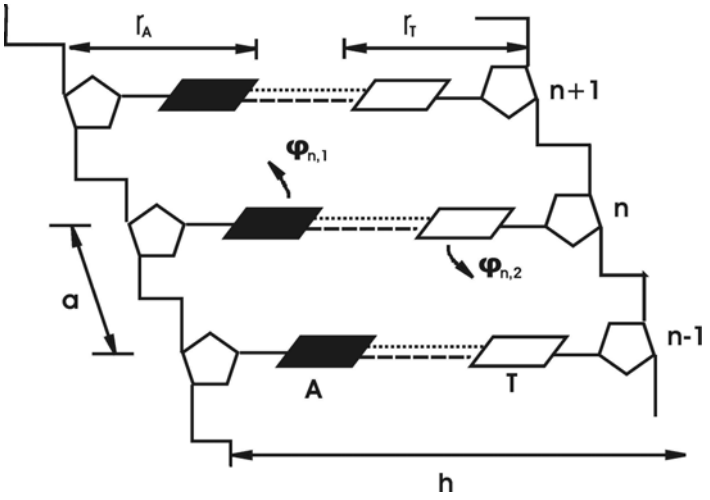
It is planer DNA model in which the chains of the macromolecule from two parallel strait lines place at a distance h from each other, the bases can make only rotation motions around their own chain, being all the time perpendicular to it. Kovaleva et al. (2007), and Kovaleva and Manevich (2005) point out that solitons and breathers play a functional role in DNA chains. They show that a localised excitation (breather) can exist in a double DNA helix. Authors formulated conditions of the breathers existence and estimate their characteristic parameters describing opening of DNA double helix. They investigated also the stability of breathers.

2.6 Multi-chain/multi-pendulum system model of double DNA

Hedrih (Stevanović) and Hedrih (2010, 2009a, 2009b, 2009c) gave several mechanical models of double DNA. In their models, DNA is in a form of homogenous multi-chain/multi-pendulum system which oscillatory signals can be considered trough a system with fixed and with free ends (see Figures 6 and 7). These figures are for the ideal elastic model and different boundary conditions. The dynamics of oscillatory signals in multi-chain systems are represented in Hedrih (Stevanović) (2006). Their basic model is linearisation of the model propose by Kovaleva and Manevich (2005). System is considered as homogeneous, witch means that all the masses are equal; rigidities of the linear-elastic spring elements are equal. The models differ in the way of coupling between the material (mass) particles. If the martial (mass) particles are coupled with

standard light hereditary elements the model has visco-elastic properties; if the martial particles are coupled with standard light fractional order elements it has visco-elastic and creep properties. There are several types of these models: *model with ideally elastic properties, model with hereditary properties and fractional order model*.

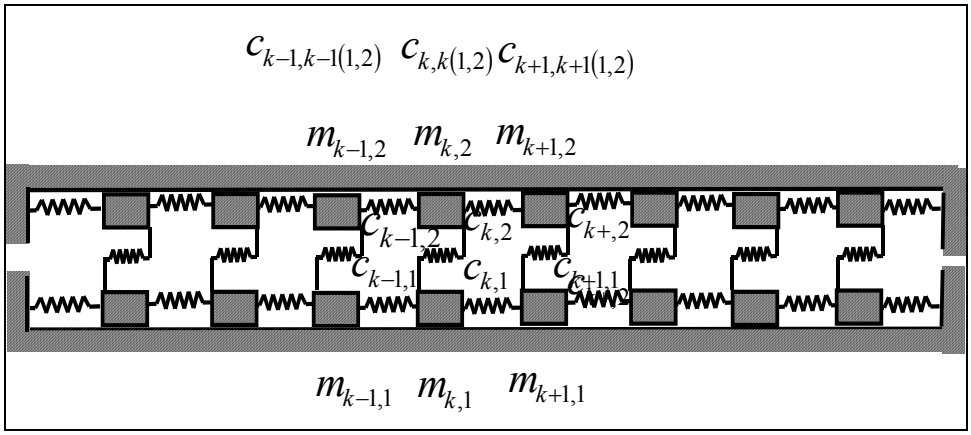
Figure 5 DNA model by N. Kovaleva and L. Manevich



Notes: Fragment of the DNA double chain consisting of three AT base pairs.
Longitudinal pitch of the helix, a = 3.4 Å, transferse pitch h = 16.15 Å.

Source: Kovaleva and Manevich (2005)

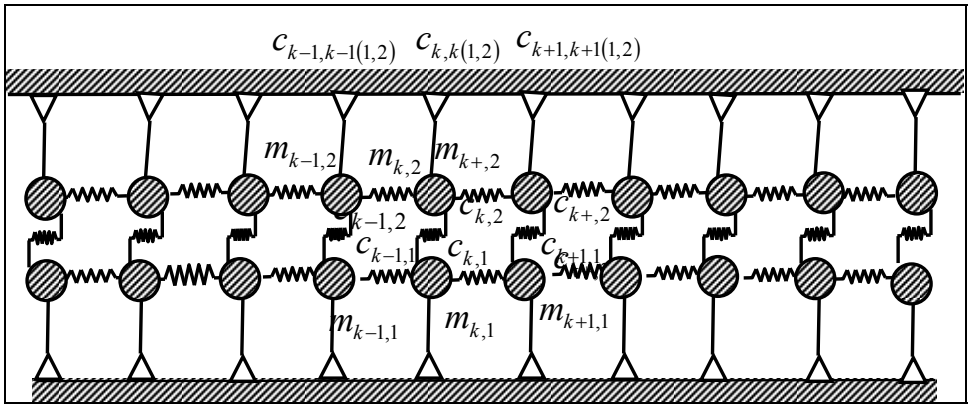
Figure 6 Model of the double DNA chain helix in the form of multi-chain system with fixed ends



For each of multi-pendulum/multi-chain models, it is possible to calculate main coordinates of eigen main chains when system is mathematically decoupled, set of eigen circular frequencies and set of characteristic numbers describing hereditary or fractional order system properties. Calculations show that there is no energy transfer between eigen main chains of double chain DNA heix system.

Using eigen main coordinates it is possible, for each of three models, to determine independent oscillators: for linear elastic model with harmonics with constant amplitudes and corresponding eigen circular frequencies; For model with hereditary properties n partial hereditary oscillators can be found. Each is defined by one eigen circular frequency and one characteristic number. Characteristic number depends on stiffness and relaxation time and determines hereditary properties of the corresponding oscillator. For fractional order model, n independent fractional order oscillators can be found, each with one eigen circular frequency and characteristic number. Characteristic number determines the properties of the fractional order system. There are full mathematical analogy and phenomenological mapping between two models: a double DNA fractional order chain helix model and a double DNA hereditary chain helix.

Figure 7 Model of the double DNA chain helix model in the form of multi-chain system with free ends



2.6.1 Model with ideally linear elastic properties

Authors of the multi-pendulum double DNA model suggest existence of new phenomena named eigen main chains of the homogeneous double DNA chain helix. These main eigen chains are partial n-frequency oscillators, and each, with n degrees of freedom. Each of these eigen main chains of the homogeneous double DNA chain helix (with $2n$ degree of freedom) is an independent partial n-frequency oscillator which oscillates with a subset of n eigen circular frequencies: first with frequencies from the set $\omega^2_{s\xi}, s = 1,2,3,4...,n$ – set described by characteristic equation of the subsystem of differential equations

$$\frac{1}{\omega_0^2}\ddot{\xi}_{\mathrm{k}} - \xi_{\mathrm{k+1}} + 2\xi_{\mathrm{k}}[1+\mu-\kappa] - \xi_{\mathrm{k-1}} = 0,\ k = 1,\ 2,\ 3,\ ...,\ n \tag{1}$$

of the n eigen circular frequencies of the first eigen main chain of the homogeneous double DNA chain helix; and second with frequencies from the set $\omega^2_{s\eta},\ s = 1,\ 2,\ 3,\ 4,\ ...,\ n$ – set described by characteristic equation of the subsystem of differential equations

$$\frac{1}{\omega_0^2}\ddot{\eta}_{\mathrm{k}} - \eta_{\mathrm{k+1}} + 2\eta_{\mathrm{k}}(1+\mu) - \eta_{\mathrm{k-1}} = 0,\ k = 1, 2, 3, ..., n \tag{2}$$

of the n eigen circular frequencies of the second eigen main chain of the homogeneous double DNA chain helix. In the case of forced oscillatory regimes, using the obtained sets of eigen circular frequencies obtained from subsystems (1)–(2), it is possible that resonant regimes on the corresponding circular frequencies are present only on one eigen main chain, while in the other eigen main chain forced oscillatory regimes are normal, without resonance. Also, in forced frequency regimes it is possible to identify phenomena of dynamical absorptions, without losing mechanical energy of the double DNA chain helix (for details see Hedrih (Stevanović) and Hedrih, 2010). Also, we calculated two subsets of the eigen circular frequencies $\left(\omega_s^2\right)$ of the vibration signal modes of separate eigen main chains *in* the double DNA chain helix using the trigonometric method (Rašković, 1965, 1985; Hedrih (Stevanović), 2006, 2008), as well as amplitudes. Two subsets of eigen circular frequencies are obtained in the following forms (for details see, Hedrih (Stevanović) and Hedrih, 2009a, 2009b, 2010):

$$\omega_s^2 = 2\omega_0^2\left[2\sin^2\frac{\varphi_s}{2} + (\mu - \kappa)\right], \omega_r^2 = 2\omega_0^2\left[2\sin^2\frac{\vartheta_s}{2} + \mu\right], s, r = 1, 2, 3, 4, ..., n \tag{3}$$

where φ_s and ϑ_r are characteristic numbers depending of boundary conditions of the model of the double DNA linear order chain helix. For specific boundary conditions it is possible to obtain coresponding values of these characteristic numbers -in a case when both ends of the double DNA chain helix are free/fixed.

2.6.2 Model with hereditary properties

In this model, double DNA is considered as a homogeneous system containing two coupled multi-pendulum subsystems. Corresponding material particles of the corresponding multi-pendulum chains are each two inter coupled by one standard light hereditary element [Hedrih (Stevanović) and Hedrih, 2009a, 2009c; Goroško and Hedrih (Stevanović), 2001, 2008]. Standard light hereditary element has relaxation time *n*. Biological materials are chancing their mechanical properties during aging. Biomaterials during aging may express relaxation properties and delay elasticity. We propose model with hereditary properties because it may be suitable for explaining this behaviour.

Two subsets of the kinetic parameters corresponding to first eigen main chain $\delta_{0(\xi,s)}$, $\delta_{(\xi,s)}$, $\omega_{(\xi,s)}$ and to second eigen main chain $\delta_{0(\eta,s)}$, $\delta_{(\eta,s)}$, $\omega_{(\eta,s)}$ of the eigen main hereditary oscillators of double DNA hereditary chain helix vibrations like one frequency oscillation modes in the second approximation are obtained in the following forms:

A *first subset:

$$\delta_{0(\xi,s)} = \frac{k}{n}\left[1 + \frac{(1-k)k}{n^2\omega_{\xi,s}^2}\right],\ \delta_{(\xi,s)} = \frac{1-k}{2n}\left[1 - k^2\frac{1}{n^2\omega_{\xi,s}^2}\right] \text{ and } \tilde{\omega}_{(\xi,s)}^2 = \omega_{(\xi,s)}^2\left[1 - (1-k)\frac{1+3k}{4}\frac{1}{4n^2\omega_{(\xi,s)}^2}\right] \tag{4}$$

$s = 1, 2, 3, 4, ..., n$

B *second subset:

$$\delta_{0(\eta,r)}=\frac{k}{n}\left[1+\frac{(1-k)k}{n^2\omega_{\eta,r}^2}\right],\ \delta_{(\eta,r)}=\frac{1-k}{2n}\left[1-k^2\frac{1}{n^2\omega_{\eta,r}^2}\right]\text{ and }\tilde{\omega}_{(\eta,r)}^2=\omega_{(\eta,r)}^2\left[1-(1-k)\frac{1+3k}{4}\frac{1}{4n^2\omega_{(\eta,r)}^2}\right] \quad (5)$$

$r=1, 2, 3, 4, ..., n$

2.6.3 Fractional order model with creeping properties

In this model, double DNA fractional order chain helix is in the form of the double chain fractional order system containing two coupled multi pendulum subsystems, with corresponding material particles of the corresponding multi-pendulum chains, that are each two inter coupled by one standard light fractional order element. System is homogenous.

We can use a system of coupled linear differential equations and modified by members with fractional order derivatives with respect to time (see Kovaleva et al., 2007; Hedrih (Stevanović), 2009a, 2009b; Hedrih (Stevanović) and Hedrih, 2009b, 2010).

The eigen main partial fractional order oscillators like one frequency oscillators of a double DNA fractional order chain helix model, we can obtain corresponding main coordinates $\zeta_{\varsigma,s}$ and $\zeta_{\eta,r}$, $r, s = 1, 2, 3, ..., n$ and corresponding two subsystems of the main partial fractional order oscillators described by the following uncoupled fractional order differential equations containing each only with one normal coordinate $\zeta_{\varsigma,s}$ and $\zeta_{\eta,r}$:

$$\ddot{\zeta}_{\varsigma,s}+\omega_{\xi,s}^2\zeta_{\varsigma,s}+\omega_{\alpha\xi,s}^2\mathrm{D}_t^{\alpha}\left[\zeta_{\varsigma,s}\right]=0,\ s=1, 2, 3, 4, ..., n \quad (6)$$

$$\ddot{\zeta}_{\eta,r}+\omega_{\eta,r}^2\zeta_{\eta,r}+\omega_{\alpha\eta,r}^2\mathrm{D}_t^{\alpha}\left[\zeta_{\eta,r}\right]=0,\ s=1, 2, 3, ..., n \quad (7)$$

Each of $2n$ fractional order differential equations (6) to (7) contains one eigen circular frequency $\omega_{\xi,s}^2$ or $\omega_{\eta,r}^2$ and one characteristic number $\omega_{\alpha\xi,s}^2$ or $\omega_{\alpha\eta,r}^2$ describing fractional order creeping properties of the double DNA chain helix. Set of one eigen circular frequency $\omega_{\xi,s}^2$ or $\omega_{\eta,r}^2$ and one characteristic number $\omega_{\alpha\xi,s}^2$ or $\omega_{\alpha\eta,r}^2$ determines fractional order properties of one fractional order oscillator [for more details, see Hedrih (Stevanović) (2008, 2009a, 2009b) and Hedrih (Stevanović) and Hedrih (2010)].

Transfer of energy of oscillations through the double DNA chain helix is why important. It is possible to analyse kinetic and potential energy of the double DNA chain helix as well as in its main chains. For the case that we compare energies of the ideally elastic DNA model with models with hereditary properties as well fractional order it is necessary to analyse dissipation of the total mechanical energy in these two models of the DNA chain helix. Total mechanical energy in this system decries with time and signal modes are damped.

2.6.4 Experimental potential of the multi-pendulum models

Ideally elastic model describes the reversible properties of the DNA system. Hereditary and fractional order model are suitable for modelling the materials with delayed deformation. Material memorises changes it sustained over time. These changes may

change the properties of material. Fractional order model with creep elements is suitable for describing (for certain boundary conditions) elastic, visco-elastic and creep properties.

These models may be suitable for explaining biochemical changes of DNA during aging of the molecule. It is possible to isolate the same DNA sequence from people in different age and to measure the visco-elastic properties of the molecules (with adequate equipment) and compare them.

The analysis showed that there is no transfer of energy between main chains of the double DNA chain helix considered as a hereditary chain helix, and that transfer of energy appears only between material particles in the corresponding subset of the corresponding main chain. These results may be important for future application in theoretical and experimental medical investigations. As we take into account a hereditary non-conservative model of the double DNA chain helix, then it is possible to conclude that main chains oscillate with no constant total mechanical energy and, also, with different initial main chain total energy values, as well as with different set of the eigen frequencies. Under the external one frequency excitation, only in one main chain is possible that resonance regime appears, but also there are possibilities for dynamical absorption existence.

3 Concluding remarks

Transcription process of DNA is well described at biochemical level. During transcription part of double DNA is unzipped, and only one chain helix is used as a matrix for transcription. For better understanding DNA and its function it is necessary to consider its behaviour through bioelectrical and mechanical point of view. If we know what is happened to DNA at biomechanical, bioelectrical and biochemical level during transcription our understanding of its function will be more complete. This may open a wide array of possibilities of using DNA as an essential structure in technical devices.

Considered as a linear mechanical system, DNA molecule as a double helix has its eigen circular frequencies and that is its characteristic. Mathematically it is possible to decouple it into two eigen main chains with their set of the eigen circular frequencies which are different. This may correspond to different chemical structure (the order of base pairs) of the complementary chains of DNA. We are free to propose that every specific set of base pair order has its eigen circular frequencies and it changes when DNA chains are coupled in the system of double helix. DNA as a double helix in a living cell can be considered to be a non-linear system but under certain condition its behaviour can be described by linear dynamics.

The phenomenon described in multi-pendulum models that there is no transfer of energy between partial eigen main oscillators each with n degrees of freedom, in double DNA chain helix, may open a new approach to understanding the transfer of genetic information. This of course needs further empirical research. It is possible to investigate the transfer of oscillatory signals through double DNA chain helix in arbitrary initial conditions only by half of the number of the eigen frequencies. Identification of two different subsets of eigen circular frequencies may correspond to base pair order in complementary chains of DNA double helix in a living cell. If the coordinates of one DNA chain is known it is possible to find the coordinates of complementary chain and to reconstruct the base pair order.

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