

MODELING DOUBLE DNA HELIX MAIN CHAINS FORCED VIBRATIONS

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ABSTRACT.

DNA transcription process is well described at biochemical level. During transcription double DNA interacts with transcription proteins; part of double DNA is unzipped, and only one chain helix is used as a matrix for transcription.

For better understanding the DNA transcription process and its behavior through biomechanical point of view, we consider double DNA (dDNA) as an oscillatory system that oscillates in forced regimes. In this paper analytical expressions of the forced oscillations of the dDNA helix chains are presented for both introduced models, ideally elastic as well as fractional order model. On the basis of previous results (DNA mathematical models published by N. Kovaleva, L. Manevich in 2005 and 2007, and multipendulum models by Hedrih (Stevanović) and Hedrih) where we obtain main chain subsystems of the double DNA helix, new results analysis of the forced vibrations is done. There are different cases of the resonant state in one of the main chains, and there are no interactions between main chains.

The possibilities of appearance of resonant regimes only in one of the two main chains is proved, as well as dynamical absorption under external one frequency forced excitations is considered.

Keywords: *Double DNA helix chain, forced vibrations, eigen main chains, resonant state, dynamical absorption, fractional order model.*

1 Introduction - DNA-structure and function

DNA is a biological polymer which can exist in different forms (A, B, Z, E ...) but only B form can be found in live organisms. Chemically, DNA consists of two long polymers of simple units called nucleotides, with backbones made of sugars and phosphate groups joined by ester bonds. To each sugar is attached one of four types of molecules called bases. (Adenine-A, thymine-T, guanine-G and cytosine-C). Two bases on opposite strands are linked via hydrogen bonds holding the two strands of DNA together. It is the sequence of these four bases along the backbone that encodes information.

The basic function of DNA 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 molecule is moving, changing its position and shape during the interactions. DNA molecules can be considered to be a mechanical structure on the nanolevel.

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. It is important to note the DNA found in many cells can be macroscopic in length - a few centimeters long for each human chromosome. Consequently, cells must compact or "package" DNA to carry it within them (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.

There are different approaches to studying the mechanical properties of the DNA molecule (experimental, theoretical modeling).

2 Mechanical properties of DNA achieved experimentally.

Experimental evidence suggests DNA mechanical properties, in particular intrinsic curvature and flexibility, have a role in many relevant biological processes.

For small distortions, DNA overwinds under tension (see Ref. [13] by Jeff Gore, Zev Bryant, Marcelo (2006)). Lowering of the temperature does increase the DNA curvature. 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 (see Ref. [1] by Javier Arsuaga, Robert K.-Z. Tan, Mariel Vazquez, De Witt Sumners, Stephen C. Harvey (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 (see Refs. [28] by Peck, L.J. and Wang, J.C. (1981) and [31] by Chang-Shung Tung and Stephen C. Harvey (1984)).

Under low tension, DNA behaves like an isotropic flexible rod. At higher tensions, the behavior of over- and underwound molecules is different. In each case, DNA undergoes a structural change before the twist density necessary for buckling is reached (see Refs. [5] by Zev Bryant, Michael D. Stone, Jeff Gore, Steven B. Smith and Nicholas R. Cozzarelli (2003)). Mg^{2+} can induce or enhance curvature in DNA fragments and helps stabilize several types of DNA structures (see Ref. [4] by Brukner, S. Susic, M. Dlakic, A. Savic, S. Pongor (1994)). DNA length varied in solution with different ionic force. It is significantly longer in solution with lower ionic force (see Ref. [10] by C. Frontali, E. Dore, A. Ferrauto, E. Gratton, A. Bettini, M.R. Pozzan, E. Valdevit (1979)).

3. Mechanical models of the DNA

A number of mechanical models of the DNA double helix have been proposed till today. 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. We are going to mention some of the models that may explain twist-opening conditions.

Bryant et al (see Ref. [5] by Bryant et al, 2003) have shown that an over- or underwound DNA molecule behaves as a constant-torque wind-up motor capable of repeatedly producing thousands of rotations, and that an overstretched molecule acts as a force-torque converter. The production of continuous directed rotation by molecular devices has potential applications in

the construction of nanomechanical systems (see Ref. [2] by Bao, 2002). Polymer 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” (see Refs. [7] by Cocco et al, 2002; and [33] by Zhou and Lai, 2001). **Eslami-Mossallam and Ejtehadi**, (see Ref. [9] by **Eslami-Mossallam and Ejtehadi, 2009**) proposed the asymmetric elastic rod model for DNA. Their model accounts for the difference between the bending energies of positive and negative rolls, which comes from the asymmetric structure of the DNA molecule. The model can explain the high flexibility of DNA at small length scales, as well as kink formation at high deformation limit. Specially type of DNA models are **soliton -existence supporting models**. One of the first of this kind was Yakushevich model of DNA and models based on it (see Ref. [11] by Gaeta, 1992). 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 (see Ref. [32] by 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. González and Martín-Landrove (see Ref. [12] by González and Martín-Landrove, 1994) gave the complete qualitative analysis of soliton interaction in DNA torsional equations. The model emphasizes the importance of the solitons for opening of the double DNA helix. The region of the chain where there is a maximum opening is larger for the general case, since the asymptotical behavior for the kink type solitons is smoother than the one corresponding to the solutions in the particular case. There is possibility that an enzyme take charge for the opening of the chain. The supersonic solutions, since they represent states that are totally open, could contribute significantly to the fusion of the DNA chain to the enzymatic activity. The presence of a propagating soliton along the chain could contribute to its opening through the interaction among different types of open states. **The composite model for DNA** is also based on Yakushevich model (Y model). The mechanism for selecting the speed of solitons by tuning the physical parameters of the non-linear medium and the hierarchical separation of the relevant degrees of freedom are described in this model (see Refs. [8] by De Leo and Demelio, 2008; [6] by Cadoni et al, 2008). **In the symmetric twist-opening model of DNA** the small amplitude dynamics of the model is shown to be governed by a solution of a set of coupled nonlinear Schrödinger equations. Conditions for modulation instability occurrence are presented and attention is paid to the impact of the backbone elastic constant K . It is shown that high values of K extend the instability region. This model can be reduced to a set of coupled discrete nonlinear system equations. The growth rate of instability has been evaluated and increases with the coupling constant K . The kink-bubble soliton, made of two part of different size, has been shown to be mobile. Authors supposed that the kink-bubble solution can be used to describe the internal dynamics which usually consists of long-range collective bending and twisting modes of the bases, short-range oscillations of individual bases, and the reorientation of the spin label (see Ref. [30] by Tabi et al, 2009).

Binding of proteins and other ligands on DNA, induces a strong deformation of the DNA structure.

The aim of our work was to model the DNA dynamics (vibrations of DNA chains) as a biological system in a specific boundary condition that are possible to occur in a life system during regular function of DNA molecule. We consider double DNA (dDNA) as an oscillatory system that oscillates in forced regimes during the DNA transcription process.

For mathematical descriptions we use References by Kovaleva and Manevich (see Refs. [26-27]), Hedrih (see Refs. [14-22]), Bačlić and Atanacković (see Ref. [3]), Hedrih and Filipovski (see Ref. [23]), Hedrih and Hedrih (see Refs. [24-25]) and Rašković P. Danilo see Ref. [29]).

4 DNA models by N. Kovaleva and L. Manevich

To model oscillation of dDNA in forced regimes we use as a basic approach model of dDNA proposed by N.Kovaleva, L.Manevich, V.Smirnov (see Ref [26]). They show that in a

double DNA helix localized excitation (breather) can exist which corresponds to predominant rotation of one chain and small perturbation of second chain using coarse-grained model of DNA double helix.

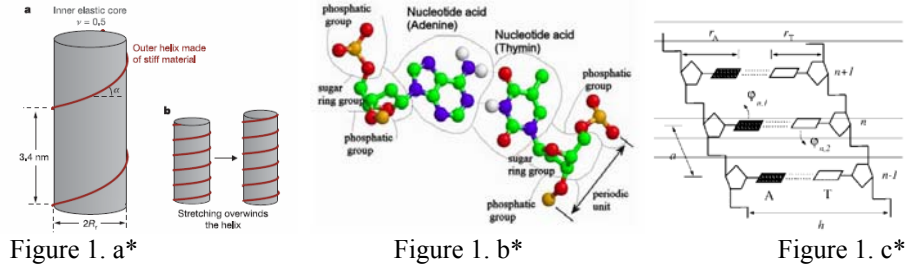


Figure 1. a* “Toy mechanical” model of DNA. a, DNA is modeled as an elastic rod (grey) wrapped helically by a stiff wire (red). see Ref. [9] by Jeff Gore, Zev Bryant, Marcelo (2006)

Figure1. b* The model scheme of a double helix on six coarse-grained particles [10].

Figure 1.c* Fragment of the DNA double chain consisting of three AT base pairs. Longitudinal pitch of the helix $a = 3.4 \text{ \AA}$; transverse pitch $h = 16.15 \text{ \AA}$ [11].

Reference [26] by N.Kovaleva, L.Manevich, V.Smirnov presented 8th conference on DSTA 2007, point out that solitons and breathers play a functional role in DNA chains. In a model, the DNA backbone is reduced to the polymeric structure and the base is covalently linked to the center of sugar ring group, thus a DNA molecule with N nucleotides corresponds to 3N interaction centers. Starting from a coarse-grained off-lattice model of DNA and using cylindrical coordinates, authors derive simplified continuum equations corresponding to vicinities of gap frequencies in the spectrum of linearized equations of motion. It is shown that obtained nonlinear continuum equations describing modulations of normal modes, admit spatially localized solitons, which can be identified with breathers. Authors formulated conditions of the breathers existence and estimate their characteristic parameters. The relationship between derived model and more simple and widely used models is discussed. The analytical results are compared with the data of numerical study of discrete equations of motion. See Figure 1.b*.

Ref. [27] by N.Kovaleva, L.Manevich (2005)) presented at the 8th conference on Dinamical systems theory and applications, presented a simplest model describing opening of DNA double helix. Corresponding differential equations are solved analytically using multiple-scale expansions after transition to complex variables. Obtained solution corresponds to localized torsional nonlinear excitation – breather. Stability of breather is also investigated.

In this Reference [27] N.Kovaleva, L.Manevich (2005)) consider B form of the DNA molecule, the fragment of which is presented in Fig.1. b*. The lines in the figure correspond to skeleton of the double helix, black and gray rectangles show the bases in pairs (AT and GC). Let us focus our attention on the rotational motions of bases around the sugarphosphate chains in the plane perpendicular to the helix axis. See Figure 1.c*

Authors deal with the planar DNA model in which the chains of the macromolecule form two parallel straight lines placed at a distance h from each other, and the bases can make only rotation motions around their own chain, being all the time perpendicular to it. Authors accepted as generalized (independent) coordinates $\varphi_{k,1}$ that are the angular displacement of the k -th base of the first chain, and as generalized (independent) coordinates $\varphi_{k,2}$ is the angular displacement of the k -th base of the second chain. Then, by using accepted generalized coordinates $\varphi_{k,1}$ and $\varphi_{k,2}$ for k -th bases of both chains in the DNA model, authors derived a system of differential equations describing DNA model vibrations in the following forms:

$$\begin{aligned}
& \mathbf{J}_{k,1} \ddot{\varphi}_{k,1} - \frac{K_{k,1}}{2} [\sin(\varphi_{k+1,1} - \varphi_{k,1}) - \sin(\varphi_{k,1} - \varphi_{k-1,1})] + K_{\alpha\beta} r_{\alpha} (r_{\alpha} - r_{\beta}) \sin \varphi_{k,1} - \\
& \quad - K_{\alpha\beta} \frac{1}{4} \left(1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}} \right) (r_{\alpha} - r_{\beta})^2 \sin(\varphi_{k,1} - \varphi_{k,2}) = 0 \\
& \mathbf{J}_{k,2} \ddot{\varphi}_{k,2} - \frac{K_{k,2}}{2} [\sin(\varphi_{k+1,2} - \varphi_{k,2}) - \sin(\varphi_{k,2} - \varphi_{k-1,2})] + K_{\alpha\beta} r_{\alpha} (r_{\alpha} - r_{\beta}) \sin \varphi_{k,2} + \\
& \quad + K_{\alpha\beta} \frac{1}{4} \left(1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}} \right) (r_{\alpha} - r_{\beta})^2 \sin(\varphi_{k,1} - \varphi_{k,2}) = 0
\end{aligned} \tag{1}$$

Here $\mathbf{J}_{k,1}$ is the axial moment of mass inertia of the k -th base of the first chain; $\mathbf{J}_{k,2}$ is the axial moment of mass inertia of the k -th base of the second chain, and the point denotes differentiation in time t . For the base pair the axial moments of mass inertia are equal to $\mathbf{J}_{k,1} = m_{\alpha} r_{\alpha}^2$, $\mathbf{J}_{k,2} = m_{\beta} r_{\beta}^2$. The value of the base mass m_{α} , the length r_{α} , and the corresponding axial moment of mass inertia $\mathbf{J}_{k,1} = m_{\alpha} r_{\alpha}^2$ for all possible base pair authors accepted as in the Reference [19]. The fourth terms in previous system equations describe interaction of the neighboring bases along each of the macromolecule chains. Parameter $K_{k,i}$, $i = 1, 2$ characterizes the energy of interaction of the k -th base with the $(k+1)$ -th one along the i -th chain $i = 1, 2$. There are different estimations of rigidity. For the calculation that the most appropriate value is close $K_{k,i} = K = 6 \times 10^3 [kJ/mol]$.

5 Consideration of the basic DNA model - linearized Kovaleva-Manevich's DNA model

Let us investigate an oscillatory model of DNA, considered in the Reference [27] by N.Kovaleva, L. Manevich, (2005) and presented in the previous chapter III, by a system of differential equations (1) expressed by generalized (independent) coordinates $\varphi_{k,1}$ and $\varphi_{k,2}$ for k -th bases of both chains in the DNA model.

For the beginning, it is necessary to consider a corresponding linearized system of the previous system of the differential equations in the following form:

$$\begin{aligned}
& \mathbf{J}_{k,1} \ddot{\varphi}_{k,1} - \frac{K_{k,1}}{2} [(\varphi_{k+1,1} - \varphi_{k,1}) - (\varphi_{k,1} - \varphi_{k-1,1})] + K_{\alpha\beta} r_{\alpha} (r_{\alpha} - r_{\beta}) \varphi_{k,1} - \\
& \quad - K_{\alpha\beta} \frac{1}{4} \left(1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}} \right) (r_{\alpha} - r_{\beta})^2 (\varphi_{k,1} - \varphi_{k,2}) = \mathfrak{M}_{0,k,1} \cos \Omega_{k,1} t
\end{aligned} \tag{2}$$

$$\begin{aligned}
& \mathbf{J}_{k,2} \ddot{\varphi}_{k,2} - \frac{K_{k,2}}{2} [(\varphi_{k+1,2} - \varphi_{k,2}) - (\varphi_{k,2} - \varphi_{k-1,2})] + K_{\alpha\beta} r_{\alpha} (r_{\alpha} - r_{\beta}) \varphi_{k,2} + \\
& \quad + K_{\alpha\beta} \frac{1}{4} \left(1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}} \right) (r_{\alpha} - r_{\beta})^2 (\varphi_{k,1} - \varphi_{k,2}) = \mathfrak{M}_{0,k,2} \cos \Omega_{k,2} t
\end{aligned} \tag{3}$$

or in the following form:

$$\begin{aligned}
& \frac{2\mathbf{J}_{k,1}}{K_{k,1}} \ddot{\varphi}_{k,1} - [(\varphi_{k+1,1} - \varphi_{k,1}) - (\varphi_{k,1} - \varphi_{k-1,1})] + \frac{2K_{\alpha\beta} r_{\alpha} (r_{\alpha} - r_{\beta})}{K_{k,1}} \varphi_{k,1} - \\
& \quad - \frac{K_{\alpha\beta}}{2K_{k,1}} \left(1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}} \right) (r_{\alpha} - r_{\beta})^2 (\varphi_{k,1} - \varphi_{k,2}) = \frac{\mathfrak{M}_{0,k,1}}{K_{k,1}} \cos \Omega_{k,1} t
\end{aligned} \tag{2*}$$

$$\begin{aligned} \frac{2\mathbf{J}_{k,2}}{K_{k,2}}\ddot{\varphi}_{k,2} - [(\varphi_{k+1,2} - \varphi_{k,2}) - (\varphi_{k,2} - \varphi_{k-1,2})] + \frac{2K_{\alpha\beta}r_{\alpha}(r_{\alpha} - r_{\beta})}{K_{k,2}}\varphi_{k,2} + \\ + \frac{K_{\alpha\beta}}{2K_{k,2}}\left(1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}}\right)(r_{\alpha} - r_{\beta})^2(\varphi_{k,1} - \varphi_{k,2}) = \frac{\mathfrak{M}_{0,k,2}}{K_{k,2}}\cos\Omega_{k,2}t \end{aligned} \quad (3*)$$

For the case of homogeneous systems we can take into consideration that are $\mathbf{J}_{k,1} = \mathbf{J}_{k,2} = \mathbf{J}$ and $K_{k,1} = K_{k,2} = K$.

By using change of the generalized coordinates $\varphi_{k,1}$ and $\varphi_{k,2}$ for k -th bases of both chains in the DNA model into following new ξ_k and η_k by the following dependence (see Hedrih and Hedrih [17, 24, 25]):

$$\xi_k = \varphi_{k,1} - \varphi_{k,2} \quad \text{and} \quad \eta_k = \varphi_{k,1} + \varphi_{k,2} \quad (4)$$

Previous system of differential equations (3) obtains the following form:

$$\frac{2\mathbf{J}}{K}\ddot{\xi}_k - \xi_{k+1} + 2\xi_k \left[1 + \frac{K_{\alpha\beta}r_{\alpha}(r_{\alpha} - r_{\beta})}{K} - \frac{K_{\alpha\beta}}{2K} \left(1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}} \right) (r_{\alpha} - r_{\beta})^2 \right] - \xi_{k-1} = \frac{\mathfrak{M}_{0,k,1}}{K}\cos\Omega_{0,k,1}t - \frac{\mathfrak{M}_{0,k,2}}{K}\cos\Omega_{0,k,2}t \quad (5)$$

$$\begin{aligned} \frac{2\mathbf{J}}{K}\ddot{\eta}_k - \eta_{k+1} + 2\eta_k \left(1 + \frac{K_{\alpha\beta}r_{\alpha}(r_{\alpha} - r_{\beta})}{K} \right) - \eta_{k-1} = \frac{\mathfrak{M}_{0,k,1}}{K}\cos\Omega_{0,k,1}t + \frac{\mathfrak{M}_{0,k,2}}{K}\cos\Omega_{0,k,2}t, \\ k = 1, 2, 3, \dots, n \end{aligned} \quad (6)$$

First series of the previous system equations are decoupled and independent with relations of the second series of the equations. *Then we can conclude that new coordinates of ξ_k and η_k are main coordinates of DNA chains and that we obtain two fictive decoupled eigen single chains of the DNA liner model. This is the first fundamental conclusion as an important property of the linear model of vibrations in a double DNA helix.*

Systems of differential equations (5)-(6) contain two separate subsystems of no autonomous differential equations expressed by *coordinates of ξ_k and η_k which are main coordinates of a double DNA chain helix system and separate linear DNA model of forced vibrations into two independent chains.*

6. Consideration of the forced vibrations of a basic DNA model - linearized Kovaleva-Manevich's DNA model

For obtaining general solutions of the both systems (5)-(6) of no autonomous differential equations which correspond to forced regimes of the main chains vibrations, for beginning it is necessary to find particular solutions of this system. Taking into account denotation

$$\mu - \kappa = \frac{K_{\alpha\beta}r_{\alpha}(r_{\alpha} - r_{\beta})}{K} - \frac{K_{\alpha\beta}}{2K} \left(1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}} \right) (r_{\alpha} - r_{\beta})^2 \quad (7)$$

$$\kappa = \frac{K_{\alpha\beta}}{2K} \left(1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}} \right) (r_{\alpha} - r_{\beta})^2, \quad \mu = \frac{K_{\alpha\beta}r_{\alpha}(r_{\alpha} - r_{\beta})}{K} \quad (8)$$

$$u = \frac{\mathbf{J}}{K}\omega^2 \quad (9)$$

previous systems (5)-(6) of no autonomous differential equations is possible to express in the form:

$$\begin{aligned} \frac{2\mathbf{J}}{K}\ddot{\xi}_k - \xi_{k+1} + 2\xi_k [1 + \mu - \kappa] - \xi_{k-1} = h_{0,k,1}\cos\Omega_{k,1}t - h_{0,k,2}\cos\Omega_{k,2}t \\ k = 1, 2, 3, \dots, n \end{aligned} \quad (10)$$

$$\begin{aligned} \frac{2\mathbf{J}}{K} \ddot{\eta}_{\mathbf{k}} - \eta_{\mathbf{k}+1} + 2\eta_{\mathbf{k}}(1+\mu) - \eta_{\mathbf{k}-1} &= h_{0,k,1} \cos \Omega_{k,1}t + h_{0,k,2} \cos \Omega_{k,2}t, \\ k &= 1, 2, 3, \dots, n \end{aligned} \quad (111)$$

where $h_{0,k,1} = \frac{\mathfrak{M}_{0,k,1}}{K}$ $h_{0,k,2} = \frac{\mathfrak{M}_{0,k,2}}{K}$, $k = 1, 2, 3, \dots, n$, reduced amplitude of external excitations..

Next, taking into account that this system is linear, for simplifications of the calculation procedure, without losing generality, we can solve system of no autonomous differential equations describing main chains forced vibrations of double DNA helix chain system under one frequency external excitation, with frequency $\Omega_{1,1}$ and reduces amplitude

applied $h_{0,k,1} = \frac{\mathfrak{M}_{0,k,1}}{K}$ applied to one mass particle to the first real chain from the coupled chains. For that reason we take for find particular solutions which correspond to forced vibrations with frequency $\Omega_{1,1}$ in the following form (see Figure 2):

$$\frac{2\mathbf{J}}{K} \ddot{\xi}_{\mathbf{k}} - \xi_{\mathbf{k}+1} + 2\xi_{\mathbf{k}}[1+\mu-\kappa] - \xi_{\mathbf{k}-1} = \begin{cases} h_{0,1,1} \cos \Omega_{1,1}t & k=1 \\ 0 & k \neq 1 \end{cases}, k=1, 2, 3, \dots, n \quad (12)$$

$$\begin{aligned} \frac{2\mathbf{J}}{K} \ddot{\eta}_{\mathbf{k}} - \eta_{\mathbf{k}+1} + 2\eta_{\mathbf{k}}(1+\mu) - \eta_{\mathbf{k}-1} &= \begin{cases} h_{0,1,1} \cos \Omega_{1,1}t & k=1 \\ 0 & k \neq 1 \end{cases}, \\ k &= 1, 2, 3, \dots, n \end{aligned} \quad (13)$$

Particular solutions for first and second system (12)-(13), we propose in the forms:

$$\xi_{port,k} = N_k \cos \Omega_{1,1}t \quad k = 1, 2, 3, \dots, n \quad (14)$$

$$\eta_{port,k} = \tilde{N}_k \cos \Omega_{1,1}t \quad k = 1, 2, 3, \dots, n \quad (15)$$

and introducing following denotations:

$$u = \frac{\mathbf{J}}{K} \omega^2 \quad v_{k,1} = \frac{\mathbf{J}}{K} \Omega_{k,1}^2 \quad v_{k,2} = \frac{\mathbf{J}}{K} \Omega_{k,2}^2 \quad (16)$$

and introducing proposed particular solutions (14)-(16) into system (12)-(13), we obtain the following system of algebra no homogeneous system::

$$-N_{\mathbf{k}+1} + 2N_{\mathbf{k}}(1+\mu-\kappa-v_{1,1}) - N_{\mathbf{k}-1} = \begin{cases} h_{0,1,1} & k=1 \\ 0 & k \neq 1 \end{cases} \quad k = 1, 2, 3, \dots, n \quad (17)$$

$$-\tilde{N}_{\mathbf{k}+1} + 2\tilde{N}_{\mathbf{k}}(1+\mu-\tilde{v}_{1,1}) - \tilde{N}_{\mathbf{k}-1} = \begin{cases} h_{0,1,1} & k=1 \\ 0 & k \neq 1 \end{cases} \quad k = 1, 2, 3, \dots, n \quad (18)$$

where $v_{1,1} = \tilde{v}_{1,1} = \frac{\mathbf{J}}{K} \Omega_{1,1}^2$.

Using Cramer low, for the amplitudes of the particular solutions we obtain the following:

$$N_k(v_{1,1}) = \frac{\Delta_k(v_{1,1})}{\Delta(v_{1,1})} \quad k = 1, 2, 3, \dots, n \quad (19)$$

$$\tilde{N}_k(\tilde{v}_{1,1}) = \frac{\tilde{\Delta}_k(\tilde{v}_{1,1})}{\tilde{\Delta}(\tilde{v}_{1,1})} \quad k = 1, 2, 3, \dots, n \quad (20)$$

where, for example, two system determinates, $\Delta(v_{1,1})$ and $\tilde{\Delta}(\tilde{v}_{1,1})$ are in the following forms (for the coupled chains each with four degree of freedom):

$$\Delta(v_{1,1}) = \begin{vmatrix} 2(1+\mu-\kappa-v_{1,1}) & -1 & & \\ -1 & 2(1+\mu-\kappa-v_{1,1}) & -1 & \\ & -1 & 2(1+\mu-\kappa-v_{1,1}) & -1 \\ & & -1 & 2(1+\mu-\kappa-v_{1,1}) \end{vmatrix} \neq 0 \quad (21)$$

$$\tilde{\Delta}(\tilde{v}_{1,1}) = \begin{vmatrix} 2(1+\mu-\tilde{v}_{1,1}) & -1 & & \\ -1 & 2(1+\mu-\tilde{v}_{1,1}) & -1 & \\ & -1 & 2(1+\mu-\tilde{v}_{1,1}) & -1 \\ & & -1 & 2(1+\mu-\tilde{v}_{1,1}) \end{vmatrix} \neq 0 \quad (22)$$

For same example other determinants $\Delta_k(v_{1,1})$ and $\tilde{\Delta}_k(\tilde{v}_{1,1})$, $k=1,2,3,\dots,n$, we obtain from corresponding two system determinates, $\Delta(v_{1,1})$ and $\tilde{\Delta}(\tilde{v}_{1,1})$, introducing into corresponding column, column with free members from right sides of the no homogeneous algebra equations (17)-(18):

$$\Delta_1(v_{1,1}) = \begin{vmatrix} h_{0,1,1} & -1 & & \\ -1 & 2(1+\mu-\kappa-v_{1,1}) & -1 & \\ & -1 & 2(1+\mu-\kappa-v_{1,1}) & -1 \\ & & -1 & 2(1+\mu-\kappa-v_{1,1}) \end{vmatrix} = h_{0,1,1} 2^{4-1} \prod_{s=1}^{s=3} (v_{1,1} - u_s^{(n=3)}) \quad (23)$$

$$\tilde{\Delta}_1(\tilde{v}_{1,1}) = \begin{vmatrix} h_{0,1,1} & -1 & & \\ -1 & 2(1+\mu-\tilde{v}_{1,1}) & -1 & \\ & -1 & 2(1+\mu-\tilde{v}_{1,1}) & -1 \\ & & -1 & 2(1+\mu-\tilde{v}_{1,1}) \end{vmatrix} = h_{0,1,1} 2^{4-1} \prod_{r=1}^{r=3} (\tilde{v}_{1,1} - \tilde{u}_r^{(n=3)}) \quad (24)$$

$$\Delta_2(v_{1,1}) = \begin{vmatrix} 2(1+\mu-\kappa-v_{1,1}) & h_{0,1,1} & & \\ -1 & & -1 & \\ & & 2(1+\mu-\kappa-v_{1,1}) & -1 \\ & & -1 & 2(1+\mu-\kappa-v_{1,1}) \end{vmatrix} = h_{0,1,1} 2^{4-2} \prod_{s=1}^{s=2} (v_{1,1} - u_s^{(n=2)}) \quad (25)$$

$$\tilde{\Delta}_2(\tilde{v}_{1,1}) = \begin{vmatrix} 2(1+\mu-\tilde{v}_{1,1}) & h_{0,1,1} & & \\ -1 & & -1 & \\ & & 2(1+\mu-\tilde{v}_{1,1}) & -1 \\ & & -1 & 2(1+\mu-\tilde{v}_{1,1}) \end{vmatrix} = h_{0,1,1} 2^{4-2} \prod_{r=1}^{r=2} (\tilde{v}_{1,1} - \tilde{u}_r^{(n=2)}) \quad (26)$$

$$\Delta_3(v_{1,1}) = \begin{vmatrix} 2(1+\mu-\kappa-v_{1,1}) & & -1 & h_{0,1,1} \\ -1 & 2(1+\mu-\kappa-v_{1,1}) & & \\ & -1 & & -1 \\ & & & 2(1+\mu-\kappa-v_{1,1}) \end{vmatrix} = h_{0,1,1} 2(\tilde{v}_{1,1} - \tilde{u}_r^{(n=1)}) \quad (27)$$

$$\tilde{\Delta}_3(\tilde{v}_{1,1}) = \begin{vmatrix} 2(1+\mu-\tilde{v}_{1,1}) & & -1 & h_{0,1,1} \\ -1 & 2(1+\mu-\tilde{v}_{1,1}) & & \\ & -1 & & -1 \\ & & & 2(1+\mu-\tilde{v}_{1,1}) \end{vmatrix} = h_{0,1,1} 2(\tilde{v}_{1,1} - \tilde{u}_r^{(n=1)}) \quad (28)$$

$$\Delta_4(v_{1,1}) = \begin{vmatrix} 2(1+\mu-\kappa-v_{1,1}) & -1 & & h_{0,1,1} \\ -1 & 2(1+\mu-\kappa-v_{1,1}) & -1 & \\ & -1 & 2(1+\mu-\kappa-v_{1,1}) & \\ & & -1 & \end{vmatrix} = h_{0,1,1} \quad (29)$$

$$\tilde{\Delta}_4(\tilde{v}_{1,1}) = \begin{vmatrix} 2(1+\mu-\tilde{v}_{1,1}) & -1 & & h_{0,1,1} \\ -1 & 2(1+\mu-\tilde{v}_{1,1}) & -1 & \\ & -1 & 2(1+\mu-\tilde{v}_{1,1}) & \\ & & -1 & \end{vmatrix} = h_{0,1,1} \quad (30)$$

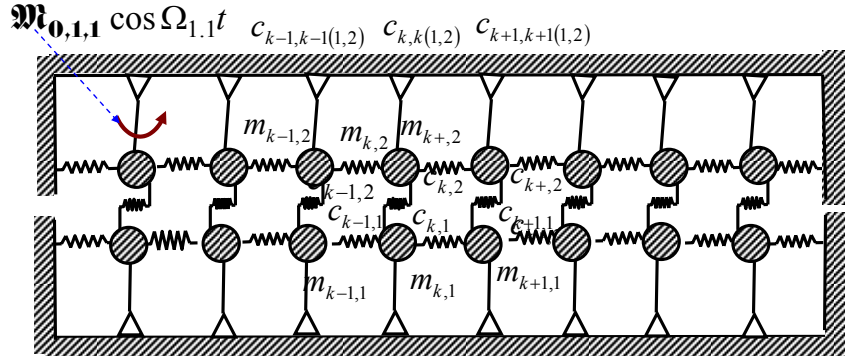


Figure 2. Double DNK Chain helix d model in the form of multipendulum system with fixed ends

Particular solutions of the considered examples with eight degree of freedom double DNA helix chain system containing two coupled chains each with four degree of freedom and excited by one frequency external excitation are in the following forms:

$$\xi_{port,1} = N_1 \cos \Omega_{1,1} t = \frac{h_{0,1,1} \prod_{s=1}^{s=3} (v_{1,1} - u_s^{(n=3)})}{2 \prod_{s=1}^{s=4} (v_{1,1} - u_s^{(4)})} \cos \Omega_{1,1} t \quad (31)$$

$$\eta_{port,1} = \tilde{N}_1 \cos \Omega_{1,1} t = \frac{h_{0,1,1} \prod_{r=1}^{r=3} (\tilde{v}_{1,1} - \tilde{u}_r^{(n=3)})}{2 \prod_{r=1}^{r=4} (\tilde{v}_{1,1} - \tilde{u}_r^{(4)})} \cos \Omega_{1,1} t \quad (32)$$

$$\xi_{port,2} = N_2 \cos \Omega_{1,1} t = \frac{h_{0,1,1} \prod_{s=1}^{s=2} (v_{1,1} - u_s^{(n=2)})}{4 \prod_{s=1}^{s=4} (v_{1,1} - u_s^{(4)})} \cos \Omega_{1,1} t \quad (33)$$

$$\eta_{port,2} = \tilde{N}_2 \cos \Omega_{1,1} t = \frac{h_{0,1,1} \prod_{r=1}^{r=2} (\tilde{v}_{1,1} - \tilde{u}_r^{(n=2)})}{4 \prod_{4r=1}^{r=4} (\tilde{v}_{1,1} - \tilde{u}_r^{(4)})} \cos \Omega_{1,1} t \quad (34)$$

$$\xi_{port,3} = N_3 \cos \Omega_{1,1} t = \frac{h_{0,1,1} (v_{1,1} - u_s^{(n=1)})}{8 \prod_{s=1}^{s=4} (v_{1,1} - u_s^{(n)})} \cos \Omega_{1,1} t \quad (35)$$

$$\eta_{port,21} = \tilde{N}_2 \cos \Omega_{1,1} t = \frac{h_{0,1,1} (\tilde{v}_{1,1} - \tilde{u}_r^{(n=1)})}{8 \prod_{r=1}^{r=4} (\tilde{v}_{1,1} - \tilde{u}_r^{(n)})} \cos \Omega_{1,1} t \quad (36)$$

$$\xi_{port,4} = N_4 \cos \Omega_{1,1} t = \frac{h_{0,1,1}}{16 \prod_{s=1}^{s=4} (v_{1,1} - u_s^{(4)})} \cos \Omega_{1,1} t \quad (37)$$

$$\eta_{port,4} = \tilde{N}_4 \cos \Omega_{1,1} t = \frac{h_{0,1,1}}{16 \prod_{r=1}^{r=4} (\tilde{v}_{1,1} - \tilde{u}_r^{(4)})} \cos \Omega_{1,1} t \quad (38)$$

Solutions of the homogeneous system for considered example are:

$$\xi_{free,k} = \sum_{s=1}^{s=4} C_s \sin k \varphi_s \cos(\omega_s t + \alpha_s), \quad k = 1, 2, 3, 4 \quad (39)$$

$$\eta_{free,k} = \sum_{r=1}^{r=4} D_r \sin k \varphi_r \cos(\tilde{\omega}_r t + \beta_r), \quad k = 1, 2, 3, 4 \quad (40)$$

General solutions are:

$$\xi_k = \xi_{free,k} + \xi_{part,k} = \sum_{s=1}^{s=4} C_s \sin k \varphi_s \cos(\omega_s t + \alpha_s) + \xi_{part,k}, \quad k = 1, 2, 3, 4 \quad (41)$$

$$\eta_k = \eta_{free,k} + \eta_{part,k} = \sum_{r=1}^{r=4} D_r \sin k \varphi_r \cos(\tilde{\omega}_r t + \beta_r) + \eta_{part,k}, \quad k = 1, 2, 3, 4 \quad (42)$$

or in the form

$$\xi_k = \xi_{free,k} + \xi_{part,k} = \sum_{s=1}^{s=4} C_s \sin k \varphi_s \cos(\omega_s t + \alpha_s) + N_k (v_{1,1}) \cos \Omega_{1,1} t, \quad k = 1, 2, 3, 4 \quad (43)$$

$$\eta_k = \eta_{free,k} + \eta_{part,k} = \sum_{r=1}^{r=4} D_r \sin k \varphi_r \cos(\tilde{\omega}_r t + \beta_r) + \tilde{N}_k (\tilde{v}_{1,1}) \cos \Omega_{1,1} t, \quad k = 1, 2, 3, 4 \quad (44)$$

For the system of double DNA helix chain system with $2n$ degrees of freedom previous two system determinates $\Delta(v_{1,1})$ and $\tilde{\Delta}(\tilde{v}_{1,1})$ are not difficult to express in the similar forms.

Then taking into account that determinates $\Delta(v_{1,1})$ and $\tilde{\Delta}(\tilde{v}_{1,1})$ are analogous as determinates, which describe frequency equations of the free vibrations of the double DNA helix chain system, which is possible express in the following forms $\Delta(u) = 0$ and $\tilde{\Delta}(u) = 0$, and that we have roots of these frequency equations in the forms (21)-(22) then we have roots of the two system determinates, $\Delta(v_{1,1})$ and $\tilde{\Delta}(\tilde{v}_{1,1})$ in the forms:

$$v_{1,1}^{(s)} = \frac{J}{K} \Omega_{1,1}^{(s)} = u_s^{(n)} = \frac{J}{K} \omega_s^2 = 2 \sin^2 \frac{\varphi_s}{2} + (\mu - \kappa), \quad s = 1, 2, 3, \dots, n \quad (45)$$

$$\tilde{v}_{1,1}^{(r)} = \frac{J}{K} \tilde{\Omega}_{1,1}^{(r)} = \tilde{u}_r^{(n)} = \frac{J}{K} \tilde{\omega}_r^2 = 2 \sin^2 \frac{\varphi_r}{2} + \mu, \quad r = 1, 2, 3, \dots, n \quad (46)$$

By use previous characteristic numbers of the previous two system determinates, these determinants $\Delta_k(v_{1,1})$ and $\tilde{\Delta}_k(\tilde{v}_{1,1})$ are possible express in the forms of products:

$$\Delta(v_{1,1}) = 2^n \prod_{s=1}^{s=n} (v_{1,1} - u_s^{(n)}) \quad (47)$$

$$\tilde{\Delta}(\tilde{v}_{1,1}) = 2^n \prod_{r=1}^{r=n} (\tilde{v}_{1,1} - \tilde{u}_r^{(n)}) \quad (48)$$

By same way, it is possible to find expressions for amplitude of the particular solutions depending of the number of degree of freedom $2n$. For example it is visible without calculations that amplitude N_1 , \tilde{N}_1 and N_2 , \tilde{N}_2 of the particular solutions of the first and second normal coordinates, $\xi_{part,1}$, $\eta_{part,1}$ and $\xi_{part,2}$, $\eta_{part,2}$ of the both main chains are in the following forms:

$$N_1 = \frac{h_{0,1,1} \prod_{s=1}^{s=n-1} (v_{1,1} - u_s^{(n-1)})}{2 \prod_{s=1}^{s=n} (v_{1,1} - u_s^{(n)})} \quad \text{and} \quad \tilde{N}_1 = \frac{h_{0,1,1} \prod_{r=1}^{r=n-1} (\tilde{v}_{1,1} - \tilde{u}_r^{(n-1)})}{2 \prod_{r=1}^{r=n} (\tilde{v}_{1,1} - \tilde{u}_r^{(n)})} \quad (49)$$

$$N_2 = \frac{h_{0,1,1} \prod_{s=1}^{s=n-2} (v_{1,1} - u_s^{(n-2)})}{2^2 \prod_{s=1}^{s=n} (v_{1,1} - u_s^{(n)})} \quad \text{and} \quad \tilde{N}_2 = \frac{h_{0,1,1} \prod_{r=1}^{r=n-1} (\tilde{v}_{1,1} - \tilde{u}_r^{(n-2)})}{2^2 \prod_{r=1}^{r=n} (\tilde{v}_{1,1} - \tilde{u}_r^{(n)})} \quad (50)$$

Then general solutions are in the following forms:

$$\xi_k = \xi_{free,k} + \xi_{part,k} = \sum_{s=1}^{s=n} C_s \sin k \varphi_s \cos(\omega_s t + \alpha_s) + \xi_{part,k}, \quad k = 1, 2, 3, \dots, n \quad (51)$$

$$\eta_k = \eta_{free,k} + \eta_{part,k} = \sum_{r=1}^{r=n} D_r \sin k \vartheta_r \cos(\tilde{\omega}_r t + \beta_r) + \eta_{part,k}, \quad k = 1, 2, 3, \dots, n \quad (52)$$

or in the form

$$\xi_k = \xi_{free,k} + \xi_{part,k} = \sum_{s=1}^{s=n} C_s \sin k \varphi_s \cos(\omega_s t + \alpha_s) + N_k(v_{1,1}) \cos \Omega_{1,1} t, \quad k = 1, 2, 3, \dots, n \quad (53)$$

$$\eta_k = \eta_{free,k} + \eta_{part,k} = \sum_{r=1}^{r=n} D_r \sin k \vartheta_r \cos(\tilde{\omega}_r t + \beta_r) + \tilde{N}_k(\tilde{v}_{1,1}) \cos \Omega_{1,1} t, \quad k = 1, 2, 3, \dots, n \quad (54)$$

For the case that one frequency external excitation, with reduced amplitude $h_{0,2,1} = \frac{\mathfrak{M}_{0,1,2}}{K}$ is with frequency $\Omega_{2,1}$, applied to the other first material particle n the other of the coupled real chains, then two subsystems of the main eigen chains are described by following subsystems of differential equations:

$$\frac{2\mathbf{J}}{K} \ddot{\xi}_k - \xi_{k+1} + 2\xi_k[1 + \mu - \kappa] - \xi_{k-1} = \begin{cases} -h_{0,2,1} \cos \Omega_{2,1} t & k = 1 \\ 0 & k \neq 1 \end{cases} \quad (55)$$

$$\frac{2\mathbf{J}}{K} \ddot{\eta}_k - \eta_{k+1} + 2\eta_k(1 + \mu) - \eta_{k-1} = \begin{cases} h_{0,2,1} \cos \Omega_{2,1} t & k = 1 \\ 0 & k \neq 1 \end{cases}, \quad (56)$$

Particular and general solutions of these previous equations is not difficult to obtain analogous by previous procedure and changing corresponding indices of the kinetic parameters of the main chains.

7. Consideration of the forced vibration regimes of a basic DNA model - linearized Kovaleva-Manevich's DNA model

From expressions (21) and (22) is possible to consider possibilities of appearance resonant regimes in eigen main chains.

For the case that determinants (21) and (22), $\Delta(v_{1,1}) = 2^n \prod_{s=1}^{s=n} (v_{1,1} - u_s^{(n)}) = 0$ and

$\tilde{\Delta}(\tilde{v}_{1,1}) = 2^n \prod_{r=1}^{r=n} (\tilde{v}_{1,1} - \tilde{u}_r^{(n)}) = 0$ are equal to zero, then we obtain two sets of external excitation

frequencies for which in the system appear resonant regime. But taking into account that eigen main chains have different sets of eigen circular frequencies as well as different sets of the resonant circular frequencies of external excitation, then we can conclude that if in one eigen main chain appear resonant regime in other no resonant regime. This is important fact to consider in the light of the real double DNA helix chain system.

Also by use expressions for amplitudes of the particular forced solutions is possible appearance of dynamical absorptions at corresponding main coordinate of main eigen chain. To obtain external excitation frequencies at which appear dynamical absorption at first or second main coordinate of the main chains are equal to zero:

$$N_1 = \frac{h_{0,1,1} \prod_{s=1}^{s=n-1} (v_{1,1} - u_s^{(n-1)})}{2 \prod_{s=1}^{s=n} (v_{1,1} - u_s^{(n)})} = 0 \quad \text{or} \quad \tilde{N}_1 = \frac{h_{0,1,1} \prod_{r=1}^{r=n-1} (\tilde{v}_{1,1} - \tilde{u}_r^{(n-1)})}{2 \prod_{r=1}^{r=n} (\tilde{v}_{1,1} - \tilde{u}_r^{(n)})} = 0 \quad (57)$$

$$N_2 = \frac{h_{0,1,1} \prod_{s=1}^{s=n-2} (v_{1,1} - u_s^{(n-2)})}{2^2 \prod_{s=1}^{s=n} (v_{1,1} - u_s^{(n)})} = 0 \quad \text{or} \quad \tilde{N}_2 = \frac{h_{0,1,1} \prod_{r=1}^{r=n-1} (\tilde{v}_{1,1} - \tilde{u}_r^{(n-2)})}{2^2 \prod_{r=1}^{r=n} (\tilde{v}_{1,1} - \tilde{u}_r^{(n)})} = 0 \quad (58)$$

and next.

$$\prod_{s=1}^{s=n-1} (v_{1,1} - u_s^{(n-1)}) = 0 \quad \text{or} \quad \prod_{r=1}^{r=n-1} (\tilde{v}_{1,1} - \tilde{u}_r^{(n-1)}) = 0 \quad (59)$$

$$\prod_{s=1}^{s=n-2} (v_{1,1} - u_s^{(n-2)}) = 0 \quad \text{or} \quad \prod_{r=1}^{r=n-2} (\tilde{v}_{1,1} - \tilde{u}_r^{(n-2)}) = 0 \quad (60)$$

From the last conditions (59) and (60), we can conclude that:

* *Dynamical absorption on the first pair of the main coordinates of the main chains appear on the resonate circular frequencies of the set of the double DNA helix chain system with one less pair of the material particles in comparison with the considered real system.*

* *Dynamical absorption on the second pair of the main coordinates of the main chains appear on the resonate circular frequencies of the set of the double DNA helix chain system with two less pairs of the material particles in comparison with considered system.*

This mathematical fact is important to considered in the light of the interruption or break of the double DNA helix chain system into finite parts.

8. The double DNA fractional order chain model on the basis of the linearized Kovaleva-Manevich's DNA models for free and forced vibrations

8.1. Constitutive relation of the standard light fractional order creep element.

Basic elements of multi mathematical pendulum system or multi coupled chain system are:

1* Material particles with mass m_k , with each particle having one degree of motion freedom, defined by following coordinate φ_k , when k changes by $k = 1, 2, 3, 4, \dots, N$.

2* Standard light fractional order coupling element of negligible mass in the form of axially stressed rod without bending, and which has the ability to resist deformation under static and dynamic conditions. **Standard light creep constraint element** for which the stress-strain relation for the restitution force as the function of element elongation is given by fractional order derivatives in the form

$$P(t) = -\{c_0 x(t) + c_\alpha \mathfrak{D}_t^\alpha [x(t)]\} \quad (61)$$

where $\mathfrak{D}_t^\alpha [\bullet]$ is operator of the α^{th} derivative with respect to time t in the following form:

$$\mathfrak{D}_t^\alpha [x(t)] = \frac{d^\alpha x(t)}{dt^\alpha} = x^{(\alpha)}(t) = \frac{1}{\Gamma(1-\alpha)} \frac{d}{dt} \int_0^t \frac{x(\tau)}{(t-\tau)^\alpha} d\tau \quad (62)$$

where c, c_α are rigidity coefficients—momentary and prolonged one, and α a rational number between 0 and 1, $0 < \alpha < 1$.

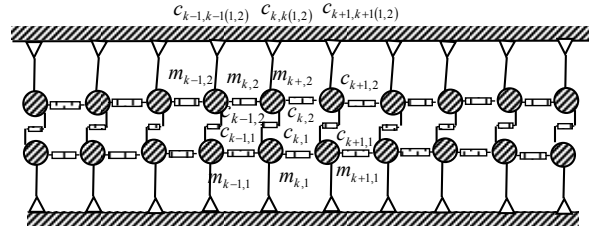


Figure 3. Double DNK fractional order chain helix in the form of multipendulum model with free ends

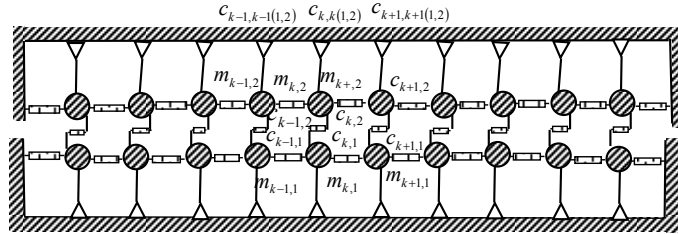


Figure 4. Double DNK fractional order chain helix d model in the form of multipendulum system with fixed ends

8.2. The double DNA fractional order chain forced vibration model on the basis of the linearized Kovaleva-Manevich's DNA model

For the fractional order forced vibrations of a fractional order double DNA chain model on the basis of the linearized Kovaleva-Manevich's DNA model, we accept a two chains as it is presented in Figure 3 or 4, in the form of the double chain fractional order system containing two coupled multi pendulum subsystem, in which corresponding material particles of the corresponding multi-pendulum chains are coupled by series of the same standard light fractional order elements.

Let's suppose that both coupled chains from system of the fractional order DNA model are excited by the system of external excitation containing two series of the one frequency excitations in the forms $\mathfrak{M}_{0,k,1} \cos \Omega_{k,1} t$ and $\mathfrak{M}_{0,k,2} \cos \Omega_{k,2} t$, $k = 1, 2, 3, \dots, n$, where $\mathfrak{M}_{0,k,1}$ and $\mathfrak{M}_{0,k,2}$ are amplitudes, $\Omega_{k,1}$ and $\Omega_{k,2}$ frequencies of the external forced couples each applied to one of the mass particles of the

double DNA model coupled chains. Then, corresponding system of the nonlinear forced vibrations of the double DNA model coupled chains are in the following forms:

Then, we can use system of the coupled fractional order coupled differential equations extended by terms containing external excitation forces or couples. Then, we can write corresponding system of the fractional order differential coupled equations in the form:

$$\begin{aligned}
& \mathbf{J}_{k,1} \ddot{\varphi}_{k,1} - \frac{K_{k,1}}{2} [(\varphi_{k+1,1} - \varphi_{k,1}) - (\varphi_{k,1} - \varphi_{k-1,1})] - \frac{K_{k,1,\sigma}}{2} \mathfrak{D}_t^\sigma [(\varphi_{k+1,1} - \varphi_{k,1}) - (\varphi_{k,1} - \varphi_{k-1,1})] + \\
& + K_{\alpha\beta} r_\alpha (r_\alpha - r_\beta) \varphi_{k,1} - K_{\alpha\beta} - \frac{1}{4} \left(1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}} \right) (r_\alpha - r_\beta)^2 (\varphi_{k,1} - \varphi_{k,2}) - \\
& - K_{\alpha\beta,\sigma} \frac{1}{4} \left(1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}} \right) (r_\alpha - r_\beta)^2 \mathfrak{D}_t^\sigma [(\varphi_{k,1} - \varphi_{k,2})] = \mathfrak{M}_{0,k,1} \cos \Omega_{k,1} t \\
& \mathbf{J}_{k,2} \ddot{\varphi}_{k,2} - \frac{K_{k,2}}{2} [(\varphi_{k+1,2} - \varphi_{k,2}) - (\varphi_{k,2} - \varphi_{k-1,2})] - \frac{K_{k,2,\sigma}}{2} \mathfrak{D}_t^\sigma [(\varphi_{k+1,2} - \varphi_{k,2}) - (\varphi_{k,2} - \varphi_{k-1,2})] + \\
& + K_{\alpha\beta} r_\alpha (r_\alpha - r_\beta) \varphi_{k,2} + K_{\alpha\beta} \frac{1}{4} \left(1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}} \right) (r_\alpha - r_\beta)^2 (\varphi_{k,1} - \varphi_{k,2}) + \\
& + K_{\alpha\beta,\sigma} \frac{1}{4} \left(1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}} \right) (r_\alpha - r_\beta)^2 \mathfrak{D}_t^\sigma [(\varphi_{k,1} - \varphi_{k,2})] = \mathfrak{M}_{0,k,2} \cos \Omega_{k,2} t
\end{aligned} \tag{63}$$

Previous system is possible to rewrite in the following form:

$$\begin{aligned}
& \frac{2\mathbf{J}_{k,1}}{K_{k,1}} \ddot{\varphi}_{k,1} - [(\varphi_{k+1,1} - \varphi_{k,1}) - (\varphi_{k,1} - \varphi_{k-1,1})] + \frac{K_{k,1,\sigma}}{K_{k,1}} \mathfrak{D}_t^\sigma [(\varphi_{k+1,1} - \varphi_{k,1}) - (\varphi_{k,1} - \varphi_{k-1,1})] + \\
& + \frac{2K_{\alpha\beta} r_\alpha (r_\alpha - r_\beta)}{K_{k,1}} \varphi_{k,1} - \frac{K_{\alpha\beta}}{2K_{k,1}} \left(1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}} \right) (r_\alpha - r_\beta)^2 (\varphi_{k,1} - \varphi_{k,2}) - \\
& - \frac{K_{\alpha\beta,\sigma}}{2K_{k,1}} \left(1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}} \right) (r_\alpha - r_\beta)^2 \mathfrak{D}_t^\sigma [(\varphi_{k,1} - \varphi_{k,2})] = \frac{\mathfrak{M}_{0,k,1}}{K_{k,1}} \cos \Omega_{k,1} t \\
& \frac{2\mathbf{J}_{k,2}}{K_{k,2}} \ddot{\varphi}_{k,2} - [(\varphi_{k+1,2} - \varphi_{k,2}) - (\varphi_{k,2} - \varphi_{k-1,2})] - \frac{K_{k,2,\sigma}}{K_{k,2}} \mathfrak{D}_t^\sigma [(\varphi_{k+1,2} - \varphi_{k,2}) - (\varphi_{k,2} - \varphi_{k-1,2})] + \\
& + \frac{2K_{\alpha\beta} r_\alpha (r_\alpha - r_\beta)}{K_{k,2}} \varphi_{k,2} + \frac{K_{\alpha\beta}}{2K_{k,2}} \left(1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}} \right) (r_\alpha - r_\beta)^2 (\varphi_{k,1} - \varphi_{k,2}) + \\
& + \frac{K_{\alpha\beta,\sigma}}{2K_{k,2}} \left(1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}} \right) (r_\alpha - r_\beta)^2 \mathfrak{D}_t^\sigma [(\varphi_{k,1} - \varphi_{k,2})] = \frac{\mathfrak{M}_{0,k,2}}{K_{k,2}} \cos \Omega_{k,2} t
\end{aligned} \tag{64}$$

As our intention is to use previous double DNA fractional order chain model for the case of the homogeneous system parameters, we take into account that: $K_{k,1,\sigma} = K_{k,2,\sigma} = K$. and $K_{\alpha\beta,\sigma} = K_{\alpha\beta,\sigma}$ and taking into account that, we introduce notation (7) and (8) then the previous system of coupled fractional order differential equations is possible write in the following form:

$$\begin{aligned}
& \frac{2\mathbf{J}}{K} \ddot{\varphi}_{k,1} - [(\varphi_{k+1,1} - \varphi_{k,1}) - (\varphi_{k,1} - \varphi_{k-1,1})] - \kappa_\sigma \mathfrak{D}_t^\sigma [(\varphi_{k+1,1} - \varphi_{k,1}) - (\varphi_{k,1} - \varphi_{k-1,1})] + \\
& + 2\mu \varphi_{k,1} - \kappa (\varphi_{k,1} - \varphi_{k,2}) - \kappa \kappa_\sigma \mathfrak{D}_t^\sigma [(\varphi_{k,1} - \varphi_{k,2})] = \frac{\mathfrak{M}_{0,k,1}}{K} \cos \Omega_{k,1} t \\
& \frac{2\mathbf{J}}{K} \ddot{\varphi}_{k,2} - [(\varphi_{k+1,2} - \varphi_{k,2}) - (\varphi_{k,2} - \varphi_{k-1,2})] - \kappa_\sigma \mathfrak{D}_t^\sigma [(\varphi_{k+1,2} - \varphi_{k,2}) - (\varphi_{k,2} - \varphi_{k-1,2})] + \\
& + 2\mu \varphi_{k,2} + \kappa (\varphi_{k,1} - \varphi_{k,2}) + \kappa \kappa_\sigma \mathfrak{D}_t^\sigma [(\varphi_{k,1} - \varphi_{k,2})] = \frac{\mathfrak{M}_{0,k,2}}{K} \cos \Omega_{k,2} t
\end{aligned} \tag{65}$$

where $\kappa_\sigma = \frac{K_{\alpha\beta,\sigma}}{K}$.

By using change of the generalized coordinates $\varphi_{k,1}$ and $\varphi_{k,2}$ for k -th bases of both chains in the DNA model into following new ξ_k and η_k by the following dependence: $\xi_k = \varphi_{k,1} - \varphi_{k,2}$ and $\eta_k = \varphi_{k,1} + \varphi_{k,2}$, previous system of differential equations (65) obtains the following form:

$$\begin{aligned} \frac{2J}{K} \ddot{\xi}_k - \xi_{k-1} + 2\xi_k - \xi_{k+1} + \kappa_\sigma \mathfrak{D}_t^\sigma [-\xi_{k-1} + 2\xi_k - \xi_{k+1}] + 2\mu\xi_k - 2\kappa\xi_k - 2\kappa\kappa_\sigma \mathfrak{D}_t^\sigma [\xi_k] = \\ = \frac{\mathfrak{M}_{0,k,1}}{K} \cos \Omega_{k,1} t - \frac{\mathfrak{M}_{0,k,2}}{K} \cos \Omega_{k,2} t \end{aligned} \quad (66)$$

$$\begin{aligned} \frac{2J}{K} \ddot{\eta}_k - \eta_{k-1} + 2\eta_k - \eta_{k+1} + \kappa_\sigma \mathfrak{D}_t^\sigma [-\eta_{k-1} + 2\eta_k - \eta_{k+1}] + 2\mu\eta_k =, \quad k=1,2,3,\dots,n \quad (67) \\ = \frac{\mathfrak{M}_{0,k,1}}{K} \cos \Omega_{k,1} t + \frac{\mathfrak{M}_{0,k,2}}{K} \cos \Omega_{k,2} t \end{aligned}$$

First series (66) and second series (67) of the previous system (64)-(65) of the fractional order differential equations are decoupled and independent. *Then, we can conclude that new coordinates ξ_k and η_k are main coordinates of fractional order double DNA helix chain model system for forced vibration regimes and that we obtain two fictive decoupled eigen single fractional order chains of the double DNA fractional order model. This is also one of the fundamental conclusion as an important property of the fractional order homogeneous model of forced vibrations in a fractional order double DNA homogeneous helix.*

Systems of fractional order differential equations (66)-(67) contains two separate subsystems of fractional order differential equations expressed by *coordinates of ξ_k and η_k which are main coordinates of a fractional order double DNA chain helix forced vibration model and separate DNA fractional order model into two independent fractional order chains.*

8.3. Analytical solutions of the subsystems of the main chains fractional order differential equations for forced regime oscillations

We solve previous subsystems (66) and (67) through the use of Laplace transformations. After conducting Laplace transformations of the previous systems (66) and (67) of differential equations with fractional order derivative and having in account that we introduced notations $\mathfrak{L}\{\xi_k(t)\}$ and $\mathfrak{L}\{\eta_k(t)\}$ for Laplace transformations, as well as having in mind, that we accepted the hypothesis that the initial conditions of fractional order derivatives of the system are given through the use of: $\left. \frac{d^{\sigma-1}\xi_k(t)}{dt^{\sigma-1}} \right|_{t=0} = 0$ and $\left. \frac{d^{\sigma-1}\eta_k(t)}{dt^{\sigma-1}} \right|_{t=0} = 0$, as well that

is

$$\mathfrak{L}\left\{ \frac{\mathfrak{M}_{0,k,1}}{K} \cos \Omega_{k,1} t \mp \frac{\mathfrak{M}_{0,k,2}}{K} \cos \Omega_{k,2} t \right\} = \frac{\mathfrak{M}_{0,k,1}}{K} \frac{p}{p^2 + \Omega_{k,1}^2} \mp \frac{\mathfrak{M}_{0,k,2}}{K} \frac{p}{p^2 + \Omega_{k,2}^2} \quad (68)$$

where ξ_{0k} and $\dot{\xi}_{0k}$ as well as η_{0k} and $\dot{\eta}_{0k}$ are initial angular positions and angular velocities defined by initial conditions of system material particles dynamics in the chains at initial moment, we can write the following system of the equations with unknown Laplace transforms:

$$\begin{aligned} \mathfrak{L}\left\{ \frac{2J}{K} \ddot{\xi}_k \right\} - \mathfrak{L}\{\xi_{k-1}\} + 2\mathfrak{L}\{\xi_k\} - \mathfrak{L}\{\xi_{k+1}\} + \kappa_\sigma \mathfrak{L}\left\{ \mathfrak{D}_t^\sigma [-\xi_{k-1} + 2\xi_k - \xi_{k+1}] \right\} + 2\mu\mathfrak{L}\{\xi_k\} - 2\kappa\mathfrak{L}\{\xi_k\} - 2\kappa\kappa_\sigma \mathfrak{L}\left\{ \mathfrak{D}_t^\sigma [\xi_k] \right\} = \\ = +h_{0,k,1} \frac{p}{p^2 + \Omega_{k,1}^2} - h_{0,k,2} \frac{p}{p^2 + \Omega_{k,2}^2} \end{aligned} \quad (69)$$

$$\begin{aligned} & \frac{2\mathbf{J}}{K} \mathfrak{L}\{\ddot{\eta}_k\} - \mathfrak{L}\{\eta_{k-1}\} + 2\mathfrak{L}\{\eta_k\} - \mathfrak{L}\{\eta_{k+1}\} + \kappa_\sigma \mathfrak{L}\{\mathfrak{L}_t^\sigma[-\eta_{k-1} + 2\eta_k - \eta_{k+1}]\} + 2\mu \mathfrak{L}\{\eta_k\} = \\ & = +h_{0,k,1} \frac{p}{p^2 + \Omega_{k,1}^2} + h_{0,k,2} \frac{p}{p^2 + \Omega_{k,2}^2} \\ & k = 1, 2, 3, \dots, n \end{aligned} \quad (79)$$

Previous system is possible to rewrite in the following form:

$$\left[\frac{2\mathbf{J}}{K} p^2 + 2\mu - 2\kappa(1 + \kappa_\sigma p^\sigma) \right] \frac{\mathfrak{L}\{\xi_k(t)\} - \mathfrak{L}\{\xi_{k-1}\} + 2\mathfrak{L}\{\xi_k(t)\} - \mathfrak{L}\{\xi_{k+1}\}}{(1 + \kappa_\sigma p^\sigma)} = \frac{2\mathbf{J}}{K} \frac{[p\xi_{0k} + \dot{\xi}_{0k}]}{(1 + \kappa_\sigma p^\sigma)} + \quad (80)$$

$$\begin{aligned} & + h_{0,k,1} \frac{p}{(p^2 + \Omega_{k,1}^2)(1 + \kappa_\sigma p^\sigma)} - h_{0,k,2} \frac{p}{(p^2 + \Omega_{k,2}^2)(1 + \kappa_\sigma p^\sigma)} \\ & \left(\frac{p^2 \frac{2\mathbf{J}}{K} + 2\mu}{(1 + \kappa_\sigma p^\sigma)} \right) \mathfrak{L}\{\eta_k\} - \mathfrak{L}\{\eta_{k-1}\} + 2\mathfrak{L}\{\eta_k\} - \mathfrak{L}\{\eta_{k+1}\} = \frac{2\mathbf{J}}{K} \frac{[p\eta_{0k} + \dot{\eta}_{0k}]}{(1 + \kappa_\sigma p^\sigma)} + \\ & + h_{0,k,1} \frac{p}{(p^2 + \Omega_{k,1}^2)(1 + \kappa_\sigma p^\sigma)} + h_{0,k,2} \frac{p}{(p^2 + \Omega_{k,2}^2)(1 + \kappa_\sigma p^\sigma)} \end{aligned} \quad (81)$$

Now, we have two separate, uncoupled non homogeneous subsystems of the algebraic equations in the following forms:

$$\begin{aligned} -\mathfrak{L}\{\xi_{k-1}\} + (2 + \nu) \mathfrak{L}\{\xi_k(t)\} - \mathfrak{L}\{\xi_{k+1}\} &= \frac{[p\xi_{0k} + \dot{\xi}_{0k}]}{\omega_0^2 [1 + \kappa_\sigma p^\sigma]} + h_{0,k,1} \frac{p}{(p^2 + \Omega_{k,1}^2)(1 + \kappa_\sigma p^\sigma)} - \\ &- h_{0,k,2} \frac{p}{(p^2 + \Omega_{k,2}^2)(1 + \kappa_\sigma p^\sigma)} \end{aligned} \quad (82)$$

$$\begin{aligned} -\mathfrak{L}\{\eta_{k-1}\} + (2 + u) \mathfrak{L}\{\eta_k\} - \mathfrak{L}\{\eta_{k+1}\} &= \frac{[p\eta_{0k} + \dot{\eta}_{0k}]}{\omega_0^2 (1 + \kappa_\sigma p^\sigma)} + h_{0,k,1} \frac{p}{(p^2 + \Omega_{k,1}^2)(1 + \kappa_\sigma p^\sigma)} + \\ &+ h_{0,k,2} \frac{p}{(p^2 + \Omega_{k,2}^2)(1 + \kappa_\sigma p^\sigma)} \end{aligned} \quad (83)$$

or in the following forms:

$$-\mathfrak{L}\{\xi_{k-1}\} + (2 + \nu) \mathfrak{L}\{\xi_k(t)\} - \mathfrak{L}\{\xi_{k+1}\} = h_{\xi hk}(p, \xi_{0k}, \dot{\xi}_{0k}) + h_{\xi pk}(p, \Omega_{k,1}^2, \Omega_{k,2}^2, h_{0k,1}, h_{0k,2}) \quad (84)$$

$$-\mathfrak{L}\{\eta_{k-1}\} + (2 + u) \mathfrak{L}\{\eta_k\} - \mathfrak{L}\{\eta_{k+1}\} = h_{\eta hk}(p, \eta_{0k}, \dot{\eta}_{0k}) + h_{\eta pk}(p, \Omega_{k,1}^2, \Omega_{k,2}^2, h_{0k,1}, h_{0k,2}) \quad (85)$$

where

$$\nu = \frac{[p^2 + 2\mu\omega_0^2]}{\omega_0^2 [1 + \kappa_\sigma p^\sigma]} - 2\kappa, \quad u = \frac{[p^2 + 2\mu\omega_0^2]}{\omega_0^2 [1 + \kappa_\sigma p^\sigma]}, \quad \omega_0^2 = \frac{K}{2\mathbf{J}} \quad (86)$$

$$h_{\xi hk}(p, \xi_{0k}, \dot{\xi}_{0k}) = \frac{[p\xi_{0k} + \dot{\xi}_{0k}]}{\omega_0^2 [1 + \kappa_\sigma p^\sigma]}, \quad h_{\eta hk}(p, \eta_{0k}, \dot{\eta}_{0k}) = \frac{[p\eta_{0k} + \dot{\eta}_{0k}]}{\omega_0^2 (1 + \kappa_\sigma p^\sigma)} \quad (87)$$

$$h_{\xi pk}(p, \Omega_{k,1}^2, \Omega_{k,2}^2, h_{0k,1}, h_{0k,2}) = h_{0,k,1} \frac{p}{(p^2 + \Omega_{k,1}^2)(1 + \kappa_\sigma p^\sigma)} - h_{0,k,2} \frac{p}{(p^2 + \Omega_{k,2}^2)(1 + \kappa_\sigma p^\sigma)} \quad (88)$$

$$h_{\eta pk}(p, \Omega_{k,1}^2, \Omega_{k,2}^2, h_{0k,1}, h_{0k,2}) = h_{0,k,1} \frac{p}{(p^2 + \Omega_{k,1}^2)(1 + \kappa_\sigma p^\sigma)} + h_{0,k,2} \frac{p}{(p^2 + \Omega_{k,2}^2)(1 + \kappa_\sigma p^\sigma)} \quad (89)$$

Both subsystems are same form and it is necessary to solve one of the subsystems and by use analogy is easy to solve other of the subsystem equations. For that reason we can use method proposed in the papers [14] and [20]. Determinate of the previous subsystem (84) as well as (85) are in following form (21) as well as (22) by similar way as for the subsystems of algebra equations in paragraph 5..

Determinates of the previous algebra subsystem (84) as well as (85) are in the same form as it is presented in (21)-(22).

Next consideration we focus to the case:

$$-\mathfrak{L}\{\xi_{k-1}\} + (2+\nu)\mathfrak{L}\{\xi_k(t)\} - \mathfrak{L}\{\xi_{k+1}\} = \begin{cases} h_{\xi h1}(p, \xi_{01}, \dot{\xi}_{01}) + h_{\xi p1}(p, \Omega_{1,1}^2, \Omega_{1,2}^2, h_{0,1,1}, h_{0,1,2}) & k=1 \\ 0 & k \neq 1 \end{cases} \quad (90)$$

$$-\mathfrak{L}\{\eta_{k-1}\} + (2+u)\mathfrak{L}\{\eta_k\} - \mathfrak{L}\{\eta_{k+1}\} = \begin{cases} h_{\eta h1}(p, \eta_{01}, \dot{\eta}_{01}) + h_{\eta p1}(p, \Omega_{1,1}^2, \Omega_{1,2}^2, h_{0,1,1}, h_{0,1,2}) & k=1 \\ 0 & k \neq 1 \end{cases} \quad (91)$$

By introduce the notation $h_{\xi h1}(p, \xi_{01}, \dot{\xi}_{01}) + h_{\xi}(p, \Omega_{1,1}^2, \Omega_{1,2}^2, h_{0,1,1}, h_{0,1,2})$ and $h_{\eta h1}(p, \eta_{01}, \dot{\eta}_{01}) + h_{\eta p1}(p, \Omega_{1,1}^2, \Omega_{1,2}^2, h_{0,1,1}, h_{0,1,2})$ defined by (86)-(87), for the determinants $\tilde{\Delta}_{(k)}(v, h_{\xi})$, we can write similar expressions as defined by (21)-(22) changing expressions $h_{\xi}(p, \xi_{01}, \dot{\xi}_{01})$ by expressions $h_{\xi h1}(p, \xi_{01}, \dot{\xi}_{01}) + h_{\xi}(p, \Omega_{1,1}^2, \Omega_{1,2}^2, h_{0,1,1}, h_{0,1,2})$ as well as by $h_{\eta h1}(p, \eta_{01}, \dot{\eta}_{01}) + h_{\eta p1}(p, \Omega_{1,1}^2, \Omega_{1,2}^2, h_{0,1,1}, h_{0,1,2})$.

For solving the system of the algebraic no homogeneous equations (90) or (91) with respect to unknown Laplace transforms $\mathfrak{L}\{\xi_k(t)\}$ or $\mathfrak{L}\{\eta_k(t)\}$ of the time function main coordinate $\xi_k(t)$ and $\eta_k(t)$ - unknown normal chain coordinates of the system main chains for forced vibrations, we can use Cramer approach by similar way as in the paragraph 5.

8.4. Forced eigen modes of the subsystems of the main chains of a fractional order double DNA helix chain system forced vibrations

In this part we start by two subsystems of fractional order differential equations (66) and (67) expressed by eigen normal chains coordinates $\xi_k = \varphi_{k,1} - \varphi_{k,2}$ and $\eta_k = \varphi_{k,1} + \varphi_{k,2}$, and we can rewrite these subsystems in the following form:

$$\begin{aligned} \frac{2J}{K} \ddot{\xi}_k - \xi_{k+1} + 2\xi_k[1 + \mu - \kappa] - \xi_{k-1} + \kappa_{\sigma} \mathfrak{L}_t^{\sigma} [-\xi_{k-1} + 2(1 - \kappa)\xi_k - \xi_{k+1}] &=, \quad k=1,2,3,\dots,n \\ &= h_{0,k,1} \cos \Omega_{k,1} t - h_{0,k,2} \cos \Omega_{k,2} t \end{aligned} \quad (92)$$

$$\begin{aligned} \frac{2J}{K} \ddot{\eta}_k - \eta_{k+1} + 2\eta_k(1 + \mu) - \eta_{k-1} + \kappa_{\sigma} \mathfrak{L}_t^{\sigma} [-\eta_{k-1} + 2\eta_k - \eta_{k+1}] &=, \quad k=1,2,3,\dots,n \\ &= h_{0,k,1} \cos \Omega_{k,1} t + h_{0,k,2} \cos \Omega_{k,2} t \end{aligned} \quad (93)$$

Without losing generality, we focused our next interest to consider two subsystems of the fractional order differential equations in the following form:

$$\frac{2J}{K} \ddot{\xi}_k - \xi_{k+1} + 2\xi_k[1 + \mu - \kappa] - \xi_{k-1} + \kappa_{\sigma} \mathfrak{L}_t^{\sigma} [-\xi_{k-1} + 2(1 - \kappa)\xi_k - \xi_{k+1}] = \begin{cases} h_{0,1,1} \cos \Omega_{1,1} t & k=1 \\ 0 & k \neq 1 \end{cases} \quad (94)$$

$$\frac{2J}{K} \ddot{\eta}_k - \eta_{k+1} + 2\eta_k(1 + \mu) - \eta_{k-1} + \kappa_{\sigma} \mathfrak{L}_t^{\sigma} [-\eta_{k-1} + 2\eta_k - \eta_{k+1}] = \begin{cases} h_{0,1,1} \cos \Omega_{1,1} t & k=1 \\ 0 & k \neq 1 \end{cases} \quad (95)$$

Previous two subsystems are for the case of fractional order forced vibrations of a double DNA helix chain system excited by one single frequency external couple $\mathfrak{M}_{0,1,1} \cos \Omega_{1,1} t$, with amplitude $\mathfrak{M}_{0,1,1}$ and frequency $\Omega_{1,1}$, applied to the first mass particle in the first chain of a double DNA helix chain system.

First series (94) and second series (95) of the previous system (94)-(95) of the fractional order differential equations for forced vibrations are decoupled and independent. Then, we can conclude that new coordinates ξ_k and η_k are main coordinates of fractional order double DNA helix chain model system for forced vibration regimes and that we obtain

two fictive decoupled eigen single fractional order chains of the double DNA fractional order model. This is also one of the fundamental conclusion as an important property of the fractional order homogeneous model of forced vibrations in a fractional order double DNA homogeneous helix.

Systems of the fractional order differential equations (94)-(95) contains two separate subsystems of fractional order differential equations expressed by *coordinates of ξ_k and η_k* which are main *coordinates of a fractional order double DNA chain helix forced vibration model and separate DNA fractional order chain model into two independent fractional order main chains.*

For first main chain of the double DNA chain helix (94), the eigen amplitudes for free vibrations are in the form $A_k^{(s)} = C_s \sin k\varphi_s$ and generalized coordinates $\xi_k(t)$ of the first main chain for forced vibrations is possible to express by set of this eigen main chain main coordinates $\zeta_{s\xi}$ for free vibrations in the following form:

$$\xi_k(t) = \sum_{s=1}^n \zeta_{s\xi} \sin k\varphi_s \quad (96)$$

$$k = 1, 2, 3, \dots, n$$

as well as for other main chain of the double DNA chain helix (95) generalized coordinates $\eta_k(t)$ of the second main chain for forced vibrations is possible to express by set of this eigen main chain main coordinates $\zeta_{s\eta}$ for free vibrations in the following form:

$$\eta_k(t) = \sum_{s=1}^n \zeta_{s\eta} \sin k\varphi_s \quad (97)$$

Normal coordinates $\zeta_{s\xi}$ or normal modes of the first main chain for forced vibrations is possible to express in the similar form as for free vibrations, but introducing suppositions that unknown amplitudes C_s and phase α_s depend of initial conditions are not constant, but functions of time, $C_s(t)$ and phase $\alpha_s(t)$, and for fractional order system main coordinate are in the form

$$\zeta_{s\xi}(t) = C_s(t) \cos(\Omega_\xi t + \alpha_s(t)), s = 1, 2, 3, \dots, n \quad (98)$$

with known frequencies (see Refs. [25] by Hedrih and Hedrih, [29] by Rašković P. Danilo) and unknown time functions - amplitudes $C_s(t)$ and phase $\alpha_s(t)$ depending of time and initial conditions.

Then, we introduce expressions (96) and (97) and their corresponding second and fractional order derivative into subsystem of the fractional order differential equations (94) and (95), we obtain the following systems:

$$\begin{aligned} & \frac{2J}{K} \sum_{s=1}^n \ddot{\zeta}_{s\xi} \sin k\varphi_s - \sum_{s=1}^n \zeta_{s\xi} \sin(k-1)\varphi_s + 2[1 + \mu - \kappa] \sum_{s=1}^n \zeta_{s\xi} \sin k\varphi_s - \sum_{s=1}^n \zeta_{s\xi} \sin(k+1)\varphi_s + \\ & + \kappa_\sigma \mathfrak{I}_t^\sigma \left[- \sum_{s=1}^n \zeta_{s\xi} \sin(k-1)\varphi_s + 2(1 - \kappa) \sum_{s=1}^n \zeta_{s\xi} \sin k\varphi_s - \sum_{s=1}^n \zeta_{s\xi} \sin(k+1)\varphi_s \right] = \begin{cases} h_{0,1,1} \cos \Omega_{1,1} t & k = 1 \\ 0 & k \neq 1 \end{cases} \\ & k = 1, 2, 3, \dots, n \end{aligned} \quad (99)$$

$$\begin{aligned} & \frac{2J}{K} \sum_{s=1}^n \ddot{\zeta}_{s\eta} \sin k\varphi_s - \sum_{s=1}^n \zeta_{s\eta} \sin(k-1)\varphi_s + 2[1 + \mu] \sum_{s=1}^n \zeta_{s\eta} \sin k\varphi_s - \sum_{s=1}^n \zeta_{s\eta} \sin(k+1)\varphi_s + \\ & + \kappa_\sigma \mathfrak{I}_t^\sigma \left[- \sum_{s=1}^n \zeta_{s\eta} \sin(k-1)\varphi_s + 2 \sum_{s=1}^n \zeta_{s\eta} \sin k\varphi_s - \sum_{s=1}^n \zeta_{s\eta} \sin(k+1)\varphi_s \right] = \\ & = \begin{cases} h_{0,1,1} \cos \Omega_{1,1} t & k = 1 \\ 0 & k \neq 1 \end{cases} \end{aligned} \quad (100)$$

$$k = 1, 2, 3, \dots, n$$

After made a group sublimations of the some terms in previous equations (99), we obtain the following subsystem:

$$\sum_{s=1}^n \frac{2\mathbf{J}}{K} \left(\ddot{\zeta}_{s\xi} + 2 \frac{K}{2\mathbf{J}} \langle [1 + \mu - \kappa] - \cos \varphi_s \rangle + \frac{K}{2\mathbf{J}} 2\kappa_\sigma \langle (1 - \kappa) - \cos \varphi_s \rangle \mathfrak{D}_t^\sigma [\zeta_{s\xi}] \right) \sin k\varphi_s =$$

$$= \begin{cases} h_{0,1,1} \cos \Omega_{1,1} t & k = 1 \\ 0 & k \neq 1 \end{cases} \quad (101)$$

$$k = 1, 2, 3, \dots, n$$

Then taking into account denotations (102)

$$\kappa_{s\sigma\xi} = \frac{K}{2\mathbf{J}} \left(2 \sin^2 \frac{\varphi_s}{2} + \mu - \kappa \right), \quad s = 1, 2, 3, \dots, n$$

$$\omega_{s\xi}^2 = \frac{K}{2\mathbf{J}} \left(2 \sin^2 \frac{\varphi_s}{2} + \mu - \kappa \right), \quad s = 1, 2, 3, \dots, n \quad (103)$$

$$\omega_{s\sigma\xi}^2 = \kappa_{s\sigma\xi} \frac{K}{2\mathbf{J}} = \kappa_\sigma \frac{K}{\mathbf{J}} \left(2 \sin^2 \frac{\varphi_s}{2} - \kappa \right), \quad s = 1, 2, 3, \dots, n \quad (104)$$

previous subsystem of fractional order differential equation (101) is possible to rewrite in the following form:

$$\sum_{s=1}^n \frac{2\mathbf{J}}{K} \left(\ddot{\zeta}_{s\xi} + \omega_{s\xi}^2 \zeta_{s\xi} + \frac{K}{2\mathbf{J}} \kappa_{s\sigma\xi} \mathfrak{D}_t^\sigma [\zeta_{s\xi}] \right) \sin k\varphi_s = \begin{cases} h_{0,1,1} \cos \Omega_{1,1} t & k = 1 \\ 0 & k \neq 1 \end{cases},$$

$$k = 1, 2, 3, \dots, n \quad (105)$$

Taking into account that it is possible to develop (to express) right hand side into series according to $\sin k\varphi_s$ in the following series:

$$\begin{cases} h_{0,1,1} \cos \Omega_{1,1} t & k = 1 \\ 0 & k \neq 1 \end{cases} = \begin{cases} \sum_{s=1}^n \frac{2\mathbf{J}}{K} h_{0,1,1(s)} \sin k\varphi_s \cos \Omega_{1,1} t & k = 1 \\ 0 & k \neq 1 \end{cases} \quad (106)$$

where

$$h_{0,1,1(s)} = \frac{K}{2\mathbf{J}} \frac{\sum_{s=1}^n h_{0,1,1} \sin k\varphi_s}{\left\langle \sum_{s=1}^n \sum_{r=1}^n \sin k\varphi_s \sin k\varphi_r \right\rangle} \quad k = 1$$

$$h_{0,1,1(s)} = 0 \quad k \neq 1$$

$$(107)$$

equations (101) is possible to rewrite in the following form:

$$\sum_{s=1}^n \frac{2\mathbf{J}}{K} \left(\ddot{\zeta}_{s\xi} + \omega_{s\xi}^2 \zeta_{s\xi} + \omega_{s\sigma\xi}^2 \mathfrak{D}_t^\sigma [\zeta_{s\xi}] - h_{0,1,1(s)} \cos \Omega_{1,1} t \right) \sin k\varphi_s = 0, \quad k = 1, 2, 3, \dots, n \quad (108)$$

Then, taking into account that $\sin k\varphi_s \neq 0$ in general case, from (108) is possible to obtain the following subsystem of fractional order differential equations:

$$\ddot{\zeta}_{s\xi} + \omega_{s\xi}^2 \zeta_{s\xi} + \omega_{s\sigma\xi}^2 \mathfrak{D}_t^\sigma [\zeta_{s\xi}] = h_{0,1,1(s)} \cos \Omega_{1,1} t, \quad s = 1, 2, 3, \dots, n \quad (109)$$

where $\omega_{s\xi}^2$ are square of eigen circular frequencies determined by expression (103) and $\omega_{s\sigma\xi}^2$ corresponding eigen characteristic numbers expressing fractional order subsystem properties, determined by expression (104).

In analogous way, taking into account denotation

$$\kappa_{s\sigma\eta} = 2\kappa_\sigma \left(\frac{2\mathbf{J}}{K} \omega_{s\eta}^2 - \mu \right), \quad s = 1, 2, 3, \dots, n \quad (110)$$

$$\omega_{s\eta}^2 = \frac{K}{2\mathbf{J}} \left(2 \sin^2 \frac{\varphi_s}{2} + \mu \right), \quad s = 1, 2, 3, \dots, n \quad (111)$$

$$\omega_{s\sigma\eta}^2 = 4\kappa_\sigma \frac{K}{2J} \sin^2 \frac{\varphi_s}{2}, \quad s = 1, 2, 3, \dots, n \quad (112)$$

and by use (100), is possible to obtain the second subsystem of fractional order differential equations in the following form:

$$\ddot{\zeta}_{s\eta} + \omega_{s\xi}^2 \zeta_{s\eta} + \omega_{s\sigma\eta}^2 \mathfrak{D}_t^\sigma [\zeta_{s\eta}] = h_{0,1,1(s)} \cos \Omega_{1,1} t, \quad s = 1, 2, 3, \dots, n \quad (113)$$

where $\omega_{s\eta}^2$ square of eigen circular frequencies determined by expression (111) and $\omega_{s\sigma\eta}^2$ corresponding eigen characteristic numbers expressing fractional order subsystem properties, determined by expression (112).

Then we have system of fractional order differential equations (109)-(1113) describing system of $2n$ fractional order oscillators, containing two subsets of the main fractional order forced oscillators, each described by n fractional order differential equations. Each of these $2n$ fractional order differential equations, contain only one main eigen coordinate $\zeta_{s\xi}$ or $\zeta_{s\eta}$ of the system.

The system (109)-(1113) represent the main fractional order forced oscillators along independent system main coordinates $\zeta_{s\xi}$ or $\zeta_{s\eta}$, $s = 1, 2, 3, \dots, n$ each with one circular frequency of external excitation and one eigen circular frequency and one eigen characteristic number from one of the two sets of: $\omega_{s\xi}$ or $\omega_{s\eta}$ eigen circular frequencies determined by expression (103) or (111) and $\omega_{s\sigma\xi}^2$ or $\omega_{s\sigma\eta}^2$ corresponding eigen characteristic numbers expressing fractional order subsystem properties, determined by expression (104) or (112).

All of fractional order differential equations of the system (109)-(1113) are same type and is possible to solve by same way by use Laplace transform $\mathfrak{L}\{\zeta_{s\xi}(t)\}$ and $\mathfrak{L}\{\zeta_{s\eta}(t)\}$. Applying Laplace transform to the system (109)-(1113) of the fractional order differential equations, we obtain the following system of the equations:

$$\mathfrak{L}\{\ddot{\zeta}_{s\xi}\} + \omega_{s\xi}^2 \mathfrak{L}\{\zeta_{s\xi}(t)\} + \omega_{s\sigma\xi}^2 \mathfrak{L}\{\mathfrak{D}_t^\sigma [\zeta_{s\xi}]\} = h_{0,1,1(s)} \mathfrak{L}\{\cos \Omega_{1,1} t\}, \quad s = 1, 2, 3, \dots, n \quad (114)$$

$$\mathfrak{L}\{\ddot{\zeta}_{s\eta}\} + \omega_{s\xi}^2 \mathfrak{L}\{\zeta_{s\eta}(t)\} + \omega_{s\sigma\eta}^2 \mathfrak{L}\{\mathfrak{D}_t^\sigma [\zeta_{s\eta}]\} = h_{0,1,1(s)} \mathfrak{L}\{\cos \Omega_{1,1} t\}, \quad s = 1, 2, 3, \dots, n \quad (115)$$

Taking into account that

$$\mathfrak{L}\left\{\frac{d^2 \zeta_{s\xi}(t)}{dt^2}\right\} = p^2 \mathfrak{L}\{\zeta_{s\xi}(t)\} - [p \zeta_{0s\xi} + \dot{\zeta}_{0s\xi}], \quad s = 1, 2, 3, \dots, n \quad (116)$$

$$\mathfrak{L}\left\{\frac{d^2 \zeta_{s\eta}(t)}{dt^2}\right\} = p^2 \mathfrak{L}\{\zeta_{s\eta}(t)\} - [p \zeta_{0s\eta} + \dot{\zeta}_{0s\eta}], \quad s = 1, 2, 3, \dots, n \quad (117)$$

$$\mathfrak{L}\{\cos \Omega_{1,1} t\} = \frac{p}{p^2 + \Omega_{1,1}^2} \quad (118)$$

$$\mathfrak{L}\left\{\frac{d^\sigma \zeta_{s\xi}}{dt^\sigma}\right\} = p^\sigma \mathfrak{L}\{\zeta_{s\xi}\} - \frac{d^{\sigma-1} \zeta_{s\xi}}{dt^{\sigma-1}} \Big|_{t=0} = p^\sigma \mathfrak{L}\{\zeta_{s\xi}\}, \quad s = 1, 2, 3, \dots, n \quad (119)$$

$$\mathfrak{L}\left\{\frac{d^\sigma \zeta_{s\eta}}{dt^\sigma}\right\} = p^\sigma \mathfrak{L}\{\zeta_{s\eta}\} - \frac{d^{\sigma-1} \zeta_{s\eta}}{dt^{\sigma-1}} \Big|_{t=0} = p^\sigma \mathfrak{L}\{\zeta_{s\eta}\}, \quad s = 1, 2, 3, \dots, n \quad (120)$$

and after introducing into system (118)-(119) for Laplace transform $\mathfrak{L}\{\zeta_{s\xi}(t)\}$ and $\mathfrak{L}\{\zeta_{s\eta}(t)\}$ of system double DNA helix chain eigen main coordinates $\zeta_{s\xi}$ and $\zeta_{s\eta}$ we obtain:

$$\mathfrak{L}\{\zeta_{s\xi}\} = \frac{[p \zeta_{0s\xi} + \dot{\zeta}_{0s\xi}]}{(p^2 + \omega_{s\xi}^2 + \omega_{s\sigma\xi}^2 p^\sigma)} + \frac{h_{0,1,1(s)}}{(p^2 + \omega_{s\xi}^2 + \omega_{s\sigma\xi}^2 p^\sigma)} \frac{p}{p^2 + \Omega_{1,1}^2}, \quad s = 1, 2, 3, \dots, n \quad (121)$$

$$\mathfrak{L}\{\zeta_{s\eta}\} = \frac{[p \zeta_{0s\eta} + \dot{\zeta}_{0s\eta}]}{(p^2 + \omega_{s\eta}^2 + \omega_{s\sigma\eta}^2 p^\sigma)} + \frac{h_{0,1,1(s)}}{(p^2 + \omega_{s\eta}^2 + \omega_{s\sigma\eta}^2 p^\sigma)} \frac{p}{p^2 + \Omega_{1,1}^2}, \quad s = 1, 2, 3, \dots, n \quad (122)$$

Then, for obtaining system double DNA helix chain eigen main coordinates $\zeta_{s\xi}(t)$ and $\zeta_{s\eta}(t)$ is necessary to applied inverse of Laplace transform to the expressions (121)-(122).

Then, we can write the following:

$$\zeta_{s\xi}(t) = \zeta_{s\xi, \text{hom}}(t) + \zeta_{s\xi, \text{part}}(t) \quad (123)$$

and

$$\zeta_{s\eta}(t) = \zeta_{s\eta, \text{hom}}(t) + \zeta_{s\eta, \text{part}}(t) \quad (124)$$

where

$\zeta_{s\xi, \text{hom}}(t)$ and $\zeta_{s\eta, \text{hom}}(t)$ are terms correspond to solutions of the homogeneous fractional order differential equations and solutions are in the following forms (see Appendix (A.1)-(A.3) and (B.1)-(B.16)):

$$\begin{aligned} \zeta_{s\xi, \text{hom}}(t) = & \zeta_{s\xi}(0) \sum_{k=0}^{\infty} (-1)^k \omega_{s\xi}^{2k} t^{2k} \sum_{j=0}^k \binom{k}{j} \frac{(\mp 1)^j \omega_{s\xi}^{2j} t^{-\alpha j}}{\omega_{s\xi}^{2j} \Gamma(2k+1-\alpha j)} + \\ & + \dot{\zeta}_{s\xi}(0) \sum_{k=0}^{\infty} (-1)^k \omega_{s\xi}^{2k} t^{2k+1} \sum_{j=0}^k \binom{k}{j} \frac{(\mp 1)^j \omega_{s\xi}^{-2j} t^{-\alpha j}}{\omega_{s\xi}^{2j} \Gamma(2k+2-\alpha j)} \end{aligned} \quad (125)$$

$$\begin{aligned} \zeta_{s\eta, \text{hom}}(t) = & \zeta_{s\eta}(0) \sum_{k=0}^{\infty} (-1)^k \omega_{s\eta}^{2k} t^{2k} \sum_{j=0}^k \binom{k}{j} \frac{(\mp 1)^j \omega_{s\eta}^{2j} t^{-\alpha j}}{\omega_{s\eta}^{2j} \Gamma(2k+1-\alpha j)} + \\ & + \dot{\zeta}_{s\eta}(0) \sum_{k=0}^{\infty} (-1)^k \omega_{s\eta}^{2k} t^{2k+1} \sum_{j=0}^k \binom{k}{j} \frac{(\mp 1)^j \omega_{s\eta}^{-2j} t^{-\alpha j}}{\omega_{s\eta}^{2j} \Gamma(2k+2-\alpha j)} \end{aligned} \quad (126)$$

$\zeta_{s\xi, \text{par}}(t)$ and $\zeta_{s\eta, \text{par}}(t)$ are terms correspond to particular solutions of the no homogeneous fractional order differential equations system (121)-(122) and solutions must to obtain as a inverse transform of the following expressions:

$$\zeta_{s\xi, \text{par}}(t) = \mathfrak{F}^{-1} \mathfrak{L} \{ \zeta_{s\xi, \text{par}} \} = \mathfrak{F}^{-1} \left\{ \frac{h_{0,1,1}(s)}{(p^2 + \omega_{s\xi}^2 + \omega_{s\xi}^2 p^\sigma)} \frac{p}{p^2 + \Omega_{1,1}^2} \right\}, s = 1, 2, 3, \dots, n \quad (127)$$

$$\zeta_{s\eta, \text{par}}(t) = \mathfrak{F}^{-1} \mathfrak{L} \{ \zeta_{s\eta, \text{par}} \} = \mathfrak{F}^{-1} \left\{ \frac{h_{0,1,1}(s)}{(p^2 + \omega_{s\eta}^2 + \omega_{s\eta}^2 p^\sigma)} \frac{p}{p^2 + \Omega_{1,1}^2} \right\}, s = 1, 2, 3, \dots, n \quad (128)$$

or in developed form

$$\begin{aligned} \zeta_{s\xi, \text{par}}(t) = & \mathfrak{F}^{-1} \mathfrak{L} \{ \zeta_{s\xi, \text{par}} \} = h_{0,1,1}(s) \mathfrak{F}^{-1} \left\{ \frac{1}{p} \frac{1}{p^2 + \Omega_{1,1}^2} \sum_{k=0}^{\infty} \frac{(-1)^k \omega_{s\xi}^{2k}}{p^{2k}} \sum_{j=0}^k \binom{k}{j} \frac{(\mp 1)^j p^{\alpha j} \omega_{s\xi}^{2(j-k)}}{\omega_{s\xi}^{2j}} \right\} \\ s = & 1, 2, 3, \dots, n \end{aligned} \quad (129)$$

$$\begin{aligned} \zeta_{s\eta, \text{par}}(t) = & \mathfrak{F}^{-1} \mathfrak{L} \{ \zeta_{s\eta, \text{par}} \} = h_{0,1,1}(s) \mathfrak{F}^{-1} \left\{ \frac{1}{p} \frac{1}{p^2 + \Omega_{1,1}^2} \sum_{k=0}^{\infty} \frac{(-1)^k \omega_{s\eta}^{2k}}{p^{2k}} \sum_{j=0}^k \binom{k}{j} \frac{(\mp 1)^j p^{\alpha j} \omega_{s\eta}^{2(j-k)}}{\omega_{s\eta}^{2j}} \right\} \\ s = & 1, 2, 3, \dots, n \end{aligned} \quad (130)$$

9. Concluding remarks

At the end, we can conclude that new coordinates of ξ_k and η_k composed to generalized coordinates by the way $\xi_k = \varphi_{k,1} - \varphi_{k,2}$ and $\eta_k = \varphi_{k,1} + \varphi_{k,2}$. These coordinates are main coordinates of the main eigen chains of a double DNA helix chain system. Also we can conclude that it is possible to obtain two fictive decoupled and separated eigen single chains of the double DNA chain helix liner model as well as fractional order model. This is important

fundamental conclusion as an important property of the linear model of vibrations in a double DNA helix.

Considered as a linear or fractional order mechanical system, DNA molecule as a double helix chain system has its eigen circular frequencies and that is its characteristic. Mathematically it is possible to decouple it into two chains with their 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 each 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 as nonlinear system but under certain condition its behavior can be describe by linear dynamics.

By use superposition's of these solutions for the case that external excitations are with same amplitudes and frequencies from system differential equations, we can see that for this case external one frequency excitations in one eigen main chain appear pure free vibrations with eigen subset of circular frequencies of its free vibrations, and in other appear forced vibrations. This conclusion is possible to generalize for same multi-frequency external excitations applied in which of the pair material particle in both chains. This conclusion is possible to extend to the fractional order double helix DNA chain system forced vibrations.

This solutions may correspond with process of binding the enzyme to the specific part of the DNA molecule. Enzyme has a role of inducer of forced vibrations. In the transcription process only one chain is used as a template for transcription other chain is control. The part of DNA chain witch is template has to make more movements than the other chain.

Dynamical absorption on the first pair of the main coordinates of the main chains appear on the resonate circular frequencies of the set of the double DNA helix chain system with one less pair of the material particles in comparison with the considered real system.

Resonant state that appear only in one main chain may be important for selecting the specific sequence for transcription and we suggest that every sequence of DNA that encodes the specific protein has its own resonate circular frequencies different from the sequences that encode other proteins.

Dynamical absorption on the second pair of the main coordinates of the main chains appear on the resonate circular frequencies of the set of the double DNA helix chain system with two less pairs of the material particles in comparison with considered system.

This mathematical fact is important to consider in the light of the interruption or break of the double DNA helix chain system on the specific places where the transcription process starts and ends.

Acknowledgements

Parts of this research were supported by the Ministry of Sciences and Technology of Republic of Serbia through Mathematical Institute SANU Belgrade Grant ONI74001 Dynamics of hybrid systems with complex structures. Mechanics of materials and Faculty of Mechanical Engineering University of Niš and Department for bio-medical science, State University of Novi Pazar in Novi Pazar.

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APPENDIX

NOMENCLATURE

DNA – Deoxyribonucleic acid (DNA)

$\varphi_{k,1} [rad]$ - generalized coordinate – angles of the k -th base of the first chain of the double DNA chain helix;

$\varphi_{k,2} [rad]$ - generalized coordinate – angles of the k -th base of the second chain of the double DNA chain helix;

$\mathbf{J}_{k,1} [kgm^2]$ - is the axial moment of mass inertia of the k -th base of the first chain of the double DNA chain helix;

$\mathbf{J}_{k,2} [kgm^2]$ - is the axial moment of mass inertia of the k -th base of the second chain of the double DNA chain helix;

$\dot{\varphi}_{k,1} [rads^{-1}]$ - angular velocity of the k -th base of the first chain of the double DNA chain helix;

$\mathbf{J}_{k,1} = m_{\alpha} r_{\alpha}^2$, $\mathbf{J}_{k,2} = m_{\beta} r_{\beta}^2 [kgm^2]$ - the base pair the axial moments of mass inertia ;

$m_{\alpha} [kg]$ - the value of the base mass

$r_{\alpha} [m]$ - the length

$\mathbf{J}_{k,1} = m_\alpha r_\alpha^2$ [kgm²] - the corresponding axial moment of mass inertia for all possible base pair authors accepted as in the Reference [17].

$K_{k,i}$, $i = 1, 2$ [KJmol⁻¹]- parameters characterize the energy of interaction of the k -th base with the $(k + 1)$ -th one along

the i -th chain $i = 1, 2$.

$K_{k,i} = K = 6 \times 10^3$ [KJmol⁻¹] - for the calculation that the most appropriate value is close /

ξ_k , η_k [rad], $k = 1, 2, 3, \dots, n$ - main orthogonal coordinates of the eigen main chains of the double DNA chain helix;

$\xi_k = \varphi_{k,1} - \varphi_{k,2}$ and $\eta_k = \varphi_{k,1} + \varphi_{k,2}$, $k = 1, 2, 3, \dots, n$ - functional dependence between main orthogonal coordinates ξ_k and η_k of the eigen main chains and generalized coordinates $\varphi_{k,1}$ and $\varphi_{k,2}$ [rad] of the double DNA chain helix;

$\omega_{\alpha\beta 2}$ [sec⁻¹] - are frequencies of rotational motions of the bases, in similar and opposite directions accordingly, of the k -th base of the first chain of the double DNA chain helix;

$\omega_{\alpha\beta 1}$ [sec⁻¹] - are frequencies of rotational motions of the bases, in similar and opposite directions accordingly, of the k -th base of the first chain of the double DNA chain helix;

$K_{k,1} = K_{k,2} = K$ - for the case of homogeneous double DNA chain helix;

$\mathbf{J}_{k,1} = \mathbf{J}_{k,2} = \mathbf{J}$ [kgm²] - for the case of homogeneous double DNA chain helix;

A_k - amplitude

$u = \mathbf{J} \mathbf{K}^{-1} \omega^2$ - eigen characteristic number of the homogeneous double DNA chain helix;

$k = K_{\alpha\beta} 2 \mathbf{K}^{-1} \{1 - \omega_{\alpha\beta 2} \omega_{\alpha\beta 1}^{-1}\} (r_\alpha - r_\beta)^2$ - parameter of the homogeneous double DNA chain helix;

$\mu = K_{\alpha\beta} r_\alpha (r_\alpha - r_\beta) \mathbf{K}^{-1}$ - parameter of the homogeneous double DNA chain helix;

$\omega_{s\xi}^2$ [sec⁻²], $s = 1, 2, 3, 4, \dots, n$ - set of the n eigen circular frequencies of the first eigen main chain of the homogeneous double DNA chain helix;

$\omega_{s\eta}^2$ [sec⁻²], $s = 1, 2, 3, 4, \dots, n$ - set of the n eigen circular frequencies of the first eigen main chain of the homogeneous double DNA chain helix;

$\omega_{s\xi}^2$ and $\omega_{s\eta}^2$, $s = 1, 2, 3, 4, \dots, n$ - two subsets of the set of the homogeneous double DNA chain helix;

APPENDIX A*

Expansion of the Laplace transform into series.

$$\mathfrak{g}\{\xi_2\} = \frac{p\varphi_{01} + \dot{\varphi}_{01}}{2(p^2 + \omega_{0\alpha}^2 p^\alpha + \tilde{\omega}_0^2 + \omega_{00}^2)} \quad (\text{A.1})$$

$$\mathfrak{g}\{\xi_2(t)\} = \frac{p\varphi_{01} + \dot{\varphi}_{01}}{2p^2 \left[1 + \frac{\omega_{0\alpha}^2}{p^2} \left(p^\alpha + \frac{\tilde{\omega}_0^2 + \omega_{00}^2}{\omega_{0\alpha}^2} \right) \right]} = \left(\varphi_{01} + \frac{\dot{\varphi}_{01}}{p} \right) \frac{1}{2p \left[1 + \frac{\omega_{0\alpha}^2}{p^2} \left(p^\alpha + \frac{\tilde{\omega}_0^2 + \omega_{00}^2}{\omega_{0\alpha}^2} \right) \right]}$$

$$\mathfrak{L}\{\xi_2(t)\} = \left(\varphi_{01} + \frac{\dot{\varphi}_{01}}{p} \right) \frac{1}{2p} \sum_{k=0}^{\infty} \frac{(-1)^k \omega_{0\alpha}^{2k}}{p^{2k}} \left(p^\alpha + \frac{\tilde{\omega}_0^2 + \omega_{00}^2}{\omega_{0\alpha}^2} \right)^k \quad (\text{A.2})$$

$$\mathfrak{L}\{\xi_2(t)\} = \left(\varphi_{01} + \frac{\dot{\varphi}_{01}}{p} \right) \frac{1}{2p} \sum_{k=0}^{\infty} \frac{(-1)^k \omega_{0\alpha}^{2k}}{p^{2k}} \sum_{j=0}^k \binom{k}{j} \frac{p^{\alpha j} \omega_{0\alpha}^{2(j-k)}}{(\tilde{\omega}_0^2 + \omega_{00}^2)^j} \quad (\text{A.3})$$

APPENDIX B*

Solution of a fractional order differential equation of a fractional order creep oscillator with single degree of freedom

The fractional order differential equations obtained and considered cases of eigen fractional order partial oscillators of the hybrid fractional order multichain system are in mathematical analogy same fractional order differential equation with corresponding unknown time-functions. We can use notation $T(t)$ and all previous derived fractional order differential equations of eigen fractional order partial oscillators with one degree of freedom, correspond to the hybrid fractional order multi-chain system dynamics with sixth degree of freedom, we can rewrite it in the following form:

$$\ddot{T}(t) \pm \omega_\alpha^2 T^{(\alpha)}(t) + \omega_0^2 T(t) = 0 \quad (\text{B.1})$$

This fractional order differential equation (B.1) on unknown time-function $T(t)$, can be solved applying Laplace transforms (see Refs. [3] by Baćlić and Atanacković (2000), [23] by Hedrih (Stevanović) and Filipovski (2002)). Upon that fact Laplace transform of solution is in form:

$$\mathfrak{L}(p) = \mathfrak{L}[T(t)] = \frac{pT(0) + \dot{T}(0)}{p^2 + \omega_0^2 \left[1 \pm \frac{\omega_\alpha^2}{\omega_0^2} \mathbf{R}(p) \right]} \quad (\text{B.2})$$

where $\mathfrak{L}[\mathfrak{D}^\alpha[T(t)]] = \mathbf{R}(p)\mathfrak{L}[T(t)]$ is Laplace transform of a fractional derivative $\frac{d^\alpha T(t)}{dt^\alpha}$ for $0 \leq \alpha \leq 1$.

For creep rheological material those Laplace transforms the form:

$$\mathfrak{L}[\mathfrak{D}^\alpha[T(t)]] = \mathbf{R}(p)\mathfrak{L}[T(t)] - \frac{d^{\alpha-1}}{dt^{\alpha-1}}T(0) = p^\alpha \mathfrak{L}[T(t)] - \frac{d^{\alpha-1}}{dt^{\alpha-1}}T(0) \quad (\text{B.3})$$

where the initial value are:

$$\left. \frac{d^{\alpha-1}T(t)}{dt^{\alpha-1}} \right|_{t=0} = 0 \quad (\text{B.4})$$

so, in that case Laplace transform of time-function is given by following expression:

$$\mathfrak{L}[T(t)] = \frac{pT_0 + \dot{T}_0}{[p^2 \pm \omega_\alpha^2 p^\alpha + \omega_0^2]} \quad (\text{B.5})$$

For boundary cases, when material parameters α take following values: $\alpha = 0$ i $\alpha = 1$ we have the two special simple cases, whose corresponding fractional-differential equations and solutions are known. In these cases fractional-differential equations are:

$$1^* \quad \ddot{T}(t) \pm \tilde{\omega}_{0\alpha}^2 T^{(0)}(t) + \omega_0^2 T(t) = 0 \quad \text{for } \alpha = 0 \quad (\text{B.6})$$

where $T^{(0)}(t) = T(t)$, and

$$2^* \quad \ddot{T}(t) \pm \omega_{1\alpha}^2 T^{(1)}(t) + \omega_0^2 T(t) = 0 \quad \text{for } \alpha = 1 \quad (\text{B.7})$$

where $T^{(1)}(t) = \dot{T}(t)$.

The solutions to equations (B.6) and (B.7) are:

$$1^* \quad T(t) = T_0 \cos t \sqrt{\omega_0^2 \pm \tilde{\omega}_{0\alpha}^2} + \frac{\dot{T}_0}{\sqrt{\omega_0^2 \pm \tilde{\omega}_{0\alpha}^2}} \sin t \sqrt{\omega_0^2 \pm \tilde{\omega}_{0\alpha}^2} \quad (\text{B.8})$$

for $\alpha = 0$.

2* a.

$$T(t) = e^{\mp \frac{\omega_\alpha^2}{2} t} \left\{ T_0 \cos t \sqrt{\omega_0^2 - \frac{\omega_{1\alpha}^4}{4}} + \frac{\dot{T}_0}{\sqrt{\omega_0^2 - \frac{\omega_{1\alpha}^4}{4}}} \sin t \sqrt{\omega_0^2 - \frac{\omega_{1\alpha}^4}{4}} \right\} \quad (\text{B.9})$$

for $\alpha = 1$ and for $\omega_0 > \frac{1}{2} \omega_{1\alpha}^2$. (for soft creep) or for strong creep:

2* b.

$$T(t) = e^{\mp \frac{\omega_\alpha^2}{2} t} \left\{ T_0 \text{Ch } t \sqrt{\frac{\omega_{1\alpha}^4}{4} - \omega_0^2} + \frac{\dot{T}_0}{\sqrt{\frac{\omega_{1\alpha}^4}{4} - \omega_0^2}} \text{Sh } t \sqrt{\frac{\omega_{1\alpha}^4}{4} - \omega_0^2} \right\} \quad (\text{B.10})$$

for $\alpha = 1$ and for $\omega_0 < \frac{1}{2} \omega_{1\alpha}^2$.

For critical case:

$$2^* \text{ c. } T(t) = e^{\mp \frac{\omega_\alpha^2}{2} t} \left\{ T_0 + \frac{2\dot{T}_0}{\omega_{1\alpha}^2} t \right\} \text{ for } \alpha = 1 \text{ and } \omega_0 = \frac{1}{2} \omega_{1\alpha}^2 . \quad (\text{B.11})$$

Fractional-differential equation (B.1) for the general case, when α is real number from interval $0 < \alpha < 1$ can be solved by using Laplace's transformation. By using that is:

$$\mathfrak{L} \left\{ \frac{d^\alpha T(t)}{dt^\alpha} \right\} = p^\alpha \mathfrak{L}\{T(t)\} - \frac{d^{\alpha-1} T(t)}{dt^{\alpha-1}} \Big|_{t=0} = p^\alpha \mathfrak{L}\{T(t)\} \quad (\text{B.12})$$

and by introducing for initial conditions of fractional derivatives in the form (B.3), and after taking Laplace's transform of the equation (B.1), we obtain a corresponding equation. *By analyzing previous Laplace transform (B.12) of solution we can conclude that we can consider two cases.*

For the case when $\omega_0^2 \neq 0$, the Laplace transform solution can be developed into series by following way:

$$\mathfrak{L}\{T(t)\} = \frac{pT_0 + \dot{T}_0}{p^2 \left[1 + \frac{\omega_\alpha^2}{p^2} \left(\pm p^\alpha + \frac{\omega_0^2}{\omega_\alpha^2} \right) \right]} = \left(T_0 + \frac{\dot{T}_0}{p} \right) \frac{1}{p \left[1 + \frac{\omega_\alpha^2}{p^2} \left(\pm p^\alpha + \frac{\omega_0^2}{\omega_\alpha^2} \right) \right]} \quad (\text{B.13})$$

$$\mathfrak{L}\{T(t)\} = \left(T_0 + \frac{\dot{T}_0}{p} \right) \frac{1}{p} \sum_{k=0}^{\infty} \frac{(-1)^k \omega_\alpha^{2k}}{p^{2k}} \left(\pm p^\alpha + \frac{\omega_0^2}{\omega_\alpha^2} \right)^k \quad (\text{B.14})$$

$$\mathfrak{L}\{T(t)\} = \left(T_0 + \frac{\dot{T}_0}{p} \right) \frac{1}{p} \sum_{k=0}^{\infty} \frac{(-1)^k \omega_\alpha^{2k}}{p^{2k}} \sum_{j=0}^k \binom{k}{j} \frac{(\mp 1)^j p^{\alpha j} \omega_\alpha^{2(j-k)}}{\omega_\alpha^{2j}} \quad (\text{B.15})$$

In writing (B.15) it is assumed that expansion leads to convergent series. The inverse Laplace transform of previous Laplace transform of solution (B.15) in term-by-term steps is based on known theorem, and yield the following solution of differential equation (B.1) of time function in the following form of time series:

$$T(t) = \mathfrak{L}^{-1} \mathfrak{L}\{T(t)\}$$

$$T(t) = T_0 \sum_{k=0}^{\infty} (-1)^k \omega_\alpha^{2k} t^{2k} \sum_{j=0}^k \binom{k}{j} \frac{(\mp 1)^j \omega_\alpha^{2j} t^{-\alpha j}}{\omega_\alpha^{2j} \Gamma(2k+1-\alpha j)} + \dot{T}_0 \sum_{k=0}^{\infty} (-1)^k \omega_\alpha^{2k} t^{2k+1} \sum_{j=0}^k \binom{k}{j} \frac{(\mp 1)^j \omega_\alpha^{-2j} t^{-\alpha j}}{\omega_\alpha^{2j} \Gamma(2k+2-\alpha j)} \quad (\text{B.16})$$