

# Modeling Double DNA Helix Main Chains of the Free and Forced Fractional Order Vibrations

ANDJELKA N. HEDRIH

Department for Bio-medical Science,  
State University of Novi Pazar, Novi Pazar,  
Niš, Trg učitelja Tase 3/9, Serbia  
e-mail: [handjelka@hm.co.rs](mailto:handjelka@hm.co.rs)

KATICA R. (STEVANOVIĆ) HEDRIH

Department for Mechanics, Mathematical Institute SANU, Belgrade,  
and Faculty of Mechanical Engineering, University of Niš, Serbia  
Niš, Vojvode Tankosić 3/22, Serbia  
e-mail: [katica@masfak.ni.ac.rs](mailto:katica@masfak.ni.ac.rs), [khedrih@eunet.rs](mailto:khedrih@eunet.rs)

**Abstract:** DNA transcription process is well described at biochemical level. During transcription, double DNA interacts with transcription proteins; a part of double DNA is unzipped, and only one chain helix is used as a matrix for transcription. Different models of two coupled homogeneous DNA chain vibrations are proposed in the literature. To better understand 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. When data from dDNA molecule are not transcribed, we consider that dDNA molecule oscillates in a manner of free fractional order vibrations. On the basis of previous results (DNA mathematical models published by N.Kovaleva, L. Manevich in 2005 and 2007, and multi-pendulum models by Hedrih (Stevanović) and Hedrih) we obtain a corresponding pair of main chain subsystems of the double DNA helix. Analytical expressions of the eigen circular frequencies and eigen fractional order characteristic numbers for the homogeneous model of the double DNA fractional order chain helix are obtained. Also, the corresponding eigen free and forced fractional order vibration modes and possibilities of the appearance of resonant regimes, as well as dynamical absorption under the external forced excitations are considered. Two sets of eigen normal coordinates of the double DNA chain helix for separation of the system into two uncoupled main eigen chains are identified. On the basis of the derived analytical expressions, a transfer of external excitation forced signals is analyzed. There are different cases of the resonant state in one of the main chains, and there are no interactions between main chains for special cases of the external one frequency forced excitation. This may correspond to the base pair order in complementary chains of DNA double helix in a living cell.

**Key-Words:** Double DNA helix chain, forced vibrations, eigen main chains, resonant state, dynamical absorption, elastic model, fractional order model, transfer of signals.

## 7.1 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.

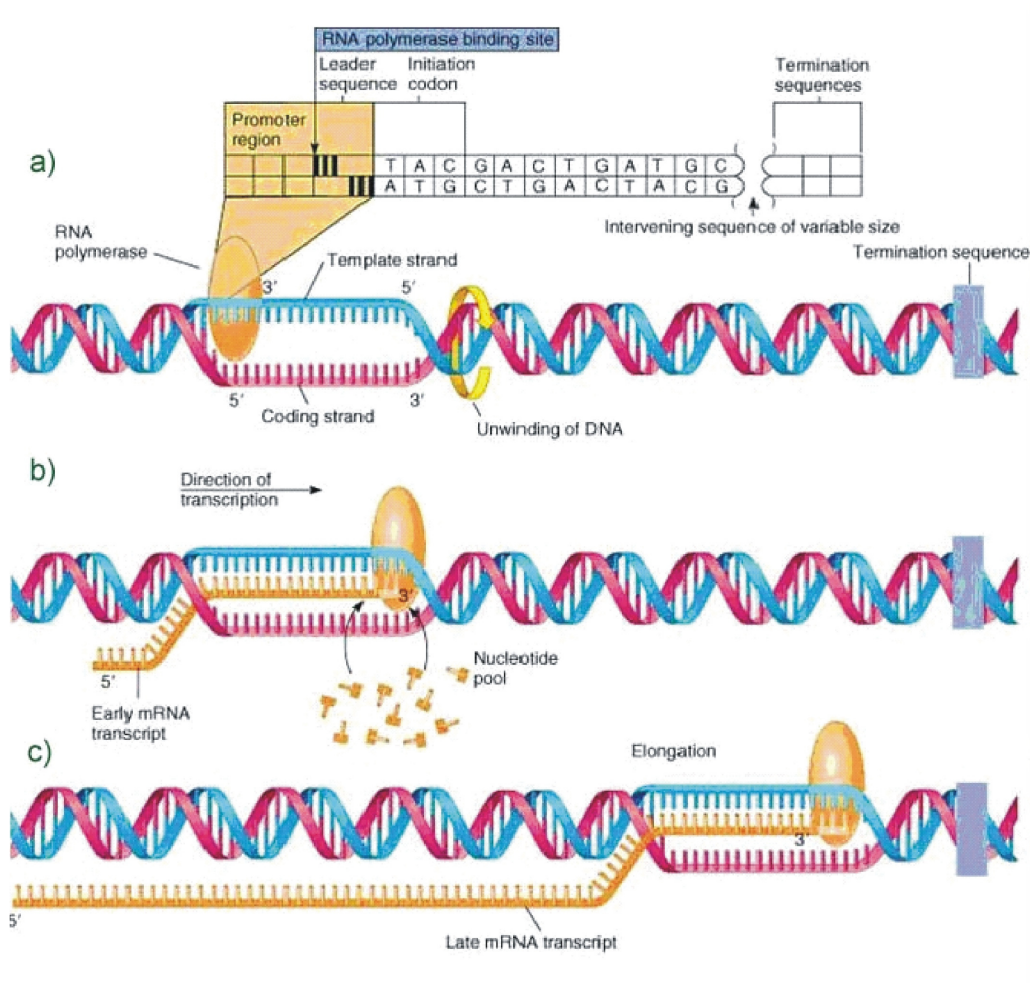


Fig.1. Model of DNA transcription (modified from, <http://www.untiredwithloving.org/satr.html>)

From the biochemical point of view, during the transcription process, genetic information is transcribing from **DNA** to RNA. The transcribed DNA message is used to produce proteins. There are three main steps to the process of DNA transcription: binding of RNA polymerase to DNA, elongation and termination. RNA polymerase is an enzyme that binds to a specific nucleotide sequences that "tell" RNA polymerase where to begin and where to end the transcription. RNA polymerase attaches to the DNA at a specific area called the promoter region. Fig 1. a) Certain proteins, called transcription factors, unwind the DNA strand and allow RNA polymerase to transcribe only a single strand of DNA into a single stranded RNA polymer called messenger RNA (mRNA). The DNA is unwound at the promoter region by RNA polymerase. The strand that serves as the template is called the antisense strand. The strand that is not transcribed is called the sense strand. RNA polymerase moves along the DNA until it reaches a terminator sequence, Fig1.b) and c). At that point, RNA polymerase releases the mRNA polymer and detaches from the DNA. The DNA that is been transcribed is rewound into original configuration. Fig.1.

Every process which binds or reads DNA is able to use or modify the mechanical properties of DNA for the purposes of recognition, packaging and modification. It is important to note that 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, [6]. Knowledge of the elastic properties of DNA is required to understand the structural dynamics of cellular processes such as replication and transcription. Binding of proteins and other ligands induces a strong deformation of the DNA structure. 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.

Single-molecule biomechanics of DNA extension, bending and twisting; protein domain motion, deformation and unfolding; the generation of mechanical forces and motions by bimolecular motors is another approach to explain the biological function of DNA in the cell, [4].

Knowledge of the elastic properties of DNA is required to understand the structural dynamics of cellular processes such as replication and transcription. For details for possible movements of DNA molecule, see Appendix E.

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

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 live system during regular function of a DNA molecule. The quick review of mechanical properties of DNA achieved experimentally and relevant existed mechanical models of specific dDNA dynamics are given below. One of soliton existence supporting model of DNA-DNA model by N. Kovaleva and L. Manevich and derived oscillatory models of DNA by Hedrih (Stevanovic) and Hedrih is specially discussed.

## 7.2 Mechanical properties of DNA achieved experimentally

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

For small distortions, DNA overwinds under tension, [18]. Lowering of the temperature does increase the DNA curvature. The DNA double helix is much more resistant to twisting deformations than to bending deformations, and almost all of the supercoiling pressure is normally relieved by writhing, [2]. 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 [47], [53].

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 [6]. The environment and its ionic strength have influence on DNA curvature.  $Mg^{2+}$  can induce or enhance curvature in DNA fragments and helps stabilize several types of DNA structures, [5]. DNA length varied in solution with different ionic force. It is significantly longer in solution with lower ionic force, [14].

## 7.3 Mechanical models of the DNA

A number of mechanical models of the DNA double helix have been proposed until 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 dDNA, twist-opening conditions. We are going to mention some of the models that can explain twist-opening conditions. Details for some types of the models are given in the Appendix E.2. (see Ref [23]).

Bryant et al. (see Ref. [6]) 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 [4]. 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 [8,56]. Eslami-Mossallam and Ejtehadi, [13] 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. A special type of DNA models are soliton-existence supporting models. One of the first of this kind was the Yakushevich model of DNA and models based on it [15]. The 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 [55] 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, [16] gave a 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 takes 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 the Yakushevich model (Y model). The mechanism for selecting the speed of solitons by tuning the physical parameters of the non-linear medium and the hierarchal separation of the relevant degrees of freedom are described in this model, see [7,11]. 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 parts 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 [52]. 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 live system during regular function of a DNA molecule. We consider double DNA (dDNA) as an oscillatory system that oscillates in forced regimes during the DNA transcription process. To model the oscillation of dDNA in free and forced regimes we use, as a basic approach, the model of dDNA proposed by N.Kovaleva, L.Manevich, V.Smirnov (see [41], [42]). Basis of the DNA models proposed by Kovaleva and Manevich, will be given in the section below.

## 7.4 DNA models by N. Kovaleva and L. Manevich

One of the soliton-existence supporting models of dDNA is also the model proposed by N.Kovaleva, L.Manevich, V.Smirnov, see [41,42]. They show that in a double DNA helix localized excitation (breather) can exist, which corresponds to predominant rotation of one chain and a small perturbation of the second chain, using a coarse-grained model of the DNA double helix. Each nucleotide is represented by three beads with interaction sites corresponding to phosphate group, group of sugar ring, and the base [41].

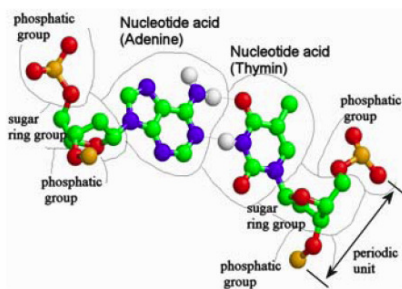


Fig. 2. a

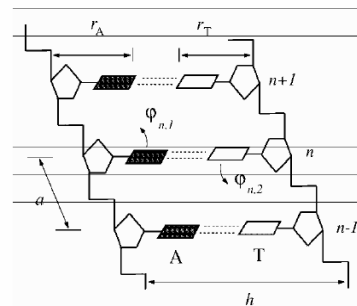


Fig. 2. b

Fig. 2. **a** The model scheme of a double helix on six coarse-grained particles (Kovaleva, Manevich, and Smirnov, 2007). Fig. 2.**b** Fragment of the DNA double chain consisting of three AT base pairs. Longitudinal pitch of the helix  $a = 3.4 \text{ \AA}$ ; transverse pitch  $h = 16.15 \text{ \AA}$  (see Ref. [42] by Kovaleva, and Manevich, 2005).

Kovaleva, Manevich, and Smirnov, [41] 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 the 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, the 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. The authors formulated conditions of the breathers' existence and estimated their characteristic parameters. The relationship between a derived model and simpler and widely used models is discussed. The analytical results are compared with the data of numerical study of discrete equations of motion. See Fig. 2.a.

Kovaleva, and Manevich, [42] developed the simplest model describing the opening of DNA double helix. The corresponding differential equations are solved analytically using multiple-scale expansions after transition to complex variables. Obtained solution corresponds to localized torsional nonlinear excitation – breather. The stability of breather is also investigated. They consider B form of the DNA molecule, the fragment of which is presented in Fig. 2b. The lines in the figure correspond to the 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 sugar-phosphate chains in the plane perpendicular to the helix axis.

The 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. The 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  $\varphi_{k,2}$  the angular displacement of the  $k$ -th base of the second chain. Then, using the accepted generalized coordinates  $\varphi_{k,1}$  and  $\varphi_{k,2}$  for the  $k$ -th bases of both chains in the DNA model, the authors derived a system of differential equations describing DNA model vibrations in the following forms:

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

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  $m_{\alpha}$ , the length  $r_{\alpha}$ , and the corresponding axial moment of mass inertia  $\mathbf{J}_{k,1} = m_{\alpha} r_{\alpha}^2$  for all possible base pairs the authors accepted as in the [42]. The fourth terms in the previous system of equations describe the interaction of the neighboring bases along each of the macromolecule chain. The 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, the most appropriate value is close to  $K_{k,i} = K = 6 \times 10^3 [kJ/mol]$ .

## 7.5 Modified DNA models by N. Kovaleva and L. Manevich for the forced regimes

We have modified the previous model by Kovaleva and Manevich [42] to investigate how the system of dDNA will behave when it is exposed to external excitation. In the process of transcription, the binding of RNA polymerase may correspond with external excitation.

Let's suppose that both coupled chains from the system of the DNA model by Kovaleva and Manevich are excited by the system of external excitation containing two series of the one frequency excitations in the forms  $M_{0,k,1} \cos \Omega_{k,1} t$  and  $M_{0,k,2} \cos \Omega_{k,2} t$ ,  $k = 1, 2, 3, \dots, n$ , where  $M_{0,k,1}$  and  $M_{0,k,2}$  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, the corresponding system of the nonlinear forced vibrations of the double DNA model coupled chains is in the following form:

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

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

Let us investigate an oscillatory model of DNA considered in the [42] by N. Kovaleva, L. Manevich, (2005) and presented in section 4 by a system of differential equations (1) expressed by generalized (independent) angular coordinates  $\varphi_{k,1}$  and  $\varphi_{k,2}$  for the  $k$ -th bases of both chains in the DNA model.

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

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

or in the following form:

$$\begin{aligned} \frac{2J_{k,1}}{K_{k,1}} \ddot{\varphi}_{k,1} - [(\varphi_{k+1,1} - \varphi_{k,1}) - (\varphi_{k,1} - \varphi_{k-1,1})] + \frac{2K_{\alpha\beta} r_{\alpha} (r_{\alpha} - r_{\beta})}{K_{k,1}} \varphi_{k,1} - \\ - \frac{K_{\alpha\beta}}{2K_{k,1}} \left( 1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}} \right) (r_{\alpha} - r_{\beta})^2 (\varphi_{k,1} - \varphi_{k,2}) = \frac{M_{0,k,1}}{K_{k,1}} \cos \Omega_{k,1} t \end{aligned}$$

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

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

Using change of the generalized independent angular coordinates  $\varphi_{k,1}$  and  $\varphi_{k,2}$  for the  $k$ -th bases of both chains in the linearized DNA model into the following new  $\xi_k$  and  $\eta_k$  by the following dependence:

$$\xi_k = \varphi_{k,1} - \varphi_{k,2} \quad \text{and} \quad \eta_k = \varphi_{k,1} + \varphi_{k,2} \quad (5)$$

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

$$\frac{2\mathbf{J}}{K}\ddot{\xi}_k - \xi_{k+1} + 2\xi_k \left[ 1 + \frac{K_{\alpha\beta}r_{\alpha}(r_{\alpha} - r_{\beta})}{K} - \frac{K_{\alpha\beta}}{2K} \left( 1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}} \right) (r_{\alpha} - r_{\beta})^2 \right] - \xi_{k-1} = \frac{M_{0,k,1}}{K}\cos\Omega_{0,k,1}t - \frac{M_{0,k,2}}{K}\cos\Omega_{0,k,2}t \quad (6)$$

$$\frac{2\mathbf{J}}{K}\ddot{\eta}_k - \eta_{k+1} + 2\eta_k \left( 1 + \frac{K_{\alpha\beta}r_{\alpha}(r_{\alpha} - r_{\beta})}{K} \right) - \eta_{k-1} = \frac{M_{0,k,1}}{K}\cos\Omega_{0,k,1}t + \frac{M_{0,k,2}}{K}\cos\Omega_{0,k,2}t, \quad k = 1, 2, 3, \dots, n \quad (7)$$

The first series of the previous system of ordinary differential equations are decoupled and independent with relations of the second series of the ordinary differential equations. We can conclude then that new coordinates of  $\xi_k$  and  $\eta_k$  are the main chain coordinates of original DNA model double chain system and that we obtain two fictive decoupled eigen single chains of the DNA linearized model. *This is the first fundamental conclusion as an important property of the linearized model of vibrations in a double DNA helix.*

The systems of differential equations (6)-(7) contain two separate independent subsystems of no autonomous differential equations expressed by *coordinates of  $\xi_k$  and  $\eta_k$  which are the main chain coordinates of a double DNA chain helix system and separate linear DNA model of forced vibrations into two independent (fictive, mathematical) chains.*

### 7.6.1. Consideration of the free vibrations of a basic DNA model - linearized Kovaleva-Manevich's DNA model

We assumed that the system of dDNA oscillates with free vibrations when it is not involved in the process of transcription and oscillates with forced vibrations during the process of transcription.

*The corresponding systems of autonomous differential equations are joined to the systems of non-autonomous differential equations (6)-(7), which also contain two separate subsystems of non-autonomous differential equations expressed by coordinates  $\xi_k$  and  $\eta_k$  which are the main chain coordinates of a double DNA chain helix system. The solutions of these corresponding systems of autonomous differential equations are  $n$ -frequency time functions which correspond to free vibrations with different subsets of  $n$  circular frequencies. The solutions of the non-autonomous differential equations (6)-(7) are multi-frequency time functions with a corresponding subset of eigen circular frequencies containing  $n$  eigen circular frequencies of free vibrations and all frequencies of external forced excitations applied to the double DNA helix chain system. So, if external excitation is with  $2n$  circular frequencies  $\Omega_{k,j}$ ,  $j = 1, 2$ ,  $k = 1, 2, 3, \dots, n$ , then forced vibrations of the independent main chain coordinate of the main chains of the linear DNA model are  $n + 2n$ -frequency time functions.*

*To prove this conclusion, for a start, it is necessary to express the solutions of the corresponding systems of autonomous differential equations and add the corresponding particular solutions of the systems of non-autonomous differential equations (6)-(7).*

*Then, for that aim, to obtain the solutions of autonomous system of differential equations, it is possible to apply the trigonometric method (see [48],[49] and [24],[25]) to both series of autonomous differential equations (both subsystems obtained from the system (6)-(7) put  $M_{0,k,j} = 0$ ,  $j = 1, 2$ ,  $k = 1, 2, 3, \dots, n$ ) in the form:*



$$\xi_k = A_k \cos(\omega t + \alpha) = C \sin k\varphi \cos(\omega t + \alpha), \quad k = 1, 2, 3, \dots, n \quad (8)$$

$$A_k = C \sin k\varphi \quad (9)$$

$$\eta_k = \tilde{A}_k \cos(\tilde{\omega} t + \beta) = D \sin k\vartheta \cos(\tilde{\omega} t + \beta), \quad k = 1, 2, 3, \dots, n \quad (10)$$

$$\tilde{A}_k = D \sin k\vartheta \quad (11)$$

where  $A_k$  and  $\tilde{A}_k$  are amplitudes of separate eigen main chain coordinates of main chains of the model of double DNA chain helix, and  $\omega$  eigen circular frequency of the one, free vibration mode.

After introducing the proposed solutions into the corresponding autonomous differential equations obtained from the previous separate subsystems (5)-(6) in which we incorporate  $M_{0,k,j} = 0, j = 1, 2, k = 1, 2, 3, \dots, n$ , we obtain the following separate subsystems of homogeneous algebraic equations along the amplitudes  $A_k$  and  $\tilde{A}_k$ :

$$-A_{k+1} + 2A_k \left\{ \left[ 1 + \frac{K_{\alpha\beta} r_\alpha (r_\alpha - r_\beta)}{K} - \frac{K_{\alpha\beta}}{2K} \left( 1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}} \right) (r_\alpha - r_\beta)^2 \right] - \frac{\mathbf{J}}{K} \omega^2 \right\} - A_{k-1} = 0 \quad (12)$$

$$-A_{k+1} + 2A_k \left( 1 + \frac{K_{\alpha\beta} r_\alpha (r_\alpha - r_\beta)}{K} - \frac{2\mathbf{J}}{K} \tilde{\omega}^2 \right) - A_{k-1} = 0 \quad (13)$$

After applying the following denotations:

$$\mu - \kappa = \frac{K_{\alpha\beta} r_\alpha (r_\alpha - r_\beta)}{K} - \frac{K_{\alpha\beta}}{2K} \left( 1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}} \right) (r_\alpha - r_\beta)^2 \quad (14)$$

$$\kappa = \frac{K_{\alpha\beta}}{2K} \left( 1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}} \right) (r_\alpha - r_\beta)^2, \quad \mu = \frac{K_{\alpha\beta} r_\alpha (r_\alpha - r_\beta)}{K} \quad (15)$$

$$u = \frac{\mathbf{J}}{K} \omega^2 \quad (16)$$

we obtain the following simple forms of the subsystems (12)-(13) in the following separate subsystems of homogeneous algebraic equations along the amplitudes  $A_k$  and  $\tilde{A}_k$ :

$$-A_{k+1} + 2A_k (1 + \mu - \kappa - u) - A_{k-1} = 0 \quad (17)$$

$$-\tilde{A}_{k+1} + 2\tilde{A}_k (1 + \mu - \tilde{u}) - \tilde{A}_{k-1} = 0 \quad (18)$$

After introducing the proposed solutions (9) and (11), the trigonometric method is applied and we obtain two equations:

$$C \sin k\varphi [-2 \cos \varphi + 2(1 + \mu - \kappa - u)] = 0 \quad (19)$$

$$D \sin k\vartheta [-2 \cos \vartheta + 2(1 + \mu - \tilde{u})] = 0 \quad (20)$$

From the previous system, we obtain the following eigen characteristic numbers for both separate eigen chains of the model of double DNA chain helix system free vibrations in the following forms:

$$u = 2 \sin^2 \frac{\varphi}{2} + (\mu - \kappa) \quad (21)$$

$$\tilde{u} = 2 \sin^2 \frac{\vartheta}{2} + \mu \quad (22)$$

and the corresponding analytical expressions of the square of  $\omega$  - eigen circular frequencies of vibration modes of separate eigen main chains in the following forms:

$$\omega_s^2 = \frac{K}{J} \left[ 2 \sin^2 \frac{\varphi_s}{2} + (\mu - \kappa) \right] \quad s = 1, 2, 3, \dots, n \quad (23)$$



$$\tilde{\omega}_r^2 = \frac{K}{J} \left[ 2 \sin^2 \frac{\vartheta_r}{2} + \mu \right] \quad r = 1, 2, 3, \dots, n \quad (24)$$

Solutions of main chains coordinates for free vibrations are in the following forms:

$$\xi_k = \sum_{s=1}^{s=n} \xi_k^{(s)} = \sum_{s=1}^{s=n} A_k^{(s)} \cos(\omega_s t + \alpha_s) = \sum_{s=1}^{s=n} C_s \sin k \varphi_s \cos(\omega_s t + \alpha_s), \quad k = 1, 2, 3, \dots, n \quad (25)$$

$$\eta_k = \sum_{r=1}^{r=n} \eta_k^{(r)} = \sum_{r=1}^{r=n} \tilde{A}_k^{(r)} \cos(\tilde{\omega}_r t + \beta_r) = \sum_{r=1}^{r=n} D_r \sin k \vartheta_r \cos(\tilde{\omega}_r t + \beta_r), \quad k = 1, 2, 3, \dots, n \quad (26)$$

### 7.6. 2. Boundary conditions of the double DNA chain helix

Now, it is necessary to consider some boundary conditions (see [48], [49] and [27]) of the double DNA chain helix in accordance with the possible real situations. For that reason, we take into account two cases of double DNA chain helix, when ends of the chains are free and when ends of the chains are fixed. Then, we can write the following boundary conditions of the double DNA chain helix:

*a\* case:* both ends of the double DNA chain helix are free:

For that case, the first and  $n$ -th equations from the subsystems are in the form:

$$A_1(1 + \mu - \kappa - 2u) - A_2 = 0 \quad (27a)$$

$$-A_{n-1} + A_n(1 + \mu - \kappa - 2u) = 0$$

$$\tilde{A}_1(1 + \mu - \kappa - 2\tilde{u}) - \tilde{A}_2 = 0$$

$$-\tilde{A}_{n-1} + \tilde{A}_n(1 + \mu - 2\tilde{u}) = 0 \quad (27b)$$

and after applying the proposed solutions (9) and (11) we obtain:

$$\varphi_s = \frac{s\pi}{n} \quad \text{and} \quad \vartheta_s = \frac{s\pi}{n} \quad s = 1, 2, 3, 4, \dots, n \quad (27c)$$

*b\* case:* both ends of the of the double DNA chain helix are fixed:

$$A_k = C \sin k \varphi \quad A_0 = 0 \quad A_{n+1} = 0 \quad A_{m+1} = C \sin(n+1)\varphi = 0 \quad (28a)$$

$$\tilde{A}_k = D \sin k \vartheta \quad \tilde{A}_0 = 0 \quad \tilde{A}_{n+1} = 0 \quad \tilde{A}_{m+1} = D \sin(n+1)\vartheta = 0 \quad (28b)$$

$$\varphi_s = \frac{s\pi}{(n+1)} \quad \vartheta_r = \frac{r\pi}{(n+1)}, \quad s = 1, 2, 3, 4, \dots, n, \quad r = 1, 2, 3, \dots, n \quad (28c)$$

Then the analytical expressions of the square of  $\omega_s$  - *eigen circular frequencies of the vibration modes of the separate main chains* in the double DNA chain helix are [35]:

$$\omega_s^2 = \frac{K}{J} \left[ 2 \sin^2 \frac{\varphi_s}{2} + \frac{K_{\alpha\beta} r_\alpha (r_\alpha - r_\beta)}{K} - \frac{K_{\alpha\beta}}{2K} \left( 1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}} \right) (r_\alpha - r_\beta)^2 \right], \quad s = 1, 2, 3, 4, \dots, n \quad (29)$$

$$\tilde{\omega}_r^2 = \frac{K}{J} \left[ 2 \sin^2 \frac{\vartheta_r}{2} + \frac{K_{\alpha\beta} r_\alpha (r_\alpha - r_\beta)}{K} \right] \quad r = 1, 2, 3, \dots, n \quad (30)$$

*a\* case:* both ends of the double DNA chain helix are free (see Fig.3.) :

$$\omega_s^2 = \frac{K}{J} \left[ 2 \sin^2 \frac{s\pi}{2n} + \frac{K_{\alpha\beta} r_\alpha (r_\alpha - r_\beta)}{K} - \frac{K_{\alpha\beta}}{2K} \left( 1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}} \right) (r_\alpha - r_\beta)^2 \right], \quad s = 1, 2, 3, 4, \dots, n \quad (31)$$

$$\tilde{\omega}_r^2 = \frac{K}{J} \left[ 2 \sin^2 \frac{r\pi}{2n} + \frac{K_{\alpha\beta} r_\alpha (r_\alpha - r_\beta)}{K} \right], \quad r = 1, 2, 3, \dots, n \quad (32)$$

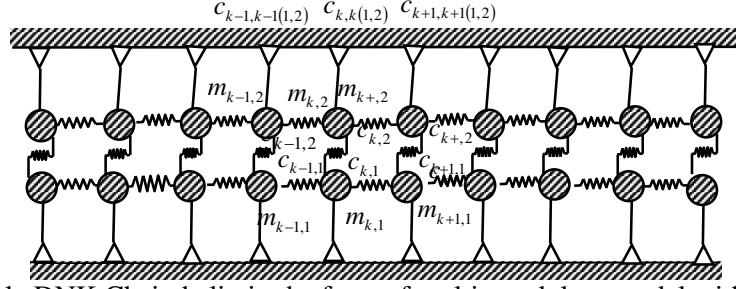


Fig 3. Double DNK Chain helix in the form of multi-pendulum model with free ends

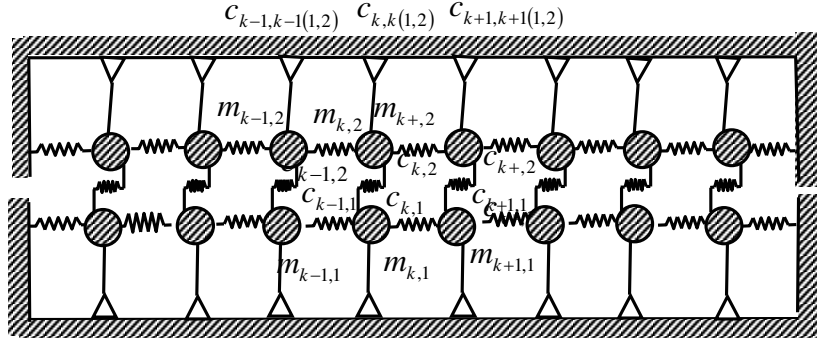


Fig.4. Double DNK Chain helix d model in the form of multi-pendulum system with fixed ends

*b\* case:* both ends of the double DNA chain helix are fixed (see Fig.4.) :

$$\omega_s^2 = \frac{K}{J} \left[ 2 \sin^2 \frac{s\pi}{2(n+1)} + \frac{K_{\alpha\beta} r_\alpha (r_\alpha - r_\beta)}{K} - \frac{K_{\alpha\beta}}{2K} \left( 1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}} \right) (r_\alpha - r_\beta)^2 \right] \quad s = 1, 2, 3, \dots, n \quad (33)$$

$$\tilde{\omega}_r^2 = \frac{K}{J} \left[ 2 \sin^2 \frac{r\pi}{2(n+1)} + \frac{K_{\alpha\beta} r_\alpha (r_\alpha - r_\beta)}{K} \right] \quad r = 1, 2, 3, \dots, n \quad (34)$$

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

In order to obtain general solutions of both systems (6)-(7) of non-autonomous differential equations corresponding to forced regimes of the main chains vibrations, it is necessary to start with finding the particular solutions for this system. Taking into account the denotation (14)-(16), the previous systems (6)-(7) of non-autonomous differential equations is possible to express in the form:

$$\frac{2J}{K} \ddot{\xi}_k - \xi_{k+1} + 2\xi_k [1 + \mu - \kappa] - \xi_{k-1} = h_{0,k,1} \cos \Omega_{k,1} t - h_{0,k,2} \cos \Omega_{k,2} t \quad k = 1, 2, 3, \dots, n \quad (35)$$

$$\frac{2J}{K} \ddot{\eta}_k - \eta_{k+1} + 2\eta_k (1 + \mu) - \eta_{k-1} = h_{0,k,1} \cos \Omega_{k,1} t + h_{0,k,2} \cos \Omega_{k,2} t, \quad k = 1, 2, 3, \dots, n \quad (36)$$

where  $h_{0,k,1} = \frac{M_{0,k,1}}{K}$ ,  $h_{0,k,2} = \frac{M_{0,k,2}}{K}$ ,  $k = 1, 2, 3, \dots, n$ , reduced external excitation amplitudes.

Next, taking into account that this system is linear, for simplifications of the calculation procedure, without loss of generality, we can solve the system of non-autonomous differential equations describing the main chains forced vibrations of the double DNA helix chain system under one frequency external excitation, with frequency  $\Omega_{1,1}$  and reduce the amplitude applied  $h_{0,k,1} = \frac{M_{0,k,1}}{K}$  to one mass particle in the first real chain from the coupled chains. For that reason, we find particular solutions that correspond to forced vibrations with frequency  $\Omega_{1,1}$  in the following form (see Fig. 5):

$$\frac{2\mathbf{J}}{K}\ddot{\xi}_k - \xi_{k+1} + 2\xi_k[1 + \mu - \kappa] - \xi_{k-1} = \begin{cases} h_{0,1,1} \cos \Omega_{1,1}t & k=1 \\ 0 & k \neq 1 \end{cases} \quad k=1,2,3,\dots,n \quad (37)$$

$$\frac{2\mathbf{J}}{K}\ddot{\eta}_k - \eta_{k+1} + 2\eta_k(1 + \mu) - \eta_{k-1} = \begin{cases} h_{0,1,1} \cos \Omega_{1,1}t & k=1 \\ 0 & k \neq 1 \end{cases}, k=1,2,3,\dots,n \quad (38)$$

Particular solutions for the first and second system (37)-(38) are proposed in the forms:

$$\xi_{port,k} = N_k \cos \Omega_{1,1}t \quad k=1,2,3,\dots,n \quad (39a)$$

$$\eta_{port,k} = \tilde{N}_k \cos \Omega_{1,1}t \quad k=1,2,3,\dots,n \quad (39b)$$

and introducing the following denotations:

$$u = \frac{\mathbf{J}}{K}\omega^2 \quad v_{k,1} = \frac{\mathbf{J}}{K}\Omega_{k,1}^2 \quad v_{k,2} = \frac{\mathbf{J}}{K}\Omega_{k,12}^2 \quad (40)$$

and introducing the proposed particular solutions (39)-(40) into the system (37)-(38), we obtain the following system of algebraic non-homogeneous system:

$$-N_{k+1} + 2N_k(1 + \mu - \kappa - v_{1,1}) - N_{k-1} = \begin{cases} h_{0,1,1} & k=1 \\ 0 & k \neq 1 \end{cases} \quad k=1,2,3,\dots,n \quad (41)$$

$$-\tilde{N}_{k+1} + 2\tilde{N}_k(1 + \mu - \tilde{v}_{1,1}) - \tilde{N}_{k-1} = \begin{cases} h_{0,1,1} & k=1 \\ 0 & k \neq 1 \end{cases} \quad k=1,2,3,\dots,n \quad (42)$$

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

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

$$N_k(v_{1,1}) = \frac{\Delta_k(v_{1,1})}{\Delta(v_{1,1})} \quad k=1,2,3,\dots,n \quad (43)$$

$$\tilde{N}_k(\tilde{v}_{1,1}) = \frac{\tilde{\Delta}_k(\tilde{v}_{1,1})}{\tilde{\Delta}(\tilde{v}_{1,1})} \quad k=1,2,3,\dots,n \quad (44)$$

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

$$\Delta(v_{1,1}) = \begin{vmatrix} 2(1 + \mu - \kappa - v_{1,1}) & -1 & & \\ -1 & 2(1 + \mu - \kappa - v_{1,1}) & -1 & \\ & -1 & 2(1 + \mu - \kappa - v_{1,1}) & -1 \\ & & -1 & 2(1 + \mu - \kappa - v_{1,1}) \end{vmatrix} \neq 0 \quad (45)$$

$$\tilde{\Delta}(\tilde{v}_{1,1}) = \begin{vmatrix} 2(1 + \mu - \tilde{v}_{1,1}) & -1 & & \\ -1 & 2(1 + \mu - \tilde{v}_{1,1}) & -1 & \\ & -1 & 2(1 + \mu - \tilde{v}_{1,1}) & -1 \\ & & -1 & 2(1 + \mu - \tilde{v}_{1,1}) \end{vmatrix} \neq 0 \quad (46)$$

For the same example the other determinants  $\Delta_k(v_{1,1})$  and  $\tilde{\Delta}_k(\tilde{v}_{1,1})$ ,  $k=1,2,3,\dots,n$ , are obtained from the corresponding two-system determinates,  $\Delta(v_{1,1})$  and  $\tilde{\Delta}(\tilde{v}_{1,1})$  introducing into the corresponding column, the column with free terms from the right sides of the non-homogeneous algebraic equations (41)-(42):

$$\Delta_1(v_{1,1}) = \begin{vmatrix} h_{0,1,1} & -1 & & \\ -1 & 2(1 + \mu - \kappa - v_{1,1}) & -1 & \\ & -1 & 2(1 + \mu - \kappa - v_{1,1}) & -1 \\ & & -1 & 2(1 + \mu - \kappa - v_{1,1}) \end{vmatrix} = h_{0,1,1} 2^{4-1} \prod_{s=1}^{s=3} (v_{1,1} - u_s^{(n=3)}) \quad (47)$$

$$\tilde{\Delta}_1(\tilde{v}_{1,1}) = \begin{vmatrix} h_{0,1,1} & -1 & & \\ -1 & 2(1+\mu-\tilde{v}_{1,1}) & -1 & \\ & -1 & 2(1+\mu-\tilde{v}_{1,1}) & -1 \\ & & -1 & 2(1+\mu-\tilde{v}_{1,1}) \end{vmatrix} = h_{0,1,1} 2^{4-1} \prod_{r=1}^{r=3} (\tilde{v}_{1,1} - \tilde{u}_r^{(n=3)}) \quad (48)$$

$$\Delta_2(v_{1,1}) = \begin{vmatrix} 2(1+\mu-\kappa-v_{1,1}) & h_{0,1,1} & & \\ -1 & & -1 & \\ & 2(1+\mu-\kappa-v_{1,1}) & & -1 \\ & & -1 & 2(1+\mu-\kappa-v_{1,1}) \end{vmatrix} = h_{0,1,1} 2^{4-2} \prod_{s=1}^{s=2} (v_{1,1} - u_s^{(n=2)}) \quad (49)$$

$$\tilde{\Delta}_2(\tilde{v}_{1,1}) = \begin{vmatrix} 2(1+\mu-\tilde{v}_{1,1}) & h_{0,1,1} & & \\ -1 & & -1 & \\ & 2(1+\mu-\tilde{v}_{1,1}) & & -1 \\ & & -1 & 2(1+\mu-\tilde{v}_{1,1}) \end{vmatrix} = h_{0,1,1} 2^{4-2} \prod_{r=1}^{r=2} (\tilde{v}_{1,1} - \tilde{u}_r^{(n=2)}) \quad (50)$$

$$\Delta_3(v_{1,1}) = \begin{vmatrix} 2(1+\mu-\kappa-v_{1,1}) & -1 & h_{0,1,1} & \\ -1 & 2(1+\mu-\kappa-v_{1,1}) & & \\ & -1 & & -1 \\ & & 2(1+\mu-\kappa-v_{1,1}) & \end{vmatrix} = h_{0,1,1} 2(\tilde{v}_{1,1} - \tilde{u}_r^{(n=1)}) \quad (51)$$

$$\tilde{\Delta}_3(\tilde{v}_{1,1}) = \begin{vmatrix} 2(1+\mu-\tilde{v}_{1,1}) & -1 & h_{0,1,1} & \\ -1 & 2(1+\mu-\tilde{v}_{1,1}) & & \\ & -1 & & -1 \\ & & 2(1+\mu-\tilde{v}_{1,1}) & \end{vmatrix} = h_{0,1,1} 2(\tilde{v}_{1,1} - \tilde{u}_r^{(n=1)}) \quad (52)$$

$$\Delta_4(v_{1,1}) = \begin{vmatrix} 2(1+\mu-\kappa-v_{1,1}) & -1 & & h_{0,1,1} \\ -1 & 2(1+\mu-\kappa-v_{1,1}) & -1 & \\ & -1 & 2(1+\mu-\kappa-v_{1,1}) & \\ & & -1 & \end{vmatrix} = h_{0,1,1} \quad (53)$$

$$\tilde{\Delta}_4(\tilde{v}_{1,1}) = \begin{vmatrix} 2(1+\mu-\tilde{v}_{1,1}) & -1 & & h_{0,1,1} \\ -1 & 2(1+\mu-\tilde{v}_{1,1}) & -1 & \\ & -1 & 2(1+\mu-\tilde{v}_{1,1}) & \\ & & -1 & \end{vmatrix} = h_{0,1,1} \quad (54)$$

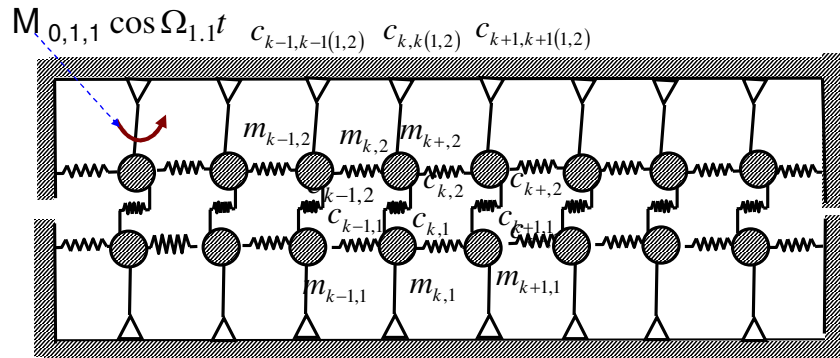


Fig. 5. Double DNK Chain helix model in the form of multi-pendulum system with fixed ends

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

$$\xi_{port,1} = N_1 \cos \Omega_{1,1} t = \frac{h_{0,1,1} \prod_{s=1}^{s=3} (v_{1,1} - u_s^{(n=3)})}{2 \prod_{s=1}^{s=4} (v_{1,1} - u_s^{(4)})} \cos \Omega_{1,1} t \quad (55)$$

$$\eta_{port,1} = \tilde{N}_1 \cos \Omega_{1,1} t = \frac{h_{0,1,1} \prod_{r=1}^{r=3} (\tilde{v}_{1,1} - \tilde{u}_r^{(n=3)})}{2 \prod_{r=1}^{r=4} (\tilde{v}_{1,1} - \tilde{u}_r^{(4)})} \cos \Omega_{1,1} t \quad (56)$$

$$\xi_{port,2} = N_2 \cos \Omega_{1,1} t = \frac{h_{0,1,1} \prod_{s=1}^{s=2} (v_{1,1} - u_s^{(n=2)})}{4 \prod_{s=1}^{s=4} (v_{1,1} - u_s^{(4)})} \cos \Omega_{1,1} t \quad (57)$$

$$\eta_{port,2} = \tilde{N}_2 \cos \Omega_{1,1} t = \frac{h_{0,1,1} \prod_{r=1}^{r=2} (\tilde{v}_{1,1} - \tilde{u}_r^{(n=2)})}{4 \prod_{r=1}^{r=4} (\tilde{v}_{1,1} - \tilde{u}_r^{(4)})} \cos \Omega_{1,1} t \quad (58)$$

$$\xi_{port,3} = N_3 \cos \Omega_{1,1} t = \frac{h_{0,1,1} (v_{1,1} - u_s^{(n=1)})}{8 \prod_{s=1}^{s=4} (v_{1,1} - u_s^{(n)})} \cos \Omega_{1,1} t \quad (59)$$

$$\eta_{port,3} = \tilde{N}_3 \cos \Omega_{1,1} t = \frac{h_{0,1,1} (\tilde{v}_{1,1} - \tilde{u}_r^{(n=1)})}{8 \prod_{r=1}^{r=4} (\tilde{v}_{1,1} - \tilde{u}_r^{(n)})} \cos \Omega_{1,1} t \quad (60)$$

$$\xi_{port,4} = N_4 \cos \Omega_{1,1} t = \frac{h_{0,1,1}}{16 \prod_{s=1}^{s=4} (v_{1,1} - u_s^{(4)})} \cos \Omega_{1,1} t \quad (61)$$

$$\eta_{port,4} = \tilde{N}_4 \cos \Omega_{1,1} t = \frac{h_{0,1,1}}{16 \prod_{r=1}^{r=4} (\tilde{v}_{1,1} - \tilde{u}_r^{(4)})} \cos \Omega_{1,1} t \quad (62)$$

Solutions of the main chains coordinates of the homogeneous system for the considered example in free vibration regime are:

$$\xi_{free,k} = \sum_{s=1}^{s=4} C_s \sin k \varphi_s \cos(\omega_s t + \alpha_s), \quad k = 1, 2, 3, 4 \quad (63)$$

$$\eta_{free,k} = \sum_{r=1}^{r=4} D_r \sin k \vartheta_r \cos(\tilde{\omega}_r t + \beta_r), \quad k = 1, 2, 3, 4 \quad (64)$$

General solutions of the main chains coordinates of the homogeneous system for the considered example in coupled free and forced vibration regimes are:

$$\xi_k = \xi_{free,k} + \xi_{part,k} = \sum_{s=1}^{s=4} C_s \sin k \varphi_s \cos(\omega_s t + \alpha_s) + \xi_{part,k}, \quad k = 1, 2, 3, 4 \quad (65)$$

$$\eta_k = \eta_{free,k} + \eta_{part,k} = \sum_{r=1}^{r=4} D_r \sin k \vartheta_r \cos(\tilde{\omega}_r t + \beta_r) + \eta_{part,k}, \quad k = 1, 2, 3, 4 \quad (66)$$

or in the form

$$\xi_k = \xi_{free,k} + \xi_{part,k} = \sum_{s=1}^{s=4} C_s \sin k \varphi_s \cos(\omega_s t + \alpha_s) + N_k(v_{1,1}) \cos \Omega_{1,1} t, \quad k = 1, 2, 3, 4 \quad (67)$$

$$\eta_k = \eta_{free,k} + \eta_{part,k} = \sum_{r=1}^{r=4} D_r \sin k \vartheta_r \cos(\tilde{\omega}_r t + \beta_r) + \tilde{N}_k(\tilde{v}_{1,1}) \cos \Omega_{1,1} t, \quad k = 1, 2, 3, 4 \quad (68)$$

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

Then, taking into account that determinates  $\Delta(v_{1,1})$  and  $\tilde{\Delta}(\tilde{v}_{1,1})$  are analogous to determinants describing the frequency equations of the free vibrations of the double DNA helix chain system, which is possible to 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 (23)-(24), then we have roots of the two-system determinates,  $\Delta(v_{1,1})$  and  $\tilde{\Delta}(\tilde{v}_{1,1})$  in the forms:

$$v_{1,1}^{(s)} = \frac{J}{K} \Omega_{1,1}^{(s)} = u_s^{(n)} = \frac{J}{K} \omega_s^2 = 2 \sin^2 \frac{\varphi_s}{2} + (\mu - \kappa) \quad s = 1, 2, 3, \dots, n \quad (69)$$

$$\tilde{v}_{1,1}^{(r)} = \frac{J}{K} \tilde{\Omega}_{1,1}^{(r)} = \tilde{u}_r^{(n)} = \frac{J}{K} \tilde{\omega}_r^2 = 2 \sin^2 \frac{\vartheta_r}{2} + \mu \quad r = 1, 2, 3, \dots, n \quad (70)$$

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

$$\Delta(v_{1,1}) = 2^n \prod_{s=1}^{s=n} (v_{1,1} - u_s^{(n)}) \quad (71)$$

$$\tilde{\Delta}(\tilde{v}_{1,1}) = 2^n \prod_{r=1}^{r=n} (\tilde{v}_{1,1} - \tilde{u}_r^{(n)}) \quad (72)$$

It is possible, in the same way, to find the expressions for the amplitude of particular solutions depending on the number of degrees of freedom  $2n$ . For example, it is obvious without calculations that the 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 each of the both main chains are in the following forms:

$$N_1 = \frac{h_{0,1,1} \prod_{s=1}^{s=n-1} (v_{1,1} - u_s^{(n-1)})}{2 \prod_{s=1}^{s=n} (v_{1,1} - u_s^{(n)})} \quad \text{and} \quad \tilde{N}_1 = \frac{h_{0,1,1} \prod_{r=1}^{r=n-1} (\tilde{v}_{1,1} - \tilde{u}_r^{(n-1)})}{2 \prod_{r=1}^{r=n} (\tilde{v}_{1,1} - \tilde{u}_r^{(n)})} \quad (73)$$

$$N_2 = \frac{h_{0,1,1} \prod_{s=1}^{s=n-2} (v_{1,1} - u_s^{(n-2)})}{2^2 \prod_{s=1}^{s=n} (v_{1,1} - u_s^{(n)})} \quad \text{and} \quad \tilde{N}_2 = \frac{h_{0,1,1} \prod_{r=1}^{r=n-1} (\tilde{v}_{1,1} - \tilde{u}_r^{(n-2)})}{2^2 \prod_{r=1}^{r=n} (\tilde{v}_{1,1} - \tilde{u}_r^{(n)})} \quad (74)$$

General solutions of the main chains coordinates of the homogeneous system for the considered example in coupled free and forced vibration regime are in the following forms:

$$\xi_k = \xi_{free,k} + \xi_{part,k} = \sum_{s=1}^{s=n} C_s \sin k \varphi_s \cos(\omega_s t + \alpha_s) + \xi_{part,k}, \quad k = 1, 2, 3, \dots, n \quad (75)$$

$$\eta_k = \eta_{free,k} + \eta_{part,k} = \sum_{r=1}^{r=n} D_r \sin k \vartheta_r \cos(\tilde{\omega}_r t + \beta_r) + \eta_{part,k}, \quad k = 1, 2, 3, \dots, n \quad (76)$$

or in the form

$$\xi_k = \xi_{free,k} + \xi_{part,k} = \sum_{s=1}^{s=n} C_s \sin k \varphi_s \cos(\omega_s t + \alpha_s) + N_k(v_{1,1}) \cos \Omega_{1,1} t, \quad k = 1, 2, 3, \dots, n \quad (77)$$

$$\eta_k = \eta_{free,k} + \eta_{part,k} = \sum_{r=1}^{r=n} D_r \sin k \vartheta_r \cos(\tilde{\omega}_r t + \beta_r) + \tilde{N}_k(\tilde{v}_{1,1}) \cos \Omega_{1,1} t, \quad k = 1, 2, 3, \dots, n \quad (78)$$

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

$$\frac{2J}{K} \ddot{\xi}_k - \xi_{k+1} + 2\xi_k [1 + \mu - \kappa] - \xi_{k-1} = \begin{cases} -h_{0,2,1} \cos \Omega_{2,1} t & k = 1 \\ 0 & k \neq 1 \end{cases} \quad (79)$$

$$\frac{2J}{K} \ddot{\eta}_k - \eta_{k+1} + 2\eta_k (1 + \mu) - \eta_{k-1} = \begin{cases} h_{0,2,1} \cos \Omega_{2,1} t & k = 1 \\ 0 & k \neq 1 \end{cases}, \quad k = 1, 2, 3, \dots, n \quad (80)$$

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

#### 7.6. 4. Consideration of the forced vibration regimes of a basic DNA model - linearized Kovaleva-Manevich's DNA model-resonance and dynamical absorption

From the expressions (73) and (74), the possibilities of the occurrence of resonant regimes in eigen main chains can be considered.

For the case when the determinants (71) and (72),  $\Delta(v_{1,1}) = 2^n \prod_{s=1}^{s=n} (v_{1,1} - u_s^{(n)}) = 0$  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, we obtain two sets of external excitation frequencies for which in

the system there appears a resonant regime. But taking into account that eigen main chains have different sets of eigen circular frequencies as well as different sets of resonant circular frequencies of external excitation, then it can be inferred that if in one eigen main chain there appears a resonant regime, then there is no resonance in the other eigen main chain. This is an important fact to consider in the light of the real double DNA helix chain system.

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

$$N_1 = \frac{h_{0,1,1} \prod_{s=1}^{s=n-1} (v_{1,1} - u_s^{(n-1)})}{2 \prod_{s=1}^{s=n} (v_{1,1} - u_s^{(n)})} = 0 \quad \text{or} \quad \tilde{N}_1 = \frac{h_{0,1,1} \prod_{r=1}^{r=n-1} (\tilde{v}_{1,1} - \tilde{u}_r^{(n-1)})}{2 \prod_{r=1}^{r=n} (\tilde{v}_{1,1} - \tilde{u}_r^{(n)})} = 0 \quad (81)$$

$$N_2 = \frac{h_{0,1,1} \prod_{s=1}^{s=n-2} (v_{1,1} - u_s^{(n-2)})}{2^2 \prod_{s=1}^{s=n} (v_{1,1} - u_s^{(n)})} = 0 \quad \text{or} \quad \tilde{N}_2 = \frac{h_{0,1,1} \prod_{r=1}^{r=n-2} (\tilde{v}_{1,1} - \tilde{u}_r^{(n-2)})}{2^2 \prod_{r=1}^{r=n} (\tilde{v}_{1,1} - \tilde{u}_r^{(n)})} = 0 \quad (82)$$

and next

$$\prod_{s=1}^{s=n-1} (v_{1,1} - u_s^{(n-1)}) = 0 \quad \text{or} \quad \prod_{r=1}^{r=n-1} (\tilde{v}_{1,1} - \tilde{u}_r^{(n-1)}) = 0 \quad (83)$$

$$\prod_{s=1}^{s=n-2} (v_{1,1} - u_s^{(n-2)}) = 0 \quad \text{or} \quad \prod_{s=1}^{s=n-2} (\tilde{v}_{1,1} - \tilde{u}_s^{(n-2)}) = 0 \quad (84)$$

From the last conditions (83) and (84) we can conclude that:



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

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

*This mathematical fact is important to consider in the light of the interruption or break of the double DNA helix chain system. By choosing the frequency of external excitation force, it is possible to define the conditions of place of the dDNA breakage.*

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

In this section fractional order model of dDNA is considered. Free and forced vibrations of this type of model are discussed. Analytical solutions for main coordinates and eigen frequencies for coupled and decoupled system are given. Visualization of the main modes of free vibrations of fractional order dDNA helix chain system and corresponding partial fractional order oscillatory modes are also presented in this section.

### 7.7.1. Constitutive relation of the standard light fractional order creep element

*Basic elements* of the 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 the following coordinate  $\varphi_k$ , 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, which has the ability to resist deformation under static and dynamic conditions (see Refs. [12], [20-22], [24-34]). *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

$$P(t) = -\{c_0 x(t) + c_\alpha D_t^\alpha [x(t)]\} \quad (85)$$

where  $D_t^\alpha [\bullet]$  is operator of the  $\alpha^{th}$  derivative with respect to time  $t$  in the following form, [19]:

$$D_t^\alpha [x(t)] = \frac{d^\alpha x(t)}{dt^\alpha} = x^{(\alpha)}(t) = \frac{1}{\Gamma(1-\alpha)} \frac{d}{dt} \int_0^t \frac{x(\tau)}{(t-\tau)^\alpha} d\tau \quad (86)$$

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

### 7.7.2. The double DNA fractional order chain free vibration model on the basis of the linearized Kovaleva-Manevich's DNA model

In this section, we will define the discrete continuum mathematical pendulum chain as a system of material particles inter-coupled by *light standard coupling elements* (*elastic, hereditary or creep*) and which are, in natural state, on defined inter-distances (when coupling elements are unstressed) (see Refs. [24-33]).

We used the fractional calculus to model the system that does not have ideally elastic properties. This concept may be incorporated into the theory of aging materials. As DNA molecule is aging it loses ideally elastic properties and expresses more visco-elastic properties.

We define *discrete homogeneous multi-mathematical pendulum chain system* as a system of discrete material particles of the same masses, which can rotate/oscillate along the corresponding circles with the same radius  $\ell$  and centers on the one horizontal line. The entire system is in the vertical plane and the gravitational field (see Fig. 6 and 7).

The number of degrees of freedom of each of these multi-pendulum chains is equal to the number of material particles in it, since we accept the previously defined character of the system.

Furthermore, we introduce the hypotheses about the homogeneity of discrete continual chain, about small deformations of light standard coupling elements, and that displacements of material particles are small.

Also, we introduce the hypothesis that the homogenous discrete continuum, chain, was in natural, non-stressed state, before the initial moment of motion observation i.e. that light standard coupling elements do not have a prehistory or memory of stress-strain state. With these hypotheses, we will direct our research to the dynamics of chain-like homogenous multi-pendulum systems.

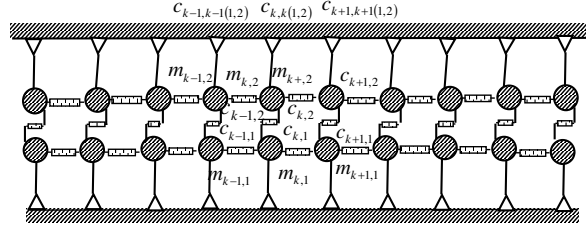


Fig. 6. Double DNK fractional order chain helix in the form of multi-pendulum model with free ends

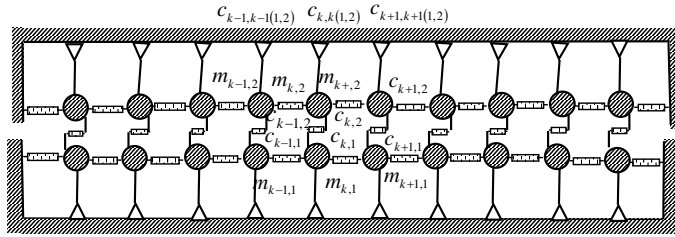


Fig.7. Double DNK fractional order chain helix d model in the form of multi-pendulum system with fixed ends

For the double DNA fractional order chain model on the basis of the linearized Kovaleva-Manevich's DNA model, we accept two chains as presented in Fig. 6 or 7, in the form of the double chain fractional order system containing two coupled multi-pendulum subsystems, in which the corresponding material particles of the corresponding multi-pendulum chains are coupled by one standard light fractional order element with stress-strain constitutive relations in the form (85).

Then, we can use the system (3) of the coupled linear differential equations extended by terms containing fractional order differential operators in the form (85). Then, we can write the corresponding system of the fractional order differential coupled equations for free fractional order vibrations of the double DNA fractional order chain system in the form:

$$\begin{aligned}
 & \mathbf{J}_{k,1} \ddot{\varphi}_{k,1} - \frac{K_{k,1}}{2} [(\varphi_{k+1,1} - \varphi_{k,1}) - (\varphi_{k,1} - \varphi_{k-1,1})] - \frac{K_{k,1,\sigma}}{2} D_t^\sigma [(\varphi_{k+1,1} - \varphi_{k,1}) - (\varphi_{k,1} - \varphi_{k-1,1})] + \\
 & \quad + K_{\alpha\beta} r_\alpha (r_\alpha - r_\beta) \varphi_{k,1} - \\
 & \quad - K_{\alpha\beta} - \frac{1}{4} \left( 1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}} \right) (r_\alpha - r_\beta)^2 (\varphi_{k,1} - \varphi_{k,2}) - K_{\alpha\beta,\sigma} \frac{1}{4} \left( 1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}} \right) (r_\alpha - r_\beta)^2 D_t^\sigma [(\varphi_{k,1} - \varphi_{k,2})] = 0 \\
 & \mathbf{J}_{k,2} \ddot{\varphi}_{k,2} - \frac{K_{k,2}}{2} [(\varphi_{k+1,2} - \varphi_{k,2}) - (\varphi_{k,2} - \varphi_{k-1,2})] - \frac{K_{k,2,\sigma}}{2} D_t^\sigma [(\varphi_{k+1,2} - \varphi_{k,2}) - (\varphi_{k,2} - \varphi_{k-1,2})] + \\
 & \quad + K_{\alpha\beta} r_\alpha (r_\alpha - r_\beta) \varphi_{k,2} + \\
 & \quad + K_{\alpha\beta} \frac{1}{4} \left( 1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}} \right) (r_\alpha - r_\beta)^2 (\varphi_{k,1} - \varphi_{k,2}) + K_{\alpha\beta,\sigma} \frac{1}{4} \left( 1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}} \right) (r_\alpha - r_\beta)^2 D_t^\sigma [(\varphi_{k,1} - \varphi_{k,2})] = 0
 \end{aligned} \tag{87}$$

where  $K_{k,1,\sigma}$ ,  $K_{k,2,\sigma}$ ,  $K_{\alpha\beta,\sigma}$  and  $K_{\alpha\beta,\sigma}$  are material constants of the double DNA fractional order chain model coupling elements pressing fractional order creep properties. The previous system is possible to rewrite in the following form:

$$\begin{aligned}
& \frac{2\mathbf{J}_{k,1}}{K_{k,1}} \ddot{\varphi}_{k,1} - [(\varphi_{k+1,1} - \varphi_{k,1}) - (\varphi_{k,1} - \varphi_{k-1,1})] + \frac{K_{k,1,\sigma}}{K_{k,1}} D_t^\sigma [(\varphi_{k+1,1} - \varphi_{k,1}) - (\varphi_{k,1} - \varphi_{k-1,1})] + \\
& \quad + \frac{2K_{\alpha\beta} r_\alpha (r_\alpha - r_\beta)}{K_{k,1}} \varphi_{k,1} - \\
& \quad - \frac{K_{\alpha\beta}}{2K_{k,1}} \left(1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}}\right) (r_\alpha - r_\beta)^2 (\varphi_{k,1} - \varphi_{k,2}) - \frac{K_{\alpha\beta,\sigma}}{2K_{k,1}} \left(1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}}\right) (r_\alpha - r_\beta)^2 D_t^\sigma [(\varphi_{k,1} - \varphi_{k,2})] = 0 \\
& \frac{2\mathbf{J}_{k,2}}{K_{k,2}} \ddot{\varphi}_{k,2} - [(\varphi_{k+1,2} - \varphi_{k,2}) - (\varphi_{k,2} - \varphi_{k-1,2})] - \frac{K_{k,2,\sigma}}{K_{k,2}} D_t^\sigma [(\varphi_{k+1,2} - \varphi_{k,2}) - (\varphi_{k,2} - \varphi_{k-1,2})] + \\
& \quad + \frac{2K_{\alpha\beta} r_\alpha (r_\alpha - r_\beta)}{K_{k,2}} \varphi_{k,2} + \\
& \quad + \frac{K_{\alpha\beta}}{2K_{k,2}} \left(1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}}\right) (r_\alpha - r_\beta)^2 (\varphi_{k,1} - \varphi_{k,2}) + \frac{K_{\alpha\beta,\sigma}}{2K_{k,2}} \left(1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}}\right) (r_\alpha - r_\beta)^2 D_t^\sigma [(\varphi_{k,1} - \varphi_{k,2})] = 0
\end{aligned} \tag{88}$$

As our intention is to use the 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  $K_{\alpha\beta,\sigma} = K_{\alpha\beta,\sigma}$ . Then, taking into account that we introduce the notation (14), (15) and (16), then the previous system of coupled fractional order differential equations is possible to write in the following form:

$$\begin{aligned}
& \frac{2\mathbf{J}}{K} \ddot{\varphi}_{k,1} - [(\varphi_{k+1,1} - \varphi_{k,1}) - (\varphi_{k,1} - \varphi_{k-1,1})] - \kappa_\sigma D_t^\sigma [(\varphi_{k+1,1} - \varphi_{k,1}) - (\varphi_{k,1} - \varphi_{k-1,1})] + \\
& \quad + 2\mu\varphi_{k,1} - \kappa(\varphi_{k,1} - \varphi_{k,2}) - \kappa\kappa_\sigma D_t^\sigma [(\varphi_{k,1} - \varphi_{k,2})] = 0 \\
& \frac{2\mathbf{J}_{k,2}}{K_{k,2}} \ddot{\varphi}_{k,2} - [(\varphi_{k+1,2} - \varphi_{k,2}) - (\varphi_{k,2} - \varphi_{k-1,2})] - \kappa_\sigma D_t^\sigma [(\varphi_{k+1,2} - \varphi_{k,2}) - (\varphi_{k,2} - \varphi_{k-1,2})] + \\
& \quad + 2\mu\varphi_{k,2} + \kappa(\varphi_{k,1} - \varphi_{k,2}) + \kappa\kappa_\sigma D_t^\sigma [(\varphi_{k,1} - \varphi_{k,2})] = 0
\end{aligned} \tag{89}$$

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

Using change of the generalized independent angular coordinates  $\varphi_{k,1}$  and  $\varphi_{k,2}$  for the  $k$ -th bases of both chains in the double DNA helix chain model into the following new coordinates  $\xi_k$  and  $\eta_k$ , as relations (5) in section 6 in the form:  $\xi_k = \varphi_{k,1} - \varphi_{k,2}$  and  $\eta_k = \varphi_{k,1} + \varphi_{k,2}$ , the previous system of ordinary differential fractional order equations (89) obtains the following form:

$$\frac{2\mathbf{J}}{K} \ddot{\xi}_k - \xi_{k-1} + 2(1 + \mu - \kappa)\xi_k - \xi_{k+1} = -\kappa_\sigma D_t^\sigma [-\xi_{k-1} + 2(1 - \kappa)\xi_k - \xi_{k+1}] \tag{90}$$

$$\frac{2\mathbf{J}}{K} \ddot{\eta}_k - \eta_{k-1} + 2(1 + \mu)\eta_k - \eta_{k+1} = -\kappa_\sigma D_t^\sigma [-\eta_{k-1} + 2\eta_k - \eta_{k+1}], \quad k = 1, 2, 3, \dots, n \tag{91}$$

The first series (89) of differential fractional order equations of the previous system (90)-(91) is decoupled and independent with relations of the second series (91) of the fractional order differential equations. *Then, we can conclude that new coordinates of  $\xi_k$  and  $\eta_k$  are the main chain coordinates of the double DNA fractional order chains and that we obtain two fictive decoupled and independent single eigen fractional order chains of the double DNA fractional order model. This is a fundamental conclusion as an important property of the fractional order homogeneous model of vibrations in a double DNA fractional order homogeneous helix.*

The systems of fractional order differential equations (90)-(91) contain two separate subsystems of fractional order differential equations expressed by *coordinates of  $\xi_k$  and  $\eta_k$  which are the main coordinates of a double DNA fractional order chain helix and separate DNA fractional order model into two independent fractional order chains.*

### 7.7.3. Analytical solutions of the subsystems of the main chains fractional order differential equations for free fractional order vibrations

We solve the previous subsystems (90) and (91) of fractional order differential equations using the Laplace transformations (for detail see Appendix E.3). After applying the Laplace transformations of the previous systems (90) and (91) of fractional order differential equations with fractional order derivative and having in mind that we introduced notations  $\mathcal{L}\{\xi_k(t)\}$  and  $\mathcal{L}\{\eta_k(t)\}$  for the Laplace transformations of unknown normal chain coordinates  $\xi_k$  and  $\eta_k$ , as well as that:

$$\mathcal{L}\left\{\frac{d^\sigma \xi_k(t)}{dt^\sigma}\right\} = p^\sigma \mathcal{L}\{\xi_k(t)\} - \frac{d^{\sigma-1} \xi_k(t)}{dt^{\sigma-1}} \Big|_{t=0} = p^\sigma \mathcal{L}\{\xi_k(t)\} \quad (92)$$

$$\mathcal{L}\left\{\frac{d^\sigma \eta_k(t)}{dt^\sigma}\right\} = p^\sigma \mathcal{L}\{\eta_k(t)\} - \frac{d^{\sigma-1} \eta_k(t)}{dt^{\sigma-1}} \Big|_{t=0} = p^\sigma \mathcal{L}\{\eta_k(t)\} \quad (93)$$

and also having in mind that we accepted the hypothesis that the initial conditions of fractional order derivatives of the system are given using:  $\frac{d^{\sigma-1} \xi_k(t)}{dt^{\sigma-1}} \Big|_{t=0} = 0$  and  $\frac{d^{\sigma-1} \eta_k(t)}{dt^{\sigma-1}} \Big|_{t=0} = 0$  as well as that:

$$\mathcal{L}\left\{\frac{d^2 \xi_k(t)}{dt^2}\right\} = p^2 \mathcal{L}\{\xi_k(t)\} - [p \xi_{0k} + \dot{\xi}_{0k}], \quad (94)$$

$$\mathcal{L}\left\{\frac{d^2 \eta_k(t)}{dt^2}\right\} = p^2 \mathcal{L}\{\eta_k(t)\} - [p \eta_{0k} + \dot{\eta}_{0k}], \quad (95)$$

where  $\xi_{0k}$  and  $\dot{\xi}_{0k}$  as well as  $\eta_{0k}$  and  $\dot{\eta}_{0k}$  are defined by initial conditions of the system material particle dynamics in the chains, we can write the following system of the algebraic equations according to the unknown Laplace transforms  $\mathcal{L}\{\xi_k(t)\}$  and  $\mathcal{L}\{\eta_k(t)\}$  of unknown normal chain coordinates  $\xi_k$  and  $\eta_k$ :

$$\frac{\left[ \frac{2\mathbf{J}}{K} p^2 + 2\mu - 2\kappa(1 + \kappa_\sigma p^\sigma) \right]}{[1 + \kappa_\sigma p^\sigma]} \mathcal{L}\{\xi_k(t)\} - \mathcal{L}\{\xi_{k-1}\} + 2\mathcal{L}\{\xi_k(t)\} - \mathcal{L}\{\xi_{k+1}\} = \frac{2\mathbf{J}}{K} \frac{[p \xi_{0k} + \dot{\xi}_{0k}]}{[1 + \kappa_\sigma p^\sigma]} \quad (96)$$

$$\frac{\left( p^2 \frac{2\mathbf{J}}{K} + 2\mu \right)}{(1 + \kappa_\sigma p^\sigma)} \mathcal{L}\{\eta_k\} - \mathcal{L}\{\eta_{k-1}\} + 2\mathcal{L}\{\eta_k\} - \mathcal{L}\{\eta_{k+1}\} = \frac{2\mathbf{J}}{K} \frac{[p \eta_{0k} + \dot{\eta}_{0k}]}{(1 + \kappa_\sigma p^\sigma)} \quad (97)$$

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

$$-\mathcal{L}\{\xi_{k-1}\} + (2 + \nu) \mathcal{L}\{\xi_k(t)\} - \mathcal{L}\{\xi_{k+1}\} = \frac{[p \xi_{0k} + \dot{\xi}_{0k}]}{\omega_0^2 [1 + \kappa_\sigma p^\sigma]} \quad (98)$$

$$-\mathcal{L}\{\eta_{k-1}\} + (2 + u) \mathcal{L}\{\eta_k\} - \mathcal{L}\{\eta_{k+1}\} = \frac{[p \eta_{0k} + \dot{\eta}_{0k}]}{\omega_0^2 (1 + \kappa_\sigma p^\sigma)} \quad (99)$$

Taking into account that at initial moment we have:  $\xi_{0k} = 0, k \neq 1$  and  $\dot{\xi}_{0k} = 0, k \neq 1$  as well as  $\eta_{0k} = 0, k \neq 1$  and  $\dot{\eta}_{0k} = 0, k \neq 1$  the previous equations obtain the following form:

$$-\mathcal{L}\{\xi_{k-1}\} + (2 + \nu) \mathcal{L}\{\xi_k(t)\} - \mathcal{L}\{\xi_{k+1}\} = \begin{cases} h_\xi(p, \xi_{01}, \dot{\xi}_{01}) & k = 1 \\ 0 & k \neq 1 \end{cases} \quad (100)$$

$$-\mathcal{L}\{\eta_{k-1}\} + (2 + \nu) \mathcal{L}\{\eta_k(t)\} - \mathcal{L}\{\eta_{k+1}\} = \begin{cases} h_\eta(p, \eta_{01}, \dot{\eta}_{01}) & k = 1 \\ 0 & k \neq 1 \end{cases} \quad (101)$$

where

$$\nu = \frac{[p^2 + 2\mu\omega_0^2]}{\omega_0^2 [1 + \kappa_\sigma p^\sigma]} - 2\kappa, \quad u = \frac{[p^2 + 2\mu\omega_0^2]}{\omega_0^2 [1 + \kappa_\sigma p^\sigma]}, \quad \omega_0^2 = \frac{K}{2\mathbf{J}} \quad (102)$$

$$h_{\xi}(p, \xi_{0k}, \dot{\xi}_{0k}) = \frac{[p\xi_{0k} + \dot{\xi}_{0k}]}{\omega_0^2[1 + \kappa_{\sigma} p^{\sigma}]}, \quad h_{\eta}(p, \eta_{0k}, \dot{\eta}_{0k}) = \frac{[p\eta_{0k} + \dot{\eta}_{0k}]}{\omega_0^2(1 + \kappa_{\sigma} p^{\sigma})} \quad (103)$$

Both subsystems (100)-(101) are of the same form and it is enough to solve one of the subsystems and applying the analogy it is easy to solve other subsystem of fractional order differential equations. For that reason, we can use the method proposed in the papers [30] and [31].

Determinates of the previous algebraic subsystem (100) as well as (101) are in the same form as presented in the following form:

$$\Delta_N(v) = \begin{vmatrix} 2+v & -1 & & \\ -1 & 2+v & & \\ & & 2+v & -1 \\ & & -1 & 2+v \end{vmatrix}_{N \times N} \neq 0 \quad (104)$$

Introducing the notation (102) and (103), for the determinants  $\tilde{\Delta}_{(k)}(v, h_{\xi})$ , we can write the following forms:

$$\tilde{\Delta}_{(1)}(v, h_{\xi}) = \begin{vmatrix} h_{\xi}(p, \xi_{01}, \dot{\xi}_{01}) & -1 & & \\ 0 & 2+v & & \\ & & 2+v & -1 \\ & & -1 & 2+v \end{vmatrix}_N = h_{\xi}(p, \xi_{01}, \dot{\xi}_{01}) \Delta_{(N-1)}(v); \quad (105)$$

$$\tilde{\Delta}_{(2)}(v, h_{\xi}) = \begin{vmatrix} 2+v & h_{\xi}(p, \xi_{01}, \dot{\xi}_{01}) & & \\ -1 & 0 & -1 & \\ & 0 & 2+v & -1 \\ & & -1 & 2+v \end{vmatrix}_N = (-1)^{2+1} h_{\xi}(p, \xi_{01}, \dot{\xi}_{01}) \Delta_{N-2}(v) \neq 0 \quad (106)$$

$$\tilde{\Delta}_{(3)}(v, h_{\xi}) = \begin{vmatrix} 2+v & -1 & h_{\xi}(p, \xi_{01}, \dot{\xi}_{01}) & & \\ -1 & 2+v & 0 & & \\ & -1 & 0 & -1 & \\ & & 0 & 2+v & -1 \\ & & & -1 & 2+v & -1 \\ & & & & -1 & 2+v \end{vmatrix}_N = (-1)^{3+1+1} h_{\xi}(p, \xi_{01}, \dot{\xi}_{01}) \Delta_{N-3}(v) \quad (107)$$

$$\tilde{\Delta}_{(4)}(v, h_{\xi}) = \begin{vmatrix} 2+v & -1 & 0 & h_{\xi}(p, \xi_{01}, \dot{\xi}_{01}) & & \\ -1 & 2+v & -1 & & & \\ & -1 & 2+v & 0 & & \\ & & -1 & 0 & -1 & \\ & & & 0 & 2+v & -1 \\ & & & & -1 & 2+v & -1 \\ & & & & & -1 & 2+v \end{vmatrix}_N = (-1)^{4+1+1+1} h_{\xi}(p, \xi_{01}, \dot{\xi}_{01}) \Delta_{N-4}(v) \quad (108)$$

$$\tilde{\Delta}_{(N)}(v, h_{\xi}) = \begin{vmatrix} 2+v & -1 & & & & & h_{\xi}(p, \xi_{01}, \dot{\xi}_{01}) \\ -1 & 2+v & -1 & & & & 0 \\ & -1 & 2+v & -1 & & & 0 \\ & & -1 & 2+v & -1 & & 0 \\ & & & -1 & 2+v & -1 & 0 \\ & & & & -1 & 2+v & 0 \\ & & & & & -1 & 0 \end{vmatrix}_N = (-1)^{2N-1} h_{\xi}(p, \xi_{01}, \dot{\xi}_{01}) \quad (109)$$

To solve the system of the algebraic non-homogeneous equations (100) or (101) with respect to unknown Laplace transforms  $\mathcal{L}\{\xi_k(t)\}$  or  $\mathcal{L}\{\eta_k(t)\}$  of the time function main chain coordinates  $\xi_k(t)$  and  $\eta_k(t)$ ,

unknown normal chain coordinates of the system main chains, we can use the Cramer approach and we can write:

$$L\{\xi_k(t)\}_N = \frac{\tilde{\Delta}_{(k)}(v, h_\xi)}{\Delta_N(v)} = \frac{(-1)^{2k-1} h_\xi(p, \xi_{0k}, \dot{\xi}_{0k}) \Delta_{N-k}(v)}{\Delta_N(v)}. \quad (110)$$

$$L\{\eta_k(t)\}_N = \frac{\tilde{\Delta}_{(k)}(u, h_\eta)}{\Delta_N(u)} = \frac{(-1)^{2k-1} h_\eta(p, \eta_{0k}, \eta_{0k}) \Delta_{N-k}(u)}{\Delta_N(u)}. \quad (111)$$

Let us first analyze the solution and characteristic equations of the homogenous subsystem as basic subsystems of the algebraic non-homogeneous equations (100) or (101) with respect to unknown Laplace transforms  $L\{\xi_k(t)\}$  or  $L\{\eta_k(t)\}$  of the time function main coordinate  $\xi_k(t)$  and  $\eta_k(t)$ , unknown normal chain coordinates of the system main chains. These two of the homogenous subsystem as basic subsystems of the algebraic non-homogeneous equations (100) or (101) are in the following forms:

$$-L\{\xi_{k-1}\} + (2+v)L\{\xi_k(t)\} - L\{\xi_{k+1}\} = 0 \quad (112)$$

$$-L\{\eta_{k-1}\} + (2+u)L\{\eta_k\} - L\{\eta_{k+1}\} = 0 \quad (113)$$

The solution of such a subsystem of algebraic homogenous equations (112) or (113), from which we obtain a series of determinants, can be obtained using the trigonometric method (see [48] or [27] ) or by obtaining the recurrent formulas. Let us use the trigonometric method and, for that reason, the solutions are assumed in the following forms:

$$L\{\xi_k(t)\} = N \sin k\phi, \quad (114)$$

and introducing into the previous subsystems (112) or (113), we have that:  $v = 2(\cos \phi - 1)$  and  $u = 2(\cos \phi - 1)$ , as well as the following two characteristic equations:

$$v = \frac{[p^2 + 2\mu\omega_0^2]}{\omega_0^2[1 + \kappa_\sigma p^\sigma]} - 2\kappa = 2(\cos \phi - 1), \quad u = \frac{[p^2 + 2\mu\omega_0^2]}{\omega_0^2[1 + \kappa_\sigma p^\sigma]} = 2(\cos \phi - 1) \quad (115)$$

or in the forms:

a\* for the first main chain with a set of main chain coordinates  $\xi_k(t)$ :

$$p^2 + 2\mu\omega_0^2 + 2\omega_0^2(1 + \kappa_\sigma p^\sigma)(1 - 2\kappa - \cos \phi_s) = 0, \quad s = 1, 2, 3, \dots, n \quad (116)$$

b\* for the second main chain with main chain coordinates  $\eta_k(t)$ :

$$p^2 + 2\mu\omega_0^2 + 2\omega_0^2(1 + \kappa_\sigma p^\sigma)(1 - \cos \phi_s) = 0, \quad s = 1, 2, 3, \dots, n \quad (117)$$

where  $\phi_s$  depends on the boundary conditions on the ends of the corresponding system main chain.

Based on the previous two characteristic equations (116) and (117), the subsystem characteristic determinants of the system can be written in the following form:

a\* for the first main chain with a set of main chain coordinates  $\xi_k(t)$ :

$$\Delta_N = \prod_{s=1}^{s=N_s} [p^2 + 2\mu\omega_0^2 + 2\omega_0^2(1 + \kappa_\sigma p^\sigma)(1 - \kappa - \cos \phi_s)] \neq 0, \quad (118)$$

b\* for the second main chain with main chain coordinates  $\eta_k(t)$ :

$$\Delta_N = \prod_{s=1}^{s=N_x} \left[ p^2 + 2\mu\omega_0^2 + 2\omega_0^2(1 + \kappa_\sigma p^\sigma)(1 - \cos \varphi_s) \right] \neq 0 \quad (119)$$

from which we obtain a series of determinants when we replace one of the columns with a column of free terms on the right side of the fractional order differential equations in system (111) as well as (112), as it is shown by the calculus in (91) - (107). Based on that, for given initial conditions for each of the particle coordinates of material particles in the corresponding chain, we can obtain the following determinants corresponding to a certain column (and to an unknown Laplace transformation  $\mathcal{L}\{\xi_k(t)\}$  of the coordinate  $\xi_k(t)$ ) in the following forms:

$$\begin{aligned} \tilde{\Delta}_{(1)}(v, h_\xi) &= h_\xi(p, \xi_{01}, \dot{\xi}_{01}) \Delta_{(N-1)}(v); \\ \tilde{\Delta}_{(2)}(v, h_\xi) &= (-1)^{2+1} h_\xi(p, \xi_{01}, \dot{\xi}_{01}) \Delta_{N-2}(v); \\ \tilde{\Delta}_{(3)}(v, h_\xi) &= (-1)^{3+1+1} h_\xi(p, \xi_{01}, \dot{\xi}_{01}) \Delta_{N-3}(v) \\ \tilde{\Delta}_{(4)}(v, h_\xi) &= (-1)^{4+1+1+1} h_\xi(p, \xi_{01}, \dot{\xi}_{01}) \Delta_{N-4}(v) \\ \tilde{\Delta}_{(5)}(v, h_\xi) &= (-1)^{5+1+1+1+1} h_\xi(p, \xi_{01}, \dot{\xi}_{01}) \Delta_{N-5}(v) \\ &\dots\dots\dots \\ \tilde{\Delta}_{(m)}(v, h_\xi) &= (-1)^{2m-1} h_\xi(p, \xi_{01}, \dot{\xi}_{01}) \Delta_{N-m}(v, h_\xi); \dots\dots\dots \end{aligned} \quad (120)$$

1.a\* for the first main chain with a set of main chain coordinates  $\xi_k(t)$  the determinate of the subsystem is:

$$\Delta_{N-k}(p) = \prod_{s=1}^{s=N-k} \left[ p^2 + 2\mu\omega_0^2 + 2\omega_0^2(1 + \kappa_\sigma p^\sigma)(1 - \kappa - \cos \varphi_s) \right] \neq 0 \quad (121)$$

1.b\* for the second main chain with main chain coordinates  $\eta_k(t)$  the determinate of the subsystem is:

$$\Delta_{N-k}(p) = \prod_{s=1}^{s=N-k} \left[ p^2 + 2\mu\omega_0^2 + 2\omega_0^2(1 + \kappa_\sigma p^\sigma)(1 - \cos \varphi_s) \right] \neq 0 \quad (122)$$

2.a\* for the first main chain with a set of main chain coordinates  $\xi_k(t)$  the particular determinates of the subsystem are:

$$\begin{aligned} \tilde{\Delta}_{(1)}(p, \xi_{01}, \dot{\xi}_{01}, h_\xi) &= h_\xi(p, \xi_{01}, \dot{\xi}_{01}) \prod_{s=1}^{s=N-1} \left[ p^2 + 2\mu\omega_0^2 + 2\omega_0^2(1 + \kappa_\sigma p^\sigma)(1 - \kappa - \cos \varphi_s) \right] \neq 0 \\ \tilde{\Delta}_{(2)}(p, \xi_{01}, \dot{\xi}_{01}, h_\xi) &= (-1)^3 h_\xi(p, \xi_{01}, \dot{\xi}_{01}) \prod_{s=1}^{s=N-2} \left[ p^2 + 2\mu\omega_0^2 + 2\omega_0^2(1 + \kappa_\sigma p^\sigma)(1 - \kappa - \cos \varphi_s) \right] \neq 0 \\ &\dots\dots\dots \\ \tilde{\Delta}_{(k)}(p, \xi_{01}, \dot{\xi}_{01}, h_\xi) &= (-1)^{2k-1} h_\xi(p, \xi_{01}, \dot{\xi}_{01}) \prod_{s=1}^{s=N-k} \left[ p^2 + 2\mu\omega_0^2 + 2\omega_0^2(1 + \kappa_\sigma p^\sigma)(1 - \kappa - \cos \varphi_s) \right] \neq 0 \\ \tilde{\Delta}_{(N)}(p, \xi_{01}, \dot{\xi}_{01}, h_\xi) &= (-1)^{N_x + N_x - 1} h_\xi(p, \xi_{01}, \dot{\xi}_{01}) \Delta_{N-N} = (-1)^{2N_x - 1} h_\xi(p, \xi_{0k}, \dot{\xi}_{0k}) \Delta_0 = (-1)^{2N-1} h_\xi(p, \xi_{0k}, \dot{\xi}_{0k}) \end{aligned} \quad (123)$$

2.b\* for the second main chain with main chain coordinates  $\eta_k(t)$   $\xi_k(t)$  the particular determinates of the subsystem are:



$$\begin{aligned}
& \tilde{\Delta}_{(1)}(p, \eta_{01}, \dot{\eta}_{01}, h_\eta) = h_\eta(p, \eta_{01}, \dot{\eta}_{01}) \prod_{s=1}^{s=N-1} [p^2 + 2\mu\omega_0^2 + 2\omega_0^2(1 + \kappa_\sigma p^\sigma)(1 - \cos \varphi_s)] \neq 0 \\
& \tilde{\Delta}_{(2)}(p, \eta_{01}, \dot{\eta}_{01}, h_\eta) = (-1)^3 h_\eta(p, \eta_{01}, \dot{\eta}_{01}) \prod_{s=1}^{s=N-2} [p^2 + 2\mu\omega_0^2 + 2\omega_0^2(1 + \kappa_\sigma p^\sigma)(1 - \cos \varphi_s)] \neq 0 \\
& \dots\dots\dots \\
& \tilde{\Delta}_{(k)}(p, \eta_{01}, \dot{\eta}_{01}, h_\eta) = (-1)^{2k-1} h_\eta(p, \eta_{01}, \dot{\eta}_{01}) \prod_{s=1}^{s=N-k} [p^2 + 2\mu\omega_0^2 + 2\omega_0^2(1 + \kappa_\sigma p^\sigma)(1 - \cos \varphi_s)] \neq 0 \\
& , \eta_{0k}, \dot{\eta}_{0k}, h_\eta) = (-1)^{N+N_x-1} h_\eta(p, \eta_{0k}, \dot{\eta}_{0k}) \Delta_{N-N} = (-1)^{2N_x-1} h_\eta(p, \eta_{01}, \dot{\eta}_{01}) \Delta_0 = (-1)^{2N-1} h_\eta(p, \eta_{01}, \dot{\eta}_{01})
\end{aligned} \tag{124}$$

Based on these previous discoveries, we can deduce the following expressions for the unknown Laplace transformations  $\mathcal{L}\{\xi_k(t)\}$  or  $\mathcal{L}\{\eta_k(t)\}$  of the time function main chain coordinates  $\xi_k(t)$  and  $\eta_k(t)$ , unknown normal chain coordinates of the sub-system main chains:

3.a\* the Laplace transformations  $L\{\xi_k(t)\}$  of the time function main chain coordinate  $\xi_k(t)$  for the first main chain with a set of main chain coordinates  $\xi_k(t)$  are:

$$\mathbb{L}_{\{\xi_k(t)\}} = \frac{P_{\xi_{01}} + \dot{\xi}_{01}}{\omega_0^2(1 + \kappa_\sigma p^\sigma)} \cdot \frac{(-1)^{2k-1} \prod_{s=1}^{s=N-k} [p^2 + 2\mu\omega_0^2 + 2\omega_0^2(1 + \kappa_\sigma p^\sigma)(1 - \kappa - \cos \varphi_s)]}{\prod_{s=1}^{s=N} [p^2 + 2\mu\omega_0^2 + 2\omega_0^2(1 + \kappa_\sigma p^\sigma)(1 - \kappa - \cos \varphi_s)]}, \quad (125)$$

3.b\* the Laplace transformations  $\mathcal{L}\{\eta_k(t)\}$  for the second main chain with main chain coordinates  $\eta_k(t)$  for the first main chain with a set of main chain coordinates  $\eta_k(t)$  are:

$$\mathbb{L}\{\eta_k(t)\} = \frac{p\eta_{01} + \dot{\eta}_{01}}{\omega_0^2(1 + \kappa_\sigma p^\sigma)} \cdot \frac{(-1)^{2k-1} \prod_{s=1}^{s=N-k} [p^2 + 2\mu\omega_0^2 + 2\omega_0^2(1 + \kappa_\sigma p^\sigma)(1 - \cos\varphi_s)]}{\prod_{s=1}^{s=N} [p^2 + 2\mu\omega_0^2 + 2\omega_0^2(1 + \kappa_\sigma p^\sigma)(1 - \cos\varphi_s)]}, k = 1, 2, 3, \dots, N \quad (126)$$

The previous solutions for the unknown Laplace transformations  $\mathcal{L}\{\xi_k(t)\}$  or  $\mathcal{L}\{\eta_k(t)\}$  of the time function main chain coordinates  $\xi_k(t)$  and  $\eta_k(t)$ , the unknown normal chain coordinates of the sub-system main chains can be written in the following form:

4.a\* the Laplace transformations  $\mathcal{L}\{\xi_k(t)\}$  of the time function main chain coordinates  $\xi_k(t)$  for the first main chain with a set of main chain coordinates  $\xi_k(t)$  are:

$$\mathbb{L}\{\xi_k(t)\} = \frac{1}{\omega_0^2} \left( \xi_{01} + \frac{\dot{\xi}_{01}}{p} \right) \frac{1}{p^{2N+1}} \frac{1}{(1 + \kappa_\sigma p^\sigma)} \cdot \frac{(-1)^{2k-1} \prod_{s=1}^{s=N-k} \left[ p^2 + 2\mu\omega_0^2 + 2\omega_0^2(1 + \kappa_\sigma p^\sigma)(1 - \kappa - \cos\varphi_s) \right]}{\prod_{s=1}^{s=N} \left\{ 1 + \frac{2\omega_0^2}{p^2} \left[ \mu + (1 + \kappa_\sigma p^\sigma)(1 - \kappa - \cos\varphi_s) \right] \right\}}$$

$$k = 1, 2, 3, \dots, N \quad (127)$$

4.b\* the Laplace transformations  $\mathcal{L}\{\eta_k(t)\}$  for the second main chain with main chain coordinates  $\eta_k(t)$  for the first main chain with a set of main chain coordinates  $\eta_k(t)$  are:

$$\mathcal{L}\{\eta_k(t)\} = \frac{1}{\omega_0^2} \left( \eta_{01} + \frac{\dot{\eta}_{01}}{p} \right) \frac{1}{p^{2N+1}} \frac{1}{(1 + \kappa_\sigma p^\sigma)} \cdot \frac{(-1)^{2k-1} \prod_{s=1}^{s=N-k} [p^2 + 2\mu\omega_0^2 + 2\omega_0^2(1 + \kappa_\sigma p^\sigma)(1 - \cos \varphi_s)]}{\prod_{s=1}^{s=N} \left\{ 1 + \frac{2\omega_0^2}{p^2} [\mu + (1 + \kappa_\sigma p^\sigma)(1 - \cos \varphi_s)] \right\}}$$

$$k = 1, 2, 3, \dots, N \quad (128)$$

5.a\* for the first main chain with a set of main chain coordinates  $\xi_k(t)$ :

$$\mathcal{L}\{\xi_k(t)\} = \frac{1}{\omega_0^2} \left( \xi_{01} + \frac{\dot{\xi}_{01}}{p} \right) \frac{1}{p^{2N-2k+1}} \frac{1}{(1 + \kappa_\sigma p^\sigma)} \cdot \frac{(-1)^{2k-1}}{\prod_{s=N-(k-1)}^{s=N} \left\{ 1 + \frac{2\omega_0^2}{p^2} [\mu + (1 + \kappa_\sigma p^\sigma)(1 - \cos \varphi_s)] \right\}},$$

$$k = 1, 2, 3, \dots, N \quad (129)$$

5.b\* for the second main chain with main chain coordinates  $\eta_k(t)$ :

$$\mathcal{L}\{\eta_k(t)\} = \frac{1}{\omega_0^2} \left( \eta_{01} + \frac{\dot{\eta}_{01}}{p} \right) \frac{1}{p^{2N-2k+1}} \frac{1}{(1 + \kappa_\sigma p^\sigma)} \cdot \frac{(-1)^{2k-1}}{\prod_{s=N-(k-1)}^{s=N} \left\{ 1 + \frac{2\omega_0^2}{p^2} [\mu + (1 + \kappa_\sigma p^\sigma)(1 - \cos \varphi_s)] \right\}}$$

$$k = 1, 2, 3, \dots, N \quad (130)$$

After developing the binomials into series of previous particular solutions, it is easy to obtain time solutions in the form of the series with respect to time (see Appendix E.3-E.4).

#### 7.7.4. Main coordinates of the fractional order double DNA helix chain system and corresponding partial fractional order oscillators

Starting from two subsystems of the main eigen chain fractional order differential equations (90)-(91) and the corresponding basic linear subsystems:

$$\frac{2\mathbf{J}}{K} \ddot{\xi}_k - \xi_{k-1} + 2\xi_k - \xi_{k+1} + 2\mu\xi_k - 2\kappa\xi_k = 0 \quad (131)$$

$$\frac{2\mathbf{J}}{K} \ddot{\eta}_k - \eta_{k-1} + 2\eta_k - \eta_{k+1} + 2\mu\eta_k = 0, \quad k = 1, 2, 3, \dots, n \quad (132)$$

we can find two subsystems of the corresponding independent partial fractional order oscillators. For that reason, we applied trigonometric method (see [48], and [24-27]) and introduce into the previous subsystem (59) the following assumed solutions:

$$\xi_k(t) = A_k \cos(\omega t + \alpha) \quad (133)$$

where  $A_k$  is unknown amplitudes, and  $\omega$  is frequency, and  $\alpha$  is phase. After introducing the notation:

$$u = 2 \left( \frac{2\mathbf{J}}{K} \omega^2 + \kappa - \mu \right) \quad (134)$$

we obtain the following system of the homogeneous algebraic equations:

$$-A_{k-1} + (2-u)A_k - A_{k+1} = 0 \quad (135)$$

Now, for the amplitudes, we assume the following:

$$A_k = C \sin k\varphi \quad (136)$$

and after introducing in the system (63) the algebraic equations

$$-C \sin(k-1)\varphi + (2-u)C \sin k\varphi - C \sin(k+1)\varphi = 0 \quad (137a)$$

$$(2 - u - 2 \cos \varphi) C \sin k \varphi = 0 \quad (137b)$$

we obtain:

$$u = 2(1 - \cos \varphi) \quad (137c)$$

as well as:

$$\omega^2 = \frac{K}{2J} (2 \sin^2 \varphi + \mu - \kappa) \quad (138)$$

The solution (133) must satisfy boundary conditions for a different case of the ends of the double DNA fractional order chain model. For that reason, we must put indices  $s$ , and two subsets of the eigen circular frequencies of the corresponding main eigen chains are:

$$\omega_{s\xi}^2 = \frac{K}{2J} \left( 2 \sin^2 \frac{\varphi_s}{2} + \mu - \kappa \right), \quad s = 1, 2, 3, \dots, n \quad (139)$$

$$\omega_{s\eta}^2 = \frac{K}{2J} \left( 2 \sin^2 \frac{\varphi_s}{2} + \mu \right), \quad s = 1, 2, 3, \dots, n \quad (140)$$

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

$$\xi_k(t) = \sum_{s=1}^n A_k^{(s)} \cos(\omega_{s\xi} t + \alpha_s) = \sum_{s=1}^n C_s \sin k \varphi_s \cos(\omega_{s\xi} t + \alpha_s) = \sum_{s=1}^n \zeta_{s\xi} \sin k \varphi_s \quad (141)$$

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

Normal coordinates  $\zeta_{s\xi}$  or normal modes of the first main chain are in the form

$$\zeta_{s\xi} = C_s \cos(\omega_{s\xi} t + \alpha_s), \quad s = 1, 2, 3, \dots, n \quad (142)$$

with known frequencies (139), and unknown amplitudes  $C_s$  and phase  $\alpha_s$  depending of initial conditions.

The transformation of the subsystem (90) of the fractional order differential equations of the first main chain by introducing (140) yields:

$$\sum_{s=1}^n \frac{2J}{K} \left( \ddot{\zeta}_{s\xi} + \omega_{s\xi}^2 \zeta_{s\xi} + \frac{K}{2J} \kappa_{s\sigma\xi} D_t^\sigma [\zeta_{s\xi}] \right) \sin k \varphi_s = 0, \quad s = 1, 2, 3, \dots, n \quad (143)$$

where characteristic numbers expressing fractional order subsystem properties are in the following form:

$$\kappa_{s\sigma\xi} = \frac{K}{2J} \left( 2 \sin^2 \frac{\varphi_s}{2} + \mu - \kappa \right), \quad s = 1, 2, 3, \dots, n \quad (144)$$

Taking into account that  $\sin k \varphi_s$  is equal to zero, only for the boundary conditions, then from (141) we can write that is necessary to be:

$$\ddot{\zeta}_{s\xi} + \omega_{s\xi}^2 \zeta_{s\xi} + \omega_{s\sigma\xi}^2 D_t^\sigma [\zeta_{s\xi}] = 0, \quad s = 1, 2, 3, \dots, n \quad (145)$$

where sets of circular frequencies  $\omega_{s\xi}^2$  and a set of characteristic fractional order numbers  $\omega_{s\sigma\xi}^2$  are in the following forms:

$$\omega_{s\xi}^2 = \frac{K}{2J} \left( 2 \sin^2 \frac{\varphi_s}{2} + \mu - \kappa \right), \quad s = 1, 2, 3, \dots, n \quad (146)$$

$$\omega_{s\sigma\xi}^2 = \kappa_{s\sigma\xi} \frac{K}{2J} = \kappa_\sigma \frac{K}{J} \left( 2 \sin^2 \frac{\varphi_s}{2} - \kappa \right), \quad s = 1, 2, 3, \dots, n \quad (147)$$

The previous system (145) of differential fractional order equations is independent containing one main chain coordinate  $\zeta_{s\xi}$  and describing creep vibration modes of the  $n$  independent partial fractional order oscillators, each of them with one degree of freedom.

On the basis of the previous approach for the second subsystems of the second main chain, for the second main chain of the fractional order double DNA chain helix, the eigen amplitudes are in the form

$B_k^{(s)} = D_s \sin k\varphi_s$  and generalized main chain coordinates  $\eta_k(t)$  of the second main chain are possible to express by a set of the corresponding main normal coordinates  $\zeta_{s\eta}$  in the following form:

$$\eta_k(t) = \sum_{s=1}^n B_k^{(s)} \cos(\omega_{s\eta} t + \beta_s) = \sum_{s=1}^n D_s \sin k\varphi_s \cos(\omega_{s\eta} t + \beta_s) = \sum_{s=1}^n \zeta_{s\eta} \sin k\varphi_s \quad (148)$$

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

Normal coordinates or normal modes  $\eta_k(t)$  of the second main chain of the fractional order double DNA helix chain are in the form:

$$\zeta_{s\eta} = B_s \cos(\omega_{s\eta} t + \beta_s), \quad s = 1, 2, 3, \dots, n \quad (149)$$

with frequencies expressed by (138), and unknown amplitudes  $B_s$  and phase  $\beta_s$  depending of initial conditions.

The transformation of the second subsystem (91) of the differential equations of the second main chain by introducing (147) yields:

$$\sum_{s=1}^n \frac{2\mathbf{J}}{K} \left( \ddot{\zeta}_{s\eta} + \omega_{s\eta}^2 \zeta_{s\eta} + \frac{K}{2\mathbf{J}} \kappa_{s\sigma\eta} \mathbf{D}_t^\sigma [\zeta_{s\eta}] \right) \sin k\varphi_s = 0 \quad (150)$$

where

$$\kappa_{s\sigma\eta} = 2\kappa_\sigma \left( \frac{2\mathbf{J}}{K} \omega_{s\eta}^2 - \mu \right), \quad s = 1, 2, 3, \dots, n \quad (151)$$

Taking into account that  $\sin k\varphi_s$  is equal to zero, only for the boundary conditions, then from (147), we can write that it is necessary to be:

$$\ddot{\zeta}_{s\eta} + \omega_{s\eta}^2 \zeta_{s\eta} + \omega_{s\sigma\eta}^2 \mathbf{D}_t^\sigma [\zeta_{s\eta}] = 0; \quad s = 1, 2, 3, \dots, n \quad (152)$$

where sets of eigen circular frequencies  $\omega_{s\eta}^2$  and a set of characteristic fractional order numbers  $\omega_{s\sigma\eta}^2$  are in the following forms:

$$\omega_{s\eta}^2 = \frac{K}{2\mathbf{J}} \left( 2\sin^2 \frac{\varphi_s}{2} + \mu \right) \quad (153)$$

$$\omega_{s\sigma\eta}^2 = 4\kappa_\sigma \frac{K}{2\mathbf{J}} \sin^2 \frac{\varphi_s}{2}, \quad s = 1, 2, 3, \dots, n \quad (154)$$

We can see that previous subsystem of the fractional order differential equations (143) with respect to their main coordinates  $\zeta_{s\eta}$ , as in the previous case corresponding subsystem of the fractional order differential equations (152) with respect to their main normal coordinates  $\zeta_{s\xi}$ , are two subsystems with independent describing creep vibration modes of the  $2n$  independent partial fractional order oscillators, each of them with one degree of freedom. Both obtained subsystems (143) and (147) of fractional order differential equations contain fractional order differential equations of the same type, each being the fractional order differential equations containing one main normal coordinate,  $\zeta_{s\xi}$  or  $\zeta_{s\eta}$ , and each of them with one degree of freedom. Then, we can conclude that we start with one fractional order double DNA helix chain system which is, in whole, with  $2n$  degrees of freedom and  $2n$  generalized independent angular coordinates  $\varphi_{k,1}$  and  $\varphi_{k,2}$ . And using two subsystems of the main chain coordinates  $\xi_k = \varphi_{k,1} - \varphi_{k,2}$  and  $\eta_k = \varphi_{k,1} + \varphi_{k,2}$  we obtained two independent subsystems, each with  $n$  degrees of freedom, and with the corresponding subsystem of independent eigen main fractional order oscillators described by the corresponding sets of eigen main chain coordinates  $\zeta_{s\xi}$  or  $\zeta_{s\eta}$ , and by subsets of the  $n$  eigen circular frequencies  $\omega_{s\xi}^2$  and  $\omega_{s\eta}^2$  and the corresponding creep properties parameters  $\omega_{s\sigma\xi}^2$  and  $\omega_{s\sigma\eta}^2$  for  $s = 1, 2, 3, \dots, n$ .

In order to solve the system of fractional order differential equations (145) and (152), we use an analogy between the obtained fractional order differential equations and the corresponding fractional order differential equation (E.4.1) in the Appendix E.4, and we can write (see [3] or [34]):

$$\begin{aligned} \zeta_{s\xi}(t) = & \zeta_{s\xi}(0) \sum_{k=0}^{\infty} (-1)^k \omega_{s\xi}^{2k} t^{2k} \sum_{j=0}^k \binom{k}{j} \frac{(\mp 1)^j \omega_{s\xi}^{2j} t^{-\alpha j}}{\omega_{s\xi}^{2j} \Gamma(2k+1-\alpha j)} + \\ & + \dot{\zeta}_{s\xi}(0) \sum_{k=0}^{\infty} (-1)^k \omega_{s\xi}^{2k} t^{2k+1} \sum_{j=0}^k \binom{k}{j} \frac{(\mp 1)^j \omega_{s\xi}^{2j} t^{-\alpha j}}{\omega_{s\xi}^{2j} \Gamma(2k+2-\alpha j)} \end{aligned} \quad (155)$$

$$\begin{aligned} \zeta_{s\eta}(t) = & \zeta_{s\eta}(0) \sum_{k=0}^{\infty} (-1)^k \omega_{s\eta}^{2k} t^{2k} \sum_{j=0}^k \binom{k}{j} \frac{(\mp 1)^j \omega_{s\eta}^{2j} t^{-\alpha j}}{\omega_{s\eta}^{2j} \Gamma(2k+1-\alpha j)} + \\ & + \dot{\zeta}_{s\eta}(0) \sum_{k=0}^{\infty} (-1)^k \omega_{s\eta}^{2k} t^{2k+1} \sum_{j=0}^k \binom{k}{j} \frac{(\mp 1)^j \omega_{s\eta}^{2j} t^{-\alpha j}}{\omega_{s\eta}^{2j} \Gamma(2k+2-\alpha j)} \end{aligned} \quad (156)$$

### 7.7.5. Visualization of the main modes of fractional order double DNA helix chain system free vibrations and corresponding partial fractional order oscillator modes

Using the previous expressions (153)-(154) we can separate the following two pairs of the main modes of a fractional order double DNA helix chain system in the following forms:

a\* the first pair for the first main chain of a fractional order double DNA helix chain system corresponds to the set of the main coordinate  $\zeta_{s\xi}$ :

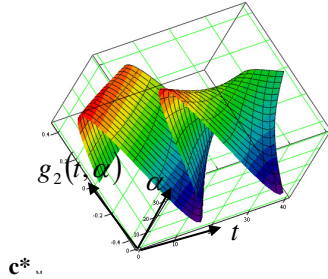
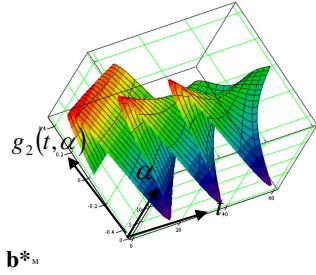
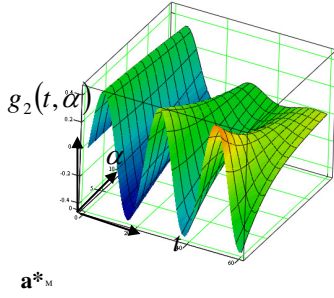


Fig.8.

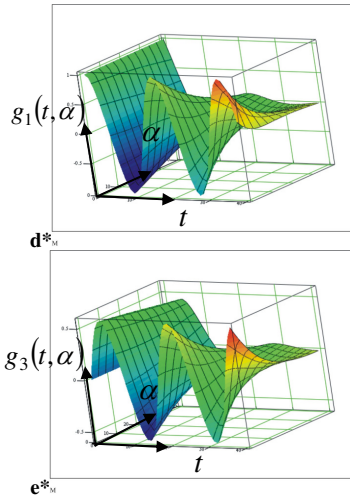


Fig.9.

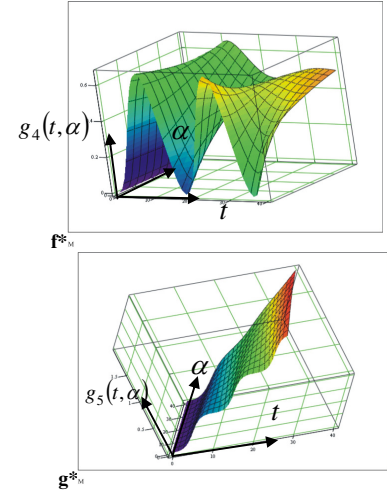


Fig.10.

Fig. 8. Time functions  $g_2(t, \alpha)$  surfaces for different multi-plate transversal vibrations kinetic and creep material parameters in the space  $(g_2(t, \alpha), t, \alpha)$  for interval  $0 \leq \alpha \leq 1$ .

Fig. 9. Time functions:  $d^* g_1(t, \alpha)$  and  $e^* g_3(t, \alpha)$  surfaces for the same multi-plate transversal vibrations kinetic and creep material parameters  $\omega_0^2 = 1, \omega_\alpha^2 = 2$  in the space  $(g_1(t, \alpha), t, \alpha)$ , as well as in corresponding  $(g_1(t, \alpha), t, \alpha)$  for interval  $0 \leq \alpha \leq 1$ .

Fig. 10. Time functions:  $f^* g_4(t, \alpha)$  and  $g^* g_5(t, \alpha)$  surfaces for the same multi-plate transversal vibrations kinetic and creep material parameters  $\omega_0^2 = 1, \omega_\alpha^2 = 2$  in the space  $(g_4(t, \alpha), t, \alpha)$ , as well as in corresponding  $(g_5(t, \alpha), t, \alpha)$  for interval  $0 \leq \alpha \leq 1$ .

$$\zeta_{s\xi(\cos)}(t) = \sum_{k=0}^{\infty} (-1)^k \omega_{s\xi}^{2k} t^{2k} \sum_{j=0}^k \binom{k}{j} \frac{(\mp 1)^j \omega_{s\xi}^{2j} t^{-\alpha j}}{\omega_{s\xi}^{2j} \Gamma(2k+1-\alpha j)} \quad (157)$$

$$\zeta_{s\xi(\sin)}(t) = \sum_{k=0}^{\infty} (-1)^k \omega_{s\xi}^{2k} t^{2k+1} \sum_{j=0}^k \binom{k}{j} \frac{(\mp 1)^j \omega_{s\xi}^{-2j} t^{-\alpha j}}{\omega_{s\xi}^{2j} \Gamma(2k+2-\alpha j)} \quad (158)$$

contains two modes like cosine and corresponding sine, with a set of the circular frequencies  $\omega_{s\xi}^{2j}$  and fractional order characteristic numbers  $\omega_{s\xi}^{2k}$ , with difference in phase analogous to that between cosine  $\cos \omega_{s\xi} t$  and sinus  $\sin \omega_{s\xi} t$  with the corresponding same circular frequency and difference in phase for  $\pi/2$ .

b\* the second pair for the second main chain of a fractional order double DNA helix chain system corresponding to the set of the main coordinate  $\zeta_{s\eta}$ :

$$\zeta_{s\eta(\cos)}(t) = \sum_{k=0}^{\infty} (-1)^k \omega_{s\eta}^{2k} t^{2k} \sum_{j=0}^k \binom{k}{j} \frac{(\mp 1)^j \omega_{s\eta}^{2j} t^{-\alpha j}}{\omega_{s\eta}^{2j} \Gamma(2k+1-\alpha j)} \quad (159)$$

$$\zeta_{s\eta(\sin)}(t) = \sum_{k=0}^{\infty} (-1)^k \omega_{s\eta}^{2k} t^{2k+1} \sum_{j=0}^k \binom{k}{j} \frac{(\mp 1)^j \omega_{s\eta}^{-2j} t^{-\alpha j}}{\omega_{s\eta}^{2j} \Gamma(2k+2-\alpha j)} \quad (160)$$

contains two modes like cosine and the corresponding sine, with a set of the circular frequencies  $\omega_{s\eta}^{2j}$  and fractional order characteristic numbers  $\omega_{s\eta}^{2k}$ , with difference in phase analogous to that between cosinus  $\cos \omega_{s\eta} t$  and sinus  $\sin \omega_{s\eta} t$  with the corresponding same circular frequency and difference in phase for  $\pi/2$ .

The previously listed analytical expressions (157)-(158) and (159)-(160) for the corresponding pairs of the first and second main chains fractional order modes of a fractional order double DNA helix chain system also correspond to  $2n$  fractional order modes of the partial fractional order oscillators (145) and (152), each for one from the set of  $2n$  main coordinates  $\zeta_{s\xi}$  and  $\zeta_{s\eta}$  of a fractional order double DNA helix chain system.

### 7.7.6. 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 two chains, as presented in Fig. 6 or 7, in the form of the double chain fractional order system containing two coupled multi-pendulum subsystems, in which the corresponding material particles of the corresponding multi-pendulum chains are coupled by series of the same standard light fractional order elements.

We assume that both coupled chains from the 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  $M_{0,k,1} \cos \Omega_{k,1} t$  and  $M_{0,k,2} \cos \Omega_{k,2} t$ ,  $k = 1, 2, 3, \dots, n$ , where  $M_{0,k,1}$  and  $M_{0,k,2}$  are amplitudes,  $\Omega_{k,1}$  and  $\Omega_{k,2}$  are frequencies of the external forced couples, each applied to one of the mass particles of the double DNA model coupled chains.

Then, we can write the corresponding system of the fractional order differential coupled equations in the form:

$$\begin{aligned}
 & \mathbf{J}_{k,1} \ddot{\varphi}_{k,1} - \frac{K_{k,1}}{2} [(\varphi_{k+1,1} - \varphi_{k,1}) - (\varphi_{k,1} - \varphi_{k-1,1})] - \frac{K_{k,1,\sigma}}{2} D_t^\sigma [(\varphi_{k+1,1} - \varphi_{k,1}) - (\varphi_{k,1} - \varphi_{k-1,1})] + \\
 & + K_{\alpha\beta} r_\alpha (r_\alpha - r_\beta) \varphi_{k,1} - K_{\alpha\beta} \frac{1}{4} \left( 1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}} \right) (r_\alpha - r_\beta)^2 (\varphi_{k,1} - \varphi_{k,2}) - \\
 & - K_{\alpha\beta,\sigma} \frac{1}{4} \left( 1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}} \right) (r_\alpha - r_\beta)^2 D_t^\sigma [(\varphi_{k,1} - \varphi_{k,2})] = M_{0,k,1} \cos \Omega_{k,1} t \\
 & \mathbf{J}_{k,2} \ddot{\varphi}_{k,2} - \frac{K_{k,2}}{2} [(\varphi_{k+1,2} - \varphi_{k,2}) - (\varphi_{k,2} - \varphi_{k-1,2})] - \frac{K_{k,2,\sigma}}{2} D_t^\sigma [(\varphi_{k+1,2} - \varphi_{k,2}) - (\varphi_{k,2} - \varphi_{k-1,2})] + \\
 & + K_{\alpha\beta} r_\alpha (r_\alpha - r_\beta) \varphi_{k,2} + K_{\alpha\beta} \frac{1}{4} \left( 1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}} \right) (r_\alpha - r_\beta)^2 (\varphi_{k,1} - \varphi_{k,2}) + \\
 & + K_{\alpha\beta,\sigma} \frac{1}{4} \left( 1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}} \right) (r_\alpha - r_\beta)^2 D_t^\sigma [(\varphi_{k,1} - \varphi_{k,2})] = M_{0,k,2} \cos \Omega_{k,2} t
 \end{aligned} \tag{161}$$

The previous system is possible to rewrite in the following form:

$$\begin{aligned}
 & \frac{2\mathbf{J}_{k,1}}{K_{k,1}} \ddot{\varphi}_{k,1} - [(\varphi_{k+1,1} - \varphi_{k,1}) - (\varphi_{k,1} - \varphi_{k-1,1})] + \frac{K_{k,1,\sigma}}{K_{k,1}} D_t^\sigma [(\varphi_{k+1,1} - \varphi_{k,1}) - (\varphi_{k,1} - \varphi_{k-1,1})] + \\
 & + \frac{2K_{\alpha\beta} r_\alpha (r_\alpha - r_\beta)}{K_{k,1}} \varphi_{k,1} - \frac{K_{\alpha\beta}}{2K_{k,1}} \left( 1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}} \right) (r_\alpha - r_\beta)^2 (\varphi_{k,1} - \varphi_{k,2}) - \\
 & - \frac{K_{\alpha\beta,\sigma}}{2K_{k,1}} \left( 1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}} \right) (r_\alpha - r_\beta)^2 D_t^\sigma [(\varphi_{k,1} - \varphi_{k,2})] = \frac{M_{0,k,1}}{K_{k,1}} \cos \Omega_{k,1} t \\
 & \frac{2\mathbf{J}_{k,2}}{K_{k,2}} \ddot{\varphi}_{k,2} - [(\varphi_{k+1,2} - \varphi_{k,2}) - (\varphi_{k,2} - \varphi_{k-1,2})] - \frac{K_{k,2,\sigma}}{K_{k,2}} D_t^\sigma [(\varphi_{k+1,2} - \varphi_{k,2}) - (\varphi_{k,2} - \varphi_{k-1,2})] + \\
 & + \frac{2K_{\alpha\beta} r_\alpha (r_\alpha - r_\beta)}{K_{k,2}} \varphi_{k,2} + \frac{K_{\alpha\beta}}{2K_{k,2}} \left( 1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}} \right) (r_\alpha - r_\beta)^2 (\varphi_{k,1} - \varphi_{k,2}) + \\
 & + \frac{K_{\alpha\beta,\sigma}}{2K_{k,2}} \left( 1 - \frac{\omega_{\alpha\beta 2}}{\omega_{\alpha\beta 1}} \right) (r_\alpha - r_\beta)^2 D_t^\sigma [(\varphi_{k,1} - \varphi_{k,2})] = \frac{M_{0,k,2}}{K_{k,2}} \cos \Omega_{k,2} t
 \end{aligned} \tag{162}$$

As our intention is to use the 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 this into account, we introduce the notation (14) and (15) and then the previous system of coupled fractional order differential equations is possible to write in the following form:

$$\begin{aligned}
 & \frac{2\mathbf{J}}{K} \ddot{\varphi}_{k,1} - [(\varphi_{k+1,1} - \varphi_{k,1}) - (\varphi_{k,1} - \varphi_{k-1,1})] - \kappa_\sigma D_t^\sigma [(\varphi_{k+1,1} - \varphi_{k,1}) - (\varphi_{k,1} - \varphi_{k-1,1})] + \\
 & + 2\mu\varphi_{k,1} - \kappa(\varphi_{k,1} - \varphi_{k,2}) - \kappa\kappa_\sigma D_t^\sigma [(\varphi_{k,1} - \varphi_{k,2})] = \frac{M_{0,k,1}}{K} \cos \Omega_{k,1} t \\
 & \frac{2\mathbf{J}_{k,2}}{K} \ddot{\varphi}_{k,2} - [(\varphi_{k+1,2} - \varphi_{k,2}) - (\varphi_{k,2} - \varphi_{k-1,2})] - \kappa_\sigma D_t^\sigma [(\varphi_{k+1,2} - \varphi_{k,2}) - (\varphi_{k,2} - \varphi_{k-1,2})] + \\
 & + 2\mu\varphi_{k,2} + \kappa(\varphi_{k,1} - \varphi_{k,2}) + \kappa\kappa_\sigma D_t^\sigma [(\varphi_{k,1} - \varphi_{k,2})] = \frac{M_{0,k,2}}{K} \cos \Omega_{k,2} t
 \end{aligned} \tag{163}$$

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

Using change of the generalized independent angular coordinates  $\varphi_{k,1}$  and  $\varphi_{k,2}$  for the  $k$ -th bases of both chains in the DNA model into the following new main chain coordinates  $\xi_k$  and  $\eta_k$  by the following dependence-relations:  $\xi_k = \varphi_{k,1} - \varphi_{k,2}$  and  $\eta_k = \varphi_{k,1} + \varphi_{k,2}$ , the previous system of fractional order differential equations (160) obtains the following form:



$$\begin{aligned} \frac{2J}{K} \ddot{\xi}_k - \xi_{k-1} + 2\xi_k - \xi_{k+1} + \kappa_\sigma D_t^\sigma [-\xi_{k-1} + 2\xi_k - \xi_{k+1}] + 2\mu\xi_k - 2\kappa\xi_k - 2\kappa\kappa_\sigma D_t^\sigma [\xi_k] = \\ = \frac{M_{0,k,1}}{K} \cos \Omega_{k,1} t - \frac{M_{0,k,2}}{K} \cos \Omega_{k,2} t \end{aligned} \quad (164)$$

$$\begin{aligned} \frac{2J}{K} \ddot{\eta}_k - \eta_{k-1} + 2\eta_k - \eta_{k+1} + \kappa_\sigma D_t^\sigma [-\eta_{k-1} + 2\eta_k - \eta_{k+1}] + 2\mu\eta_k = \\ = \frac{M_{0,k,1}}{K} \cos \Omega_{k,1} t + \frac{M_{0,k,2}}{K} \cos \Omega_{k,2} t \end{aligned} \quad , k = 1, 2, 3, \dots, n \quad (165)$$

The first series (161) and second series (163) of the previous system (164)-(165) of the fractional order differential equations are decoupled and independent. Then, we can conclude that new main chain coordinates  $\xi_k$  and  $\eta_k$  are the main chain 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 conclusions as an important property of the fractional order homogeneous model of forced vibrations in a fractional order double DNA homogeneous helix.

The systems of fractional order differential equations (164)-(165) contain two separate subsystems of fractional order differential equations expressed by main chain coordinates of  $\xi_k$  and  $\eta_k$  which are the main chain coordinates of a fractional order double DNA chain helix forced vibration model and separate DNA fractional order model into two independent fractional order chains.

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

We solve the previous subsystems (164) and (165) using the Laplace transformations, as in section 7.3. After applying the Laplace transformations to the previous systems (164) and (165) of differential equation's with fractional order derivative and having in mind that we introduced the notations  $L\{\xi_k(t)\}$  and  $L\{\eta_k(t)\}$  for the Laplace transformations, as well as that: (92), (93), (94) and (95) and also having in mind that we accepted the hypothesis that the initial conditions of fractional order derivatives of the system are given using:

$$\begin{aligned} \left. \frac{d^{\sigma-1} \xi_k(t)}{dt^{\sigma-1}} \right|_{t=0} = 0 \quad \text{and} \quad \left. \frac{d^{\sigma-1} \eta_k(t)}{dt^{\sigma-1}} \right|_{t=0} = 0, \quad \text{as well as that:} \\ L\left\{ \frac{M_{0,k,1}}{K} \cos \Omega_{k,1} t \mp \frac{M_{0,k,2}}{K} \cos \Omega_{k,2} t \right\} = \frac{M_{0,k,1}}{K} \frac{p}{p^2 + \Omega_{k,1}^2} \mp \frac{M_{0,k,2}}{K} \frac{p}{p^2 + \Omega_{k,2}^2} \end{aligned} \quad (166)$$

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

$$\begin{aligned} L\left\{ \frac{2J}{K} \ddot{\xi}_k \right\} - L\{\xi_{k-1}\} + 2L\{\xi_k\} - L\{\xi_{k+1}\} + \kappa_\sigma L\{D_t^\sigma [-\xi_{k-1} + 2\xi_k - \xi_{k+1}]\} + 2\mu L\{\xi_k\} - 2\kappa L\{\xi_k\} - 2\kappa\kappa_\sigma L\{D_t^\sigma [\xi_k]\} = \\ = +h_{0,k,1} \frac{p}{p^2 + \Omega_{k,1}^2} - h_{0,k,2} \frac{p}{p^2 + \Omega_{k,2}^2} \end{aligned} \quad (167)$$

$$\begin{aligned} \frac{2J}{K} L\{\ddot{\eta}_k\} - L\{\eta_{k-1}\} + 2L\{\eta_k\} - L\{\eta_{k+1}\} + \kappa_\sigma L\{D_t^\sigma [-\eta_{k-1} + 2\eta_k - \eta_{k+1}]\} + 2\mu L\{\eta_k\} = \\ = +h_{0,k,1} \frac{p}{p^2 + \Omega_{k,1}^2} + h_{0,k,2} \frac{p}{p^2 + \Omega_{k,2}^2} \end{aligned} \quad , k = 1, 2, 3, \dots, n \quad (168)$$

The previous system is possible to rewrite in the following form:

$$\begin{aligned} & \left[ \frac{2\mathbf{J}}{K} p^2 + 2\mu - 2\kappa(1 + \kappa_\sigma p^\sigma) \right] \mathcal{L}\{\xi_k(t)\} - \mathcal{L}\{\xi_{k-1}\} + 2\mathcal{L}\{\xi_k(t)\} - \mathcal{L}\{\xi_{k+1}\} = \frac{2\mathbf{J}}{K} \left[ \frac{p\xi_{0k} + \dot{\xi}_{0k}}{(1 + \kappa_\sigma p^\sigma)} \right] + \\ & + h_{0,k,1} \left( \frac{p}{(p^2 + \Omega_{k,1}^2)(1 + \kappa_\sigma p^\sigma)} \right) - h_{0,k,2} \left( \frac{p}{(p^2 + \Omega_{k,2}^2)(1 + \kappa_\sigma p^\sigma)} \right) \end{aligned} \quad (169)$$

$$\begin{aligned} & \left( \frac{p^2 \frac{2\mathbf{J}}{K} + 2\mu}{(1 + \kappa_\sigma p^\sigma)} \right) \mathcal{L}\{\eta_k\} - \mathcal{L}\{\eta_{k-1}\} + 2\mathcal{L}\{\eta_k\} - \mathcal{L}\{\eta_{k+1}\} = \frac{2\mathbf{J}}{K} \left[ \frac{p\eta_{0k} + \dot{\eta}_{0k}}{(1 + \kappa_\sigma p^\sigma)} \right] + \\ & + h_{0,k,1} \left( \frac{p}{(p^2 + \Omega_{k,1}^2)(1 + \kappa_\sigma p^\sigma)} \right) + h_{0,k,2} \left( \frac{p}{(p^2 + \Omega_{k,2}^2)(1 + \kappa_\sigma p^\sigma)} \right) \end{aligned} \quad (170)$$

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

$$\begin{aligned} -\mathcal{L}\{\xi_{k-1}\} + (2 + \nu)\mathcal{L}\{\xi_k(t)\} - \mathcal{L}\{\xi_{k+1}\} &= \frac{p\xi_{0k} + \dot{\xi}_{0k}}{\omega_0^2(1 + \kappa_\sigma p^\sigma)} + h_{0,k,1} \left( \frac{p}{(p^2 + \Omega_{k,1}^2)(1 + \kappa_\sigma p^\sigma)} \right) - \\ &- h_{0,k,2} \left( \frac{p}{(p^2 + \Omega_{k,2}^2)(1 + \kappa_\sigma p^\sigma)} \right) \end{aligned} \quad (171)$$

$$\begin{aligned} -\mathcal{L}\{\eta_{k-1}\} + (2 + u)\mathcal{L}\{\eta_k\} - \mathcal{L}\{\eta_{k+1}\} &= \frac{p\eta_{0k} + \dot{\eta}_{0k}}{\omega_0^2(1 + \kappa_\sigma p^\sigma)} + h_{0,k,1} \left( \frac{p}{(p^2 + \Omega_{k,1}^2)(1 + \kappa_\sigma p^\sigma)} \right) + \\ &+ h_{0,k,2} \left( \frac{p}{(p^2 + \Omega_{k,2}^2)(1 + \kappa_\sigma p^\sigma)} \right) \end{aligned} \quad (172)$$

or in the following forms:

$$-\mathcal{L}\{\xi_{k-1}\} + (2 + \nu)\mathcal{L}\{\xi_k(t)\} - \mathcal{L}\{\xi_{k+1}\} = h_{\xi hk}(p, \xi_{0k}, \dot{\xi}_{0k}) + h_{\xi pk}(p, \Omega_{k,1}^2, \Omega_{k,2}^2, h_{0k,1}, h_{0k,2}) \quad (174)$$

$$-\mathcal{L}\{\eta_{k-1}\} + (2 + u)\mathcal{L}\{\eta_k\} - \mathcal{L}\{\eta_{k+1}\} = h_{\eta hk}(p, \eta_{0k}, \dot{\eta}_{0k}) + h_{\eta pk}(p, \Omega_{k,1}^2, \Omega_{k,2}^2, h_{0k,1}, h_{0k,2}) \quad (175)$$

where

$$\nu = \frac{p^2 + 2\mu\omega_0^2}{\omega_0^2(1 + \kappa_\sigma p^\sigma)} - 2\kappa, \quad u = \frac{p^2 + 2\mu\omega_0^2}{\omega_0^2(1 + \kappa_\sigma p^\sigma)}, \quad \omega_0^2 = \frac{K}{2\mathbf{J}} \quad (176)$$

$$h_{\xi hk}(p, \xi_{0k}, \dot{\xi}_{0k}) = \frac{p\xi_{0k} + \dot{\xi}_{0k}}{\omega_0^2(1 + \kappa_\sigma p^\sigma)}, \quad h_{\eta hk}(p, \eta_{0k}, \dot{\eta}_{0k}) = \frac{p\eta_{0k} + \dot{\eta}_{0k}}{\omega_0^2(1 + \kappa_\sigma p^\sigma)} \quad (177)$$

$$h_{\xi pk}(p, \Omega_{k,1}^2, \Omega_{k,2}^2, h_{0k,1}, h_{0k,2}) = h_{0,k,1} \left( \frac{p}{(p^2 + \Omega_{k,1}^2)(1 + \kappa_\sigma p^\sigma)} \right) - h_{0,k,2} \left( \frac{p}{(p^2 + \Omega_{k,2}^2)(1 + \kappa_\sigma p^\sigma)} \right) \quad (178)$$

$$h_{\xi pk}(p, \Omega_{k,1}^2, \Omega_{k,2}^2, h_{0k,1}, h_{0k,2}) = h_{0,k,1} \left( \frac{p}{(p^2 + \Omega_{k,1}^2)(1 + \kappa_\sigma p^\sigma)} \right) + h_{0,k,2} \left( \frac{p}{(p^2 + \Omega_{k,2}^2)(1 + \kappa_\sigma p^\sigma)} \right) \quad (179)$$

Both subsystems are of the same form and it is necessary to solve one of the subsystems and applying the analogy it is easy to solve the other of the subsystem equations. For that reason, we can use the method proposed in the papers [32] and [31]. The determinate of the previous subsystem (174) as well as (165) is in the following form (104) as for the subsystems of algebraic equations (100) and (101) in section 7.3.

The algebra no homogenous algebra equations (171) and (172) for special case as in section 7.3 are of the same form, as presented in (101) and (102), and we can write:

$$-\mathcal{L}\{\xi_{k-1}\} + (2 + \nu)\mathcal{L}\{\xi_k(t)\} - \mathcal{L}\{\xi_{k+1}\} = \begin{cases} h_{\xi h1}(p, \xi_{01}, \dot{\xi}_{01}) + h_{\xi p1}(p, \Omega_{1,1}^2, \Omega_{1,2}^2, h_{01,1}, h_{01,2}) & k = 1 \\ 0 & k \neq 1 \end{cases} \quad (180)$$

$$-\mathcal{L}\{\eta_{k-1}\} + (2 + u)\mathcal{L}\{\eta_k\} - \mathcal{L}\{\eta_{k+1}\} = \begin{cases} h_{\eta h1}(p, \eta_{01}, \dot{\eta}_{01}) + h_{\eta p1}(p, \Omega_{1,1}^2, \Omega_{1,2}^2, h_{01,1}, h_{01,2}) & k = 1 \\ 0 & k \neq 1 \end{cases} \quad (181)$$

The determinates of the previous algebraic subsystems (180) as well as (181) are of the same form, as presented in (104). Introducing the notation  $h_{\xi h1}(p, \xi_{01}, \dot{\xi}_{01}) + h_{\xi}(p, \Omega_{1,1}^2, \Omega_{1,2}^2, h_{0k,1}, h_{0k,2})$  and  $h_{\eta h1}(p, \eta_{01}, \eta_{01}) + h_{\eta p1}(p, \Omega_{1,1}^2, \Omega_{1,2}^2, h_{01,1}, h_{01,2})$  defined by (178) and (179), for the determinants  $\tilde{\Delta}_{(k)}(v, h_{\xi})$ , we can write similar expressions, as defined by (105)-(109), changing the expressions  $h_{\xi}(p, \xi_{01}, \dot{\xi}_{01})$  by expressions  $h_{\xi h1}(p, \xi_{01}, \dot{\xi}_{01}) + h_{\xi}(p, \Omega_{1,1}^2, \Omega_{1,2}^2, h_{0k,1}, h_{0k,2})$  as well as by  $h_{\eta h1}(p, \eta_{01}, \eta_{01}) + h_{\eta p1}(p, \Omega_{1,1}^2, \Omega_{1,2}^2, h_{01,1}, h_{01,2})$ .

To solve the system of the algebraic non-homogeneous equations (180) or (181) with respect to unknown Laplace transforms  $L\{\xi_k(t)\}$  or  $L\{\eta_k(t)\}$  of the time function main chain coordinates  $\xi_k(t)$  and  $\eta_k(t)$ -unknown normal chain coordinates of the system main chains for forced vibrations, we can use the Cramer approach in a similar way as in section 7.3.

### 7.7.8. 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 with two subsystems of fractional order differential equations (164) and (165) expressed by eigen a normal chain coordinates  $\xi_k = \varphi_{k,1} - \varphi_{k,2}$  and  $\eta_k = \varphi_{k,1} + \varphi_{k,2}$ , and these subsystems can be rewritten in the following form:

$$\begin{aligned} \frac{2J}{K} \ddot{\xi}_k - \xi_{k+1} + 2\xi_k[1 + \mu - \kappa] - \xi_{k-1} + \kappa_{\sigma} D_t^{\sigma} [-\xi_{k-1} + 2(1 - \kappa)\xi_k - \xi_{k+1}] &= h_{0,k,1} \cos \Omega_{k,1} t - h_{0,k,2} \cos \Omega_{k,2} t \\ k &= 1, 2, 3, \dots, n \end{aligned} \quad (182)$$

$$\begin{aligned} \frac{2J}{K} \ddot{\eta}_k - \eta_{k+1} + 2\eta_k(1 + \mu) - \eta_{k-1} + \kappa_{\sigma} D_t^{\sigma} [-\eta_{k-1} + 2\eta_k - \eta_{k+1}] &= h_{0,k,1} \cos \Omega_{k,1} t + h_{0,k,2} \cos \Omega_{k,2} t \\ k &= 1, 2, 3, \dots, n \end{aligned} \quad (183)$$

Without loss of generality, our interest was focused next on considering two subsystems of the fractional order differential equations in the following form:

$$\begin{aligned} \frac{2J}{K} \ddot{\xi}_k - \xi_{k+1} + 2\xi_k[1 + \mu - \kappa] - \xi_{k-1} + \kappa_{\sigma} D_t^{\sigma} [-\xi_{k-1} + 2(1 - \kappa)\xi_k - \xi_{k+1}] &= \begin{cases} h_{0,1,1} \cos \Omega_{1,1} t & k = 1 \\ 0 & k \neq 1 \end{cases} \\ k &= 1, 2, 3, \dots, n \end{aligned} \quad (184)$$

$$\begin{aligned} \frac{2J}{K} \ddot{\eta}_k - \eta_{k+1} + 2\eta_k(1 + \mu) - \eta_{k-1} + \kappa_{\sigma} D_t^{\sigma} [-\eta_{k-1} + 2\eta_k - \eta_{k+1}] &= \begin{cases} h_{0,1,1} \cos \Omega_{1,1} t & k = 1 \\ 0 & k \neq 1 \end{cases} \\ k &= 1, 2, 3, \dots, n \end{aligned} \quad (185)$$

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

The first series (184) and second series (185) of the previous system (164)-(165) of the fractional order differential equations for forced vibrations are decoupled and independent. *Then, we can conclude that new coordinates  $\xi_k$  and  $\eta_k$  are the main chain 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 conclusions as an important property of the fractional order homogeneous model of forced vibrations in a fractional order double DNA homogeneous helix.*

The systems of the fractional order differential equations (184)-(185) contain two separate subsystems of fractional order differential equations expressed by *coordinates of  $\xi_k$  and  $\eta_k$  which are the main chain 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 the first main chain of the double DNA chain helix (184), 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 a set of this eigen main chain main coordinates  $\zeta_{s\xi}$  for free vibrations (149) in the following form:

$$\xi_k(t) = \sum_{s=1}^n \zeta_{s\xi} \sin k\varphi_s \quad (186)$$

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

and for the other main chain of the double DNA chain helix (185) generalized coordinates  $\eta_k(t)$  of the second main chain for forced vibrations is possible to express by a set of this eigen main chain main coordinates  $\zeta_{s\eta}$  for free vibrations (146) in the following form:

$$\eta_k(t) = \sum_{s=1}^n \zeta_{s\eta} \sin k\varphi_s \quad (187)$$

Normal coordinates  $\zeta_{s\xi}$  or normal modes of the first main chain for forced vibrations is possible to express in the form similar to that for free vibrations (142), but introducing the assumption that unknown amplitudes  $C_s$  and phase  $\alpha_s$  depending of initial conditions are not constant, but functions of time,  $C_s(t)$  and phase  $\alpha_s(t)$ , and for fractional order system the main coordinates are in the form

$$\zeta_{s\xi}(t) = C_s(t) \cos(\Omega_{\xi} t + \alpha_s(t)), s = 1, 2, 3, \dots, n \quad (188)$$

with known frequencies (139), and unknown time functions - amplitudes  $C_s(t)$  and phase  $\alpha_s(t)$  depending of time and initial conditions.

Then, we introduce the expressions (186) and (187) and their corresponding second and fractional order derivative into the subsystem of the fractional order differential equations (184) and (185), and we obtain the following sub-systems:

$$\begin{aligned} & \frac{2J}{K} \sum_{s=1}^n \ddot{\zeta}_{s\xi} \sin k\varphi_s - \sum_{s=1}^n \zeta_{s\xi} \sin(k-1)\varphi_s + 2[1 + \mu - \kappa] \sum_{s=1}^n \zeta_{s\xi} \sin k\varphi_s - \sum_{s=1}^n \zeta_{s\xi} \sin(k+1)\varphi_s + \\ & + \kappa_{\sigma} D_t^{\sigma} \left[ - \sum_{s=1}^n \zeta_{s\xi} \sin(k-1)\varphi_s + 2(1 - \kappa) \sum_{s=1}^n \zeta_{s\xi} \sin k\varphi_s - \sum_{s=1}^n \zeta_{s\xi} \sin(k+1)\varphi_s \right] = \begin{cases} h_{0,1,1} \cos \Omega_{1,1} t & k = 1 \\ 0 & k \neq 1 \end{cases} \\ & k = 1, 2, 3, \dots, n \end{aligned} \quad (189)$$

$$\begin{aligned} & \frac{2J}{K} \sum_{s=1}^n \ddot{\zeta}_{s\eta} \sin k\varphi_s - \sum_{s=1}^n \zeta_{s\eta} \sin(k-1)\varphi_s + 2[1 + \mu] \sum_{s=1}^n \zeta_{s\eta} \sin k\varphi_s - \sum_{s=1}^n \zeta_{s\eta} \sin(k+1)\varphi_s + \\ & + \kappa_{\sigma} D_t^{\sigma} \left[ - \sum_{s=1}^n \zeta_{s\eta} \sin(k-1)\varphi_s + 2 \sum_{s=1}^n \zeta_{s\eta} \sin k\varphi_s - \sum_{s=1}^n \zeta_{s\eta} \sin(k+1)\varphi_s \right] = \begin{cases} h_{0,1,1} \cos \Omega_{1,1} t & k = 1 \\ 0 & k \neq 1 \end{cases} \\ & k = 1, 2, 3, \dots, n \end{aligned} \quad (190)$$

After making group sublimations of some terms in the previous equations (189), we obtain the following subsystem:

$$\sum_{s=1}^n \frac{2J}{K} \left( \ddot{\zeta}_{s\xi} + 2 \frac{K}{2J} \langle [1 + \mu - \kappa] - \cos \varphi_s \rangle + \frac{K}{2J} 2\kappa_{\sigma} \langle (1 - \kappa) - \cos \varphi_s \rangle D_t^{\sigma} [\zeta_{s\xi}] \right) \sin k\varphi_s = \begin{cases} h_{0,1,1} \cos \Omega_{1,1} t & k = 1 \\ 0 & k \neq 1 \end{cases} \quad (191)$$

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

Then, taking into account the denotations (144), (146) and (145), the previous subsystem of equation is possible to rewrite in the following form:

$$\sum_{s=1}^n \frac{2J}{K} \left( \ddot{\zeta}_{s\xi} + \omega_{s\xi}^2 \zeta_{s\xi} + \frac{K}{2J} \kappa_{\sigma} D_t^{\sigma} [\zeta_{s\xi}] \right) \sin k\varphi_s = \begin{cases} h_{0,1,1} \cos \Omega_{1,1} t & k = 1 \\ 0 & k \neq 1 \end{cases}, k = 1, 2, 3, \dots, n \quad (192)$$

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

$$\begin{cases} h_{0,1,1} \cos \Omega_{1,1} t & k=1 \\ 0 & k \neq 1 \end{cases} = \begin{cases} \sum_{s=1}^n \frac{2J}{K} h_{0,1,1(s)} \sin k \varphi_s \cos \Omega_{1,1} t & k=1 \\ 0 & k \neq 1 \end{cases} \quad (193)$$

where

$$h_{0,1,1(s)} = \frac{K}{2J} \frac{\sum_{s=1}^n h_{0,1,1} \sin k \varphi_s}{\left\langle \sum_{s=1}^n \sum_{r=1}^n \sin k \varphi_s \sin k \varphi_r \right\rangle_{r=s}} \quad k=1 \quad (194)$$

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

It is possible to rewrite the equations (192) in the following form:

$$\sum_{s=1}^n \frac{2J}{K} \left( \ddot{\zeta}_{s\xi} + \omega_{s\xi}^2 \zeta_{s\xi} + \omega_{s\sigma\xi}^2 D_t^\sigma [\zeta_{s\xi}] - h_{0,1,1(s)} \cos \Omega_{1,1} t \right) \sin k \varphi_s = 0, \quad k=1,2,3,\dots,n \quad (195)$$

Then, taking into account that  $\sin k \varphi_s \neq 0$ , in a general case, from (195) it is possible to obtain the following subsystem of fractional order differential equations along main chain normal coordinates  $\zeta_{s\xi}$  in the following form:

$$\ddot{\zeta}_{s\xi} + \omega_{s\xi}^2 \zeta_{s\xi} + \omega_{s\sigma\xi}^2 D_t^\sigma [\zeta_{s\xi}] = h_{0,1,1(s)} \cos \Omega_{1,1} t, \quad s=1,2,3,\dots,n \quad (196)$$

where  $\omega_{s\xi}^2$  square of eigen circular frequencies determined by expression (146) and  $\omega_{s\sigma\xi}^2$  the corresponding eigen characteristic numbers expressing fractional order subsystem properties, are determined by the expression (147).

Analogously, using (187) and (180) from (190), it is possible to obtain the second subsystem of fractional order differential equations along main chain normal coordinates  $\zeta_{s\eta}$  in the following form:

$$\ddot{\zeta}_{s\eta} + \omega_{s\xi}^2 \zeta_{s\eta} + \omega_{s\sigma\eta}^2 D_t^\sigma [\zeta_{s\eta}] = h_{0,1,1(s)} \cos \Omega_{1,1} t, \quad s=1,2,3,\dots,n \quad (197)$$

where  $\omega_{s\eta}^2$  the square of eigen circular frequencies is determined by the expression (153) and  $\omega_{s\sigma\eta}^2$  the corresponding eigen characteristic numbers expressing fractional order subsystem properties are determined by the expression (154).

Then, we have the system (196)-(197) containing two subsets of the main fractional order forced oscillators, each with  $n$  fractional order differential equations along one main chain main coordinates  $\zeta_{s\xi}$  and  $\zeta_{s\eta}$ . Each of these  $2n$  fractional order differential equations contains only one main eigen coordinate  $\zeta_{s\xi}$  or  $\zeta_{s\eta}$  of the system.

The system (196)-(197) represents the main fractional order forced oscillators along the independent system of main chain 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 the expression (146) or (153) and  $\omega_{s\sigma\xi}^2$  or  $\omega_{s\sigma\eta}^2$  the corresponding eigen characteristic numbers expressing fractional order subsystem properties, determined by the expression (147) or (154).

All fractional order differential equations of the system (196)-(197) are the same type and it is possible to solve them in the same way using the Laplace transform  $L\{\zeta_{s\xi}(t)\}$  and  $L\{\zeta_{s\eta}(t)\}$ . Applying the Laplace transform to the system (196)-(197) of the fractional order differential equations, we obtain the following two subsystems of equations:

$$L\{\ddot{\zeta}_{s\xi}\} + \omega_{s\xi}^2 L\{\zeta_{s\xi}(t)\} + \omega_{s\sigma\xi}^2 L\{D_t^\sigma [\zeta_{s\xi}]\} = h_{0,1,1(s)} L\{\cos \Omega_{1,1} t\}, \quad s=1,2,3,\dots,n \quad (198)$$

$$L\{\ddot{\zeta}_{s\eta}\} + \omega_{s\xi}^2 L\{\zeta_{s\eta}(t)\} + \omega_{s\sigma\eta}^2 L\{D_t^\sigma [\zeta_{s\eta}]\} = h_{0,1,1(s)} L\{\cos \Omega_{1,1} t\}, \quad s=1,2,3,\dots,n \quad (199)$$

Taking into account that:

$$\mathcal{L}\left\{\frac{d^2\zeta_{s\xi}(t)}{dt^2}\right\} = p^2\mathcal{L}\{\zeta_{s\xi}(t)\} - [p\zeta_{0s\xi} + \dot{\zeta}_{0s\xi}], \quad s = 1, 2, 3, \dots, n \quad (200)$$

$$\mathcal{L}\left\{\frac{d^2\zeta_{s\eta}(t)}{dt^2}\right\} = p^2\mathcal{L}\{\zeta_{s\eta}(t)\} - [p\zeta_{0s\eta} + \dot{\zeta}_{0s\eta}], \quad s = 1, 2, 3, \dots, n \quad (201)$$

$$\mathcal{L}\{\cos\Omega_{1,1}t\} = \frac{p}{p^2 + \Omega_{1,1}^2} \quad (202)$$

$$\mathcal{L}\left\{\frac{d^\sigma\zeta_{s\xi}}{dt^\sigma}\right\} = p^\sigma\mathcal{L}\{\zeta_{s\xi}\} - \frac{d^{\sigma-1}\zeta_{s\xi}}{dt^{\sigma-1}}\bigg|_{t=0} = p^\sigma\mathcal{L}\{\zeta_{s\xi}\}, \quad s = 1, 2, 3, \dots, n \quad (203)$$

$$\mathcal{L}\left\{\frac{d^\sigma\zeta_{s\eta}}{dt^\sigma}\right\} = p^\sigma\mathcal{L}\{\zeta_{s\eta}\} - \frac{d^{\sigma-1}\zeta_{s\eta}}{dt^{\sigma-1}}\bigg|_{t=0} = p^\sigma\mathcal{L}\{\zeta_{s\eta}\}, \quad s = 1, 2, 3, \dots, n \quad (204)$$

and after introducing into the sub-systems (198)-(199) for the Laplace transform  $\mathcal{L}\{\zeta_{s\xi}(t)\}$  and  $\mathcal{L}\{\zeta_{s\eta}(t)\}$  of the system double DNA helix chain eigen main coordinates  $\zeta_{s\xi}$  and  $\zeta_{s\eta}$  for forced regime, we obtain:

$$\mathcal{L}\{\zeta_{s\xi}\} = \frac{[p\zeta_{0s\xi} + \dot{\zeta}_{0s\xi}]}{(p^2 + \omega_{s\xi}^2 + \omega_{s\sigma\xi}^2 p^\sigma)} + \frac{h_{0,1,1}(s)}{(p^2 + \omega_{s\xi}^2 + \omega_{s\sigma\xi}^2 p^\sigma)} \frac{p}{p^2 + \Omega_{1,1}^2}, \quad s = 1, 2, 3, \dots, n \quad (205)$$

$$\mathcal{L}\{\zeta_{s\eta}\} = \frac{[p\zeta_{0s\eta} + \dot{\zeta}_{0s\eta}]}{(p^2 + \omega_{s\eta}^2 + \omega_{s\sigma\eta}^2 p^\sigma)} + \frac{h_{0,1,1}(s)}{(p^2 + \omega_{s\eta}^2 + \omega_{s\sigma\eta}^2 p^\sigma)} \frac{p}{p^2 + \Omega_{1,1}^2}, \quad s = 1, 2, 3, \dots, n \quad (206)$$

Then, to obtain the system double DNA helix chain eigen main coordinates  $\zeta_{s\xi}(t)$  and  $\zeta_{s\eta}(t)$  it is necessary to apply the inverse Laplace transform to the expressions (205)-(206). Then we can write the following:

$$\zeta_{s\xi}(t) = \zeta_{s\xi, \text{hom}}(t) + \zeta_{s\xi, \text{part}}(t) \quad (207)$$

and

$$\zeta_{s\eta}(t) = \zeta_{s\eta, \text{hom}}(t) + \zeta_{s\eta, \text{part}}(t) \quad (208)$$

where

$a^*)$   $\zeta_{s\xi, \text{hom}}(t)$  and  $\zeta_{s\eta, \text{hom}}(t)$  are terms corresponding to the solutions of the homogeneous fractional order differential equations and the solutions are in the forms (155) and (156) (see Appendix (E.4.1)):

$$\begin{aligned} \zeta_{s\xi, \text{hom}}(t) = & \zeta_{s\xi}(0) \sum_{k=0}^{\infty} (-1)^k \omega_{s\sigma\xi}^{2k} t^{2k} \sum_{j=0}^k \binom{k}{j} \frac{(\mp 1)^j \omega_{s\sigma\xi}^{2j} t^{-\alpha j}}{\omega_{s\xi}^{2j} \Gamma(2k+1-\alpha j)} + \\ & + \dot{\zeta}_{s\xi}(0) \sum_{k=0}^{\infty} (-1)^k \omega_{s\sigma\xi}^{2k} t^{2k+1} \sum_{j=0}^k \binom{k}{j} \frac{(\mp 1)^j \omega_{s\sigma\xi}^{-2j} t^{-\alpha j}}{\omega_{s\xi}^{2j} \Gamma(2k+2-\alpha j)} \end{aligned} \quad (209)$$

$$\begin{aligned} \zeta_{s\eta, \text{hom}}(t) = & \zeta_{s\eta}(0) \sum_{k=0}^{\infty} (-1)^k \omega_{s\sigma\eta}^{2k} t^{2k} \sum_{j=0}^k \binom{k}{j} \frac{(\mp 1)^j \omega_{s\sigma\eta}^{2j} t^{-\alpha j}}{\omega_{s\eta}^{2j} \Gamma(2k+1-\alpha j)} + \\ & + \dot{\zeta}_{s\eta}(0) \sum_{k=0}^{\infty} (-1)^k \omega_{s\sigma\eta}^{2k} t^{2k+1} \sum_{j=0}^k \binom{k}{j} \frac{(\mp 1)^j \omega_{s\sigma\eta}^{-2j} t^{-\alpha j}}{\omega_{s\eta}^{2j} \Gamma(2k+2-\alpha j)} \end{aligned} \quad (210)$$

$b^*)$   $\zeta_{s\xi, \text{par}}(t)$  and  $\zeta_{s\eta, \text{par}}(t)$  are terms corresponding to particular solutions of the non-homogeneous fractional order differential equations system (196)-(197) and the solutions must be obtained as an inverse transform of the following expressions:

$$\zeta_{s\xi, \text{par}}(t) = \mathcal{L}^{-1}\{\zeta_{s\xi, \text{par}}\} = \mathcal{L}^{-1}\left\{\frac{h_{0,1,1}(s)}{(p^2 + \omega_{s\xi}^2 + \omega_{s\sigma\xi}^2 p^\sigma)} \frac{p}{p^2 + \Omega_{1,1}^2}\right\}, \quad s = 1, 2, 3, \dots, n \quad (211)$$

$$\zeta_{s\eta, \text{par}}(t) = \mathcal{L}^{-1}\{\zeta_{s\eta, \text{par}}\} = \mathcal{L}^{-1}\left\{\frac{h_{0,1,1}(s)}{(p^2 + \omega_{s\eta}^2 + \omega_{s\sigma\eta}^2 p^\sigma)} \frac{p}{p^2 + \Omega_{1,1}^2}\right\}, \quad s = 1, 2, 3, \dots, n \quad (212)$$

or in a developed form

$$\zeta_{s\xi,par}(t) = L^{-1}L\{\zeta_{s\xi,par}\} = h_{0,1,l(s)}L^{-1}\left\{\frac{1}{p}\frac{1}{p^2 + \Omega_{1,1}^2}\sum_{k=0}^{\infty}\frac{(-1)^k\omega_{s\xi}^2}{p^{2k}}\sum_{j=0}^k\binom{k}{j}\frac{(\mp 1)^j p^{\alpha j}\omega_{s\xi}^{2(j-k)}}{\omega_{s\xi}^{2j}}\right\}, s = 1,2,3,\dots,n \quad (213)$$

$$\zeta_{s\eta,par}(t) = L^{-1}L\{\zeta_{s\eta,par}\} = h_{0,1,l(s)}L^{-1}\left\{\frac{1}{p}\frac{1}{p^2 + \Omega_{1,1}^2}\sum_{k=0}^{\infty}\frac{(-1)^k\omega_{s\eta}^2}{p^{2k}}\sum_{j=0}^k\binom{k}{j}\frac{(\mp 1)^j p^{\alpha j}\omega_{s\eta}^{2(j-k)}}{\omega_{s\eta}^{2j}}\right\}, s = 1,2,3,\dots,n \quad (214)$$

## 7.8 Concluding remarks

Finally, we can conclude that new main chain coordinates of  $\xi_k$  and  $\eta_k$ ,  $k = 1,2,3,\dots,n$  composed of the generalized independent coordinates in the way  $\xi_k = \varphi_{k,1} - \varphi_{k,2}$  and  $\eta_k = \varphi_{k,1} + \varphi_{k,2}$ ,  $k = 1,2,3,\dots,n$  are the main chain coordinates of the main eigen chains of a double DNA helix chain system and that it is possible to obtain two fictive decoupled and separated eigen single chains of the double DNA chain helix linear model as well as fractional order model. This is an important fundamental conclusion as a significant 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 a 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 conditions its behavior can be described by linear dynamics.

Then, analytical expressions of the square of  $\omega_s$  - eigen circular frequencies of the vibration modes of the separate chains of the homogeneous double DNA chain helix are obtained. By using these results it is easy to consider these values of the system  $\omega_s$  - eigen circular frequencies of free vibrations as series of resonant frequencies under external multi frequencies excitations, and also possibilities for the appearance of dynamical absorption phenomena and find explanation with real processes in the homogeneous double DNA chain helix.

By using superposition's of these solutions for the case that external excitation are with the same amplitudes and frequencies from the system of differential equations, we can see that for this case of external one frequency excitation in one eigen main chain there appear pure free vibrations with eigen subset of circular frequencies of its free vibrations, and in the other there appear forced vibrations. This conclusion is possible to generalize for the same multi-frequency external excitations applied to each of the material particle pairs in double DNA helix chain system. Eigen main chain in which there occur pure free vibrations with eigen subset of circular frequencies of its free vibrations may correspond with real chain of DNA that is not used as a template in the process of transcription- sense strand. The eigen main chain that oscillates in forced regime may correspond with real antisense strand of DNA –one that is transcribed.

\* 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 pair of the material particles less compared to 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 pairs of the material particles compared to the considered system.

This mathematical fact is important to consider in the light of the interruption or break of the double DNA helix chain system. In order to transcribe specific DNA sequence, RNA polymerase has to recognize the specific region of DNA where the sequence starts. Promoter regions make the recognition possible. We are free to suggest that, from the mechanical point of view, if specific one frequency excitation caused by RNA polymerase is the same as eigen oscillatory frequency of specific promoter region resonance appears, that is the condition for starting the transcription from the mechanical point of view. This means that every gene has its specific “starting” oscillatory frequency that will correspond with one frequency external excitation. This may also correspond with spatially localized solitons in Soliton –existence supporting models of DNA.

Our next considerations will focus on the small nonlinearity in the double DNA chain helix vibrations and rare nonlinear phenomena such as resonant jumps and energy interactions between nonlinear modes.



## Acknowledgements

Parts of this research were supported by the Ministry of Sciences and Technology of the Republic of Serbia through Mathematical Institute SANU Belgrade, Grant ON174001 Dynamics of hybrid systems with complex structures. Mechanics of materials and Faculty of Mechanical Engineering University of Niš and Department for Bio-chemical and Medical Science, State University of Novi Pazar in Novi Pazar.

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