Appendix A

A1. Gamma Function

Euler's gamma function is defined by the so-called *Euler integral of the second kind*

$$\Gamma(z) = \int_0^\infty e^{-t} t^{z-1} dt, \quad z \in \mathbb{C} \quad . \tag{A.1.1}$$

Thus

$$\Gamma(1) = \int_0^\infty e^{-t} dt = 1, \tag{A.1.2}$$

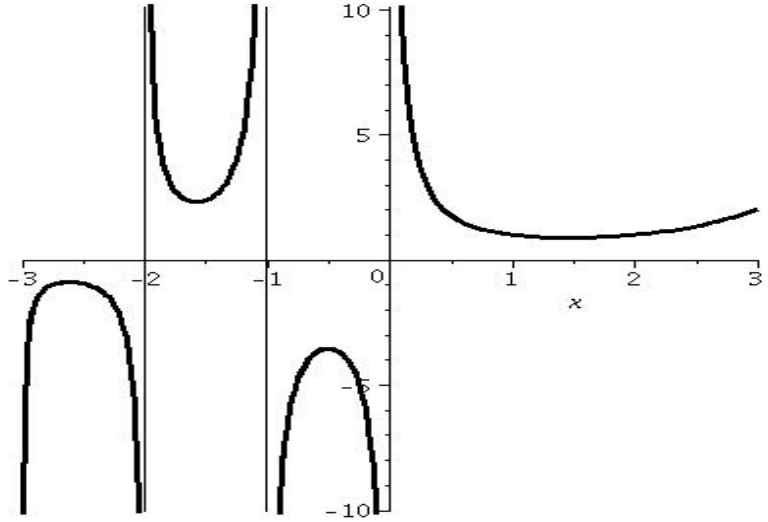

Fig.A.1: The real Gamma function Γ

The integral in the right side of (A.1.1) is convergent for all values of complex argument z with positive real part. However, by means of an analytic continuation it can be extended to the entire complex plane, excluding negative integers and zero.
Gamma function has several well established properties, the first of which is that it can be seen as a generalization of the factorial function. The so called *reduction formula* holds, for $z \in \mathbb{C} \setminus \{0, -1, -2, -3, ...\}$

$$\Gamma(z+1) = z\Gamma(z), \ \Rightarrow \Gamma(n+1) = n(n-1)! = n! \quad n \in \mathbb{N}_0 . \tag{A.1.3}$$

This reduction formula (A.1.2) can easily be proven starting from the integral (A.1.1). The analytic continuation of (A.1.1) is then conducted by application of this formula to arguments with negative real parts. Points at which the Gamma function is not well defined, i.e. negative integers and zero, are its simple poles. Another important relationship for the gamma function is the Legendre formula:

$$\Gamma(z)\Gamma(z+1/2) = \sqrt{\pi}\, 2^{2z-1}\Gamma(2z), \quad 2z \neq 0, -1, -2, ..., \tag{A.1.4}$$

Taking $z = n + 1/2$ in the previous relation, and utilizing the fact that for integer arguments Gamma function can be evaluated by means of the factorial function, one can obtain a set of particular values of the Gamma function:

$$\Gamma(n+1/2) = \frac{\sqrt{\pi}\Gamma(2n+1)}{2^{2n}\Gamma(n+1)} = \frac{\sqrt{\pi}(2n)!}{2^{2n} n!}, \tag{A.1.5}$$

[A1] Podlubny, I. *Fractional Differential Equations*, volume 198 of *Mathematics in Science and Engineering*. Academic Press, San Diego, 1999.

A2. Beta Function

Beta function, also known as the *Euler Integral of the First Kind*, is an important special function in general, very widely used in fractional calculus. The importance of Beta function in this context is that its form is similar to the fractional integral and derivative of a number of elementary functions, polynomials in particular, but also Mittag-Leffler function (to be introduced next). Beta integral is defined in the following way

$$B(\alpha,\beta)=\int_0^1(1-u)^{\alpha-1}u^{\beta-1}du=\frac{\Gamma(\alpha)\Gamma(\beta)}{\Gamma(\alpha+\beta)}=B(\beta,\alpha) \tag{A.2.1}$$

Obviously, the Beta-integral is convergent only for and with positive real parts. However, by means of its relation with the Gamma function, it can be continued analytically to the entire complex plane, excluding negative integers and zero.

Appendix B

Table A. A comparison of S-Z approximations of the first order, taken from a broad literature, which represent special cases of a T-integrator [B1]

α	r	$a\equiv\chi_2$	χ_1	$s-z$ approximation	Name of approximation
0	-	-	1	$\frac{1}{s}\approx f_{\mathrm{FD}}(z)=\frac{T}{z-1}$	Euler approximation of first order (FD)
$\alpha\in[0,0.5]$ $\alpha=(1-\chi_1)/2$	-	-	$\chi_1\in[0,1]$	$\frac{1}{s}\approx f_{\mathrm{Le1}}(z,\chi_1)=T\frac{1+\chi_1+(1-\chi_1)z}{2(z-1)}$	parametric FD-BL approximation [45]
$\frac{1}{2}$	1	0	0	$\frac{1}{s}\approx f_{\mathrm{BL}}(z)=\frac{T}{2}\frac{z+1}{z-1}$	Tustin approximation (BL)
0.7736	0.2927	0.5471	0.5471	$\frac{1}{s}\approx=\frac{T}{1.2927}\frac{z+0.2927}{z-1}$	Dostál rule [47]
$\frac{7}{8}$	$\frac{1}{7}$	$\frac{3}{4}$	-	$\frac{1}{s}\approx\frac{7T}{8}\frac{z+1/7}{z-1}$	Al-Alaoui rule [64]
1	0	1	-	$\frac{1}{s}\approx f_{\mathrm{BD}}(z)=\frac{1}{T}\frac{z}{z-1}$	Euler approximation of second order (BD)
$\alpha\in[0,1]$	-	-	-	$\frac{1}{s}\approx f_{\mathrm{Se}}(z,\alpha)=T\frac{1+\alpha(z-1)}{z-1}$	α-approximation of first order (parametric FD-BD approximation) [42-44, 53-55]
$\alpha\in[0.5,1]$ $\alpha=(1+\chi_2)/2$	$r\in[0,1]$ $r=\frac{1-\chi_2}{1+\chi_2}$	$a\equiv\chi_2\in[0,1]$	-	$\frac{1}{s}\approx f_{\mathrm{Le2}}(z,\chi_2)=T\frac{1+\chi_2+(1-\chi_2)z}{2(z-1)}$	parametric BD-BL approximation [46]
$\alpha\in[0.5,1]$ $\alpha=1/(1+r)$ $\alpha=(1+a)/2$	$r\in[0,1]$ $r=\frac{1-a}{1+a}$	$a\in[0,1]$ $a=\frac{1-r}{1+r}$	-	$\frac{1}{s}\approx f_{\mathrm{DP}}(z,r)=\frac{T}{1+r}\frac{z+r}{z-1}$ $\frac{1}{s}\approx f_{\mathrm{AL}}(z,a)=T\frac{1+a+(1-a)z}{2(z-1)}$	Parametric BD-BL approximation [64, 65]

[B1] K. J. Åström, B. Wittenmark, *Computer Controlled Systems: Theory and Design, 3. ed.*, Prentice-Hall, 1997

Appendix C

Appendix C1 *Gronwall-Bellman lemma*

Lemma (*Gronwall-Bellman lemma*), [C.1]

Let $u(t), c(t)$ and $k(t)$ be real continuous functions defined in $[a,b], k(t) \geq 0$ for $t \in [a,b]$. We suppose that on $[a,b]$ we have the inequality

$$u(t) \leq c(t) + \int_a^t k(\tau) u(\tau) d\tau, \tag{C.1.1}$$

then

$$u(t) \leq c(t) + \int_a^t k(\tau) c(\tau) \exp\left[\int_\tau^t k(s) ds\right] d\tau. \tag{C.1.2}$$

in $[a,b]$.

Corollary 1: If $c(t)$ is differentiable, then from (C.1.1) it follows that

$$u(t) \leq c(a)\left(\int_a^t k(s) ds\right) + \int_a^t \exp\left[\int_\tau^t k(s) ds\right] c'(\tau) d\tau. \tag{C.1.3}$$

for all $t \in [a,b]$.

Corollary 2: If $c(t)$ be a positive, monotonic decreasing function, then from (C.1.1) it follows that

$$u(t) \leq c(t) \exp\left(\int_a^t k(\tau) d\tau\right), \tag{C.1.4}$$

for all $t \in [a,b]$.

[C.1] J.K. Hale, *Functional Differential Equations,* Springer, New York,1971

Appendix C.2 Mittag-Leffler function

Mittag-Leffler function appears in two forms and can be considered as a generalization of the exponential function. Mittag-Leffler function generalizes the exponential in two ways. First, its series expansion is a straightforward generalization of the exponential series. Second, solutions to a number of fractional differential equations are expressed in terms of the Mittag-Leffler function just in the same way as the solutions to a number of ordinary differential equations are expressed in terms of the exponential (and its trigonometric relatives). The *single-parameter Mittag-Leffler function* (in fact, the only form actually considered by Mittag-Leffler) is defined as [C2]

$$E_\alpha(z) = \sum_{k=0}^{\infty} \frac{z^k}{\Gamma(k\alpha + 1)}, \tag{C.2.1}$$

where $\alpha > 0$ and z is an arbitrary complex number. The *two-parameter Mittag-Leffler function* appears most frequently and has the following form

$$E_{\alpha,\beta}(z)=\sum_{k=0}^{\infty}\frac{z^k}{\Gamma(k\alpha+\beta)}, \tag{C.2.2}$$

where $\alpha>0$, $\beta>0$, and z is an arbitrary complex number.

The importance of the Mittag-Leffler function in a broader concept lays in the fact that for specific values of its parameters, the Mittag-Leffler function reduces to a number of special functions appearing in various fields of engineering. For example, $E_{\alpha,1}(z)=E_{\alpha}(z)$, $E_{1,1}(z)=e^{z}$, $E_{2,1}(z)=\cosh(\sqrt{z})$, $E_{2,1}\left(-z^2\right)=\cos(z)$.

The Laplace transform of the Mittag-Leffler function can be easily found to be

$$\int_0^{\infty}e^{-st}t^{\alpha k-\beta-1}E_{\alpha,\beta}^{(k)}\left(\pm at^{\alpha}\right)dt=\frac{k!s^{\alpha-\beta}}{\left(s^{\alpha}\mp a\right)^{k+1}},\left(\Re(s)>|a|^{1/n}\right) \tag{C.2.3}$$

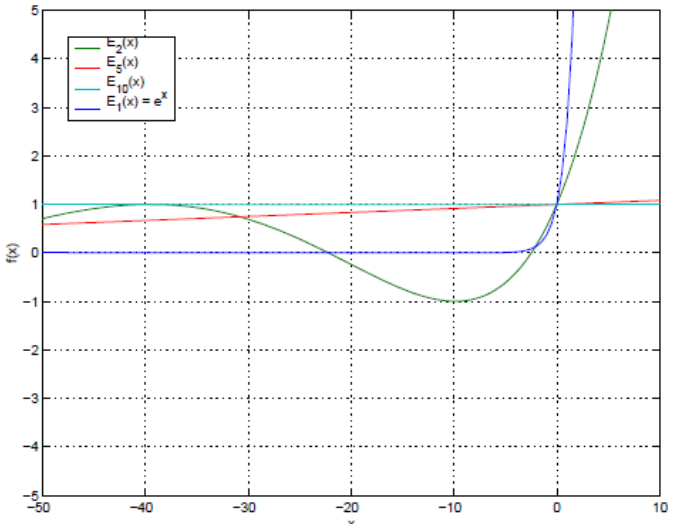

Fig.C.1: The Mittag-Leffler function for different $\alpha,\beta=1$

[C2] A.A. Kilbas, H.M. Srivastava, J.J. Trujillo,*Theory and applications of Fractional Differential equations*, edited by J.V. Mill.Elsevier, Amsterdam,2006.

Appendix D

Human Skin

Human skin is the body`s largest organ. It is a major part of integumentary system which comprises between 15-20 % of the total body weight, and covers 1,5-2 m^2 of surface area. Each square centimeter of human skin has $6*10^6$ cells, $5*10^3$ sensory points, 15 sebaceous glands and 100 sweat glands.

Functions of Human Skin

As an organ that interfaces with the environment, skin plays a key role in *protecting* the body from damage and against pathogens (see [D1,D2]). In the human skin Langerhans cells play a protective role since they are a part of the adaptive immune system. Important functions of human skin are insulation and temperature regulation. Skin *heat regulation* is performed by controlling blood supply. Since skin blood supply is far greater than its requirements heat regulation is controlled by vasodilatation and vasoconstriction (constricted blood vessels reduce cutaneous blood flow and conserve heat, while dilated blood vessels increase heat loss).
Another important function of skin is *control of evaporation*. The skin provides semi-impermeable barrier controlling the body fluid loss. Sweat *excretion* containing small amount of urea is accomplished by skin. However, excretion by sweating is at most a secondary function to *temperature regulation*. *Absorption* is also one of the functions of skin. Oxygen (see [D.3]), nutrients or synthetic chemicals, applied topically are adsorbed and/or transported through skin (see [D.4,D.5]). The skin acts also as water resistant barrier so essential nutrients could not be washed out of body. The other important function of human skin is *sensation*. Skin tissue contains variety of nerve endings that react to variety of sensations such as touch, pressure, vibration, heat and cold and tissue injury. Finally, function of human skin is *storage* and synthesis: skin acts as a storage center for lipids and water; synthesis of vitamin D by action of UV.

Structure of Human Skin

Human skin (Figure 1.) is composed of three major layers:

- epidermis
- dermis
- hypodermis

EPIDERMIS

The epidermis (Fig.D.1.) is the top layer of human skin, and therefore it is the first barrier between body and outside world. The thickness of the epidermis is approximately 0,5-1mm. The epidermis contains four types of cells: Merkel cells, keratinocites, melanocites and Langerhans cells. Epidermis consists of five sub layers which are usually named as five strata (Fig.D.1.):

- stratum corneum,
-stratum lucidum,
-stratum granulosum,
-stratum spinosum,
-stratum germinativum (stratum basale)

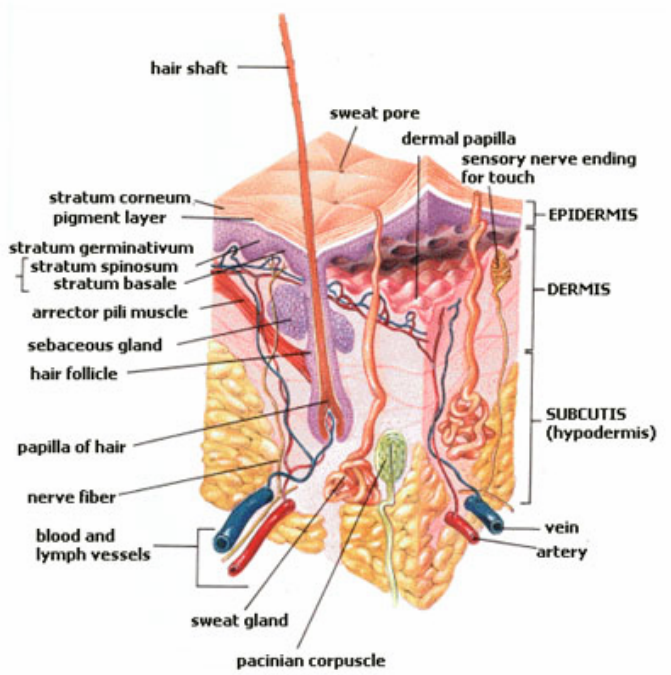

Fig D.1. Structure of human skin (see [D.6])

Keratinocites are formed through mitotic cell division at the lowermost portion of epidermis-stratum basale. The daughter cells move upwards. As they mature, these cells lose water, flatten out and at the end of their life cycle they reach the uppermost layer of the epidermis – stratum corneum. Therefore, stratum corneum contains mainly dead keratinocites, keratin proteins and lipids forming a protective barrier. Dead cells from stratum corneum permanently slough of and are replaced by new cells coming from below. Human skin completely renews itself for approximately 3-5 weeks.
Melanocites are another significant group of cells. These cells produce melanin the pigment responsible for skin color. Langerhans cells are the front door of the immune system and they prevent foreign substances from penetrating the skin. As shown in Fig. D.1. epidermis consists of many layers. Stratum corneum is outer layer made of flattened epithelial dead cells organized in multiple sub layers. Next layer below is translucent and transitional thin layer of cells which might be visible in thick skin. However, nuclei and/or other organelles are not visible. Cytoplasm of these cells is mostly made of keratin filaments. Next three to five layers (supra basal layers) consist of flattened polygonal cells that have granules in cytoplasm. Below them is a layer of cells that contains bundles of keratin filaments and these cells are cube-shaped. The last layer positioned above the basement membrane and the dermis is basal or cell division layer. It is a single layer of cells that undergo mitosis to renew the epidermal upper layers.

DERMIS
The dermis is the middle layer of the skin positioned between the epidermis and hypodermis. It is the thickest skin layer. The major components of the dermis are collagen and elastin fibers. These macromolecular proteins are important for resilience of the skin tissue. The dermis fibroblasts synthesize collagen and elastin as well as other structural molecules. Lymph nodes and capillaries are also important constituents of the dermis. Capillaries are essential for nourishing, oxygenating and temperature regulation of the human skin. They are also very important for protecting the skin from invading microorganisms. Sweat glands, hair follicles, sebaceous glands as well as small number of muscle and nerve cells are also present in the dermis. Sebaceous glands are of particular importance for skin health since they produce sebum oily protective substance that lubricates and water proofs the skin.

HYPODERMIS
The hypodermis is located below the dermis. The purpose of this layer is to attach the skin to bone and muscle and to supply it with nerves and blood vessels. It contains a loose connective tissue and elastin. Hypodermis contains fibroblasts, adipocytes and macrophagues as a main cell types. In the subcutaneous tissue the

predominant type of cells are fat cells. The fat acts as heat insulator protecting underlying tissue from cold and mechanical trauma.

D.1 Proksch, E; Brandner, JM; Jensen, JM (2008). "The skin: an indispensable barrier.". *Experimental Dermatology* **17** (12): 1063–72.

D.2 Madison, KC. (2003). "Barrier function of the skin: "la raison d'être" of the epidermis",*J Invest Dermatol* **121** (2): 231–41.

D.3 Stücker, M., A. Struk, P. Altmeyer, M. Herde, H. Baumgärtl & D.W. Lübbers (2002). The cutaneous uptake of atmospheric oxygen contributes significantly to the oxygen supply of human dermis and epidermis., *Journal of Physiology* **538**(3): 985–994.

D.4 Felipe, P., Silva, J.N., Silva, R., Cirne de Castro, J.L., Gomes, M., Alves, L.C., et al. Stratum Corneum Is an Effective Carrier to TiO2 and ZnO Nanoparticle Percutaneous Absorption. Skin Pharmacology and Physiology 2009;22:266-275

D.5 Vogt, A., Combadiere, B., Hadam, S., Stieler, K., Lademann, J., Schaefer, H., et al. 40nm, but not 750 or 1,500 nm, Nanoparticles Enter Epidermal CD1a+ Cells after Transcutaneous Application on Human Skin. Journal of Investigative Dermatology

D.6 Wikipedia: http://en.wikipedia.org/wiki/Skin

APPENDIX E

APPENDIX E.1 NOMENCLATURE

DNA – Deoxyribonucleic acid (DNA)

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

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

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

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

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

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

m_α $[\,kg\,]$- the value of the base mass

$r_\alpha[\,m\,]$ - the length

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

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

$K_{k,i} = K = 6\times10^3[\text{KJmol-1}]$- for the calculation that the most appropriate value is close /

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

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

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

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

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

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

A_k - amplitude

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

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

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

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

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

APPENDIX E.2

dDNA is biological molecule involved in two very important processes in the living cell: replication (doubling the DNA molecule and consequently the genetic material) and transcription (transcribing the information from DNA to RNA). Replication is a part of the cell division process when one cell is dividing into two new cells but with same genetic information. Translation occurs in all metabolically active cells and it is necessary for one cell to live. As dDNA is placed in nucleus (in 46 chromosomes in somatic cells) and cell organelles called mitochondria in the form of very long polymers it is packed and condensed and in that form it is inactive. Only parts of dDNA that are currently in function are decondensed, unzipped and transcribed. The condensed form of dDNA is possible gratefully to the special type of proteins called histons and special elastic properties of dDNA that are also relevant for DNA's physiological function." The elastic properties of a molecule of duplex DNA are strongly dependent on nucleotide sequence." (see Ref [9] by Coleman et al. 2003). They proposed the theoretical model where the sequence dependence of elastic properties of dDNA is determined by the kinematical variables, called tilt, roll, twist, shift, slide, and rise, (see Fig E.2.1) that describe the relative orientation and displacement of the *n*th and (*n*11)th base pairs. Very important are the symmetry imposed on previous mentioned kinematic variables by the complementarities of bases, i.e., of A to T and C to G, the antiparallel nature of the DNA sugar–phosphate chains, and the requirement that kinematic variables are independent of the choice of the direction of increasing *n,*(see Ref [9] by Coleman at al. 2003).

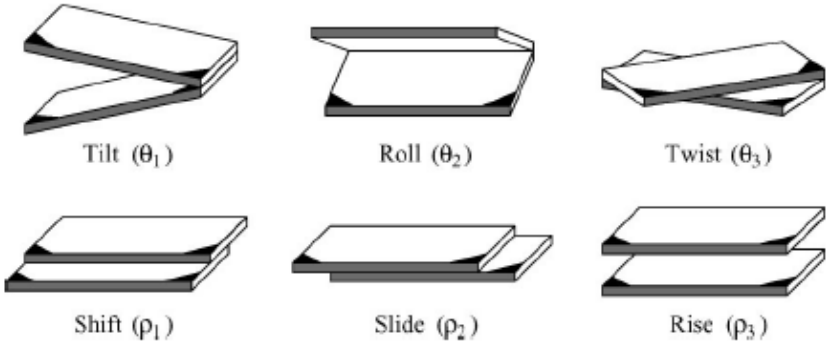

Fig E2.1. Relative orientation and displacement of successive base pairs. From Coleman B.D., Olson W.K., and Swigon, 2003. (Ref [9])

The special enzymes, named topoisomerases, unzipped and zipped dDNA in process of replication and transcription." Topoisomerases relieve the torsional strain in DNA that is built up during replication and transcription." (See [40] by Koster et al, 2005). Using real-time single-molecule observation, Koster et al. (See [40] by Koster et al, 2005) show that Topoisomeras B releases supercoils by a swivel mechanism that involves friction between the rotating DNA and the enzyme cavity: the DNA does not freely rotate. TopIB does not release all the supercoils at once, but in multiple steps. "The number of supercoils removed per step follows an exponential distribution. The enzyme is found to be torque-sensitive, as the mean number of supercoils per step increases with the torque stored in the DNA." (See [40] by Koster et al, 2005).

DNA mechanical models

A number of models have been constructed to describe different kinds of movements in a DNA molecule: asymmetric and symmetric motion; movements of long and short segments; twisting and stretching of dsDNA, twist-opening conditions. Some models have, for example, been made for circular double-stranded DNA molecules in viral capsids. We are discussing here *polymer models, elastic rod models, network models, torsional springs models, soliton -existence supporting models***,**(see [23] by Hedrih, 2011).

Polymer models

In polymer models DNA molecule is considered to be a polymer and calculations are done as for other polymers.There are several DNA polymer models:

- Gaussian polymer (GP) model

- Freely Jointed Chains (FJC) model,
- Worm –Like Chain (WLC) model
- Worm –Like Rod Chain (WLRC) model (see Ref [8] by Cocco et al, 2002).see Fig. E.2.2.
- bead–spring model

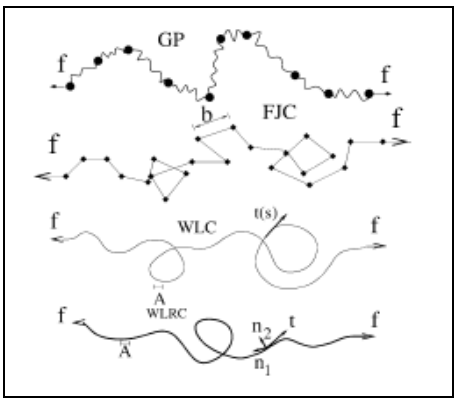

Fig E.2.2 Polimer models. From: Cocco,et al. 2002. (Ref [8])

Double strained DNA differs from simple polymers because it exhibits torsional and bending stiffness and under tension DNA supercoiles. These models are used to interpret single-molecule force-extension experiments on single strand DNA and dDNA. They show how combining the elasticity of two single nucleic acid strands with a description of the base-pairing interactions between them explains much of the phenomenology and kinetics of RNA and DNA 'unzipping' experiments" (see [8] by Cocco et al, 2002 and [56] by Zhou and Lai, 2001).

"A limitation of the initial WLC model was the assumption of intrinsically straight homogeneous polymers whose thermal fluctuations are quantified as deviations from the straight line. DNA almost always contains curved regions, which can strongly affect the persistence length", (see [1] by Anselmi et al, 2005).

"For better fitting the experimental data in to the WLC polymer model Seol et al, (see [50] by Seol et al, 2007) develop finite wormlike chain (FWLC) model. FWLC models are suitable for both short (a few hundred nanometers in contour length) and very long (microns in contour length) molecule." (See [23] by Hedrih, 2011).

In the *bead–spring model* the DNA chain is modeled as a bead–rod system with the first-order effective bead–spring integration scheme. The proposed effective bead–spring model may help simulate the dynamic behaviors of many types of polymer chains with different chain elasticity via an efficient unified integration scheme with large time steps. Combining with angular springs, this model can also be used to simulate the bending behaviors of semiflexible polymers, (see ref [44] by Liu et al, 2008).

Elastic rod models

DNA can be modeled as an ideally elastic rod, or as an anisotropic rod. There are several types of elastic rod models:

- simple elastic rod models
- sequence-dependent anisotropic elastic model
- asymmetric elastic rod model

"In *simple elastic rod models* rod is ideally elastic which means that it will return to its original shape after deformation; one can compute the energy necessary for bending, stretching or torsional deformation. The model is not sequence dependent (i.e. all segments are equal) and the model is equally bendable (deformable) in all directions. The phenomena that can be described using such simplified elastic model include gross shape changes in DNA, such as supercoiling, the response of plasmids to stress, etc. A technique of finite element analysis has been applied successfully for small DNA deformations. Model is suitable for DNA in plasmids (see [46] by Munteanu et al, 1998). If DNA is modeled as a homogeneous and isotropic elastic rod, the DNA chain is characterized by three parameters: The bending rigidity, the torsional rigidity, and the DNA effective diameter,(see [45] by Maxim and Kamenetskii, 1997).

In *sequence-dependent anisotropic elastic model* DNA is considered to be an initially straight, segmented, elastic rod, in which the flexibility of each segment is greater towards the major groove than it is in other directions. This model can predict local bending phenomena and explains phenomena as the affinity of protein binding and kinking (see [46] by Munteanu et al, 1998). Goyal and Perkins (see [17] by Goyal and Perkins, 2008) extend a computational rod model that captures the non-linear dynamics of hyperelastic, isotropic rods to accommodate large and discontinuous variations in bending and torsional stiffness.

Modeling DNA, as an isotropic rod can't explain some mechanical properties of DNA molecule achieved experimentally (twist-strech coupling in single DNA measured by rotor bead tracking technique) like overwinding of DNA molecule under tensions. DNA molecule reaches the maximum twist level at a tension of 30 pN, as tension is increased above this critical value, the DNA begins to unwind. Elastic rod model can explain these unusual mechanical properties.

DNA is modeled as an elastic rod wrapped helically by a stiff wire. The inner core of radius R is assumed to have a Poisson's ratio v= 0.5. "The outer wire is affixed to the inner rod helically with a pitch of 3.4 nm, and contributes to the overall mechanical properties because it resists stretching and compression. The outer helix increases the torsional rigidity and yields a twist–stretch coupling that depends upon the helix angle. Stretching generates an overwinding of the helix because the inner rod decreases in diameter as it is stretched. The outer helix is then able to wrap a larger number of times over the length of the molecule."…"These results have implications for the action of DNA-binding proteins that must stretch and twist DNA to compensate for variability in the lengths of their binding sites." (See Ref [18] by Gore et al, 2006). Linear isotropic rod model has some limitations in predicting DNA supercoiling of long molecules under applied tension and twist. There is coupling between bending and stretching (See Ref [51] by Smith and Healey 2008). Bend-twist coupling is important in predicting the stability boundary. Eslami-Mossallam and Ejtehadi, (See Ref [13] by Eslami-Mossallam and Ejtehadi, 2009) proposed the asymmetric elastic rod model for DNA.

Model of Leburn and Lavery (See Ref [43] by Lebrun and Lavery, 1996) show how the double helix can be extended to twice its normal length before its base pairs break. Results correlate well with nanomanipulation experiments." (See Ref [23] by Hedrih, 2011).

The network model

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

No inner dynamical degrees of freedom of the nucleotides are taken into account that is justified by the time scale separation between the small-amplitude and fast vibrational motions of the individual atoms and the slower and relatively large-amplitude motions of the atom groups constituting the nucleotides. The nucleotides are considered as identical objects of fixed mass all of four types of bases are treated as equal. The network model can explain the mechanical stability and elasticity properties of dsDNA molecules. This model is suitable for studying the opening-closing dynamics of dsDNA molecules that are forced into non-equilibrium conformations, which are relevant for bimolecular processes. Hennig and Archilla (see Ref [39] by Hening and Archilla, 2004) show that the attainment of a quasi-equilibrium regime proceeds faster in the case of the twisted DNA form, than for its thus less flexible ladder counterpart (see Ref [23] by Hedrih, 2011).

Torsional spring model

In torsional springs model Tung et al (see Ref [53] by Tung and Harvey, 1984) made a distinction between purine bases (adenine and guanine) and also between pyrimidines, (cytosine and thymine), using the atomic resolution of conformational energy calculations. See Fig E.2.3.

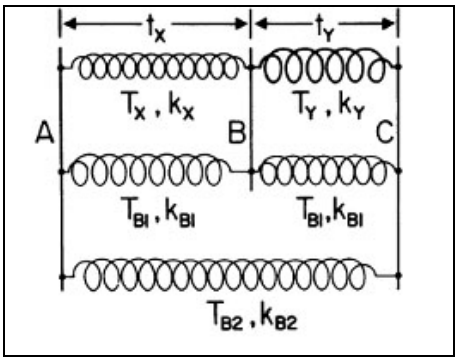

Fig E.2.3 Torsional spring model- Torsional spring model for helix twist angles of a trimer. Distances in this figure correspond to angels not to lengths. From : Tung, CS, and S.C. Harvey, 1984. (ref [53]).

The model predicts a macroscopic torsional stiffness and a longitudinal compressibility (Young's modulus) that are both in good agreement with experiment. They use conformational energy calculations to determine the parameters of the model, and can quantitatively predict helix twist angles (see [53] by Tung and Harvey, 1984), (see [23] by Hedrih, 2011**).**

Soliton -existence supporting models

There several types and its modifications of soliton- existence supporting models:

- *Yakushevich model (Y model)*
- *The composite model (Y based model)*
- *Dynamic plane–base rotator model (See [54] byVasumathi and Daniel, 2008).*
- *Symmetric twist-opening model of DNA. (See f [52] Tabi et al, 2009),*
- *Nonlinear Volkov-Kosevich DNA model*
- *Peyrard–Bishop–Dauxois (PBD)*
- *Cross-grained model by Kovaleva and L. Manevich* (*Y based model) (see [41,42] by Kovaleva et al, 2007; Kovaleva and Manevich, 2005)*

One of the first of this kind was *Yakushevich model (Y model) of DNA* and models based on it (see [15] by Gaeta, 1992, as well as [16] by González and Martín-Landrove,1994)). Dynamics of topological solitons describing open states in the DNA double helix are studied in the framework of a model that takes into account asymmetry of the helix. Yakushevich, et al (see [55] by Yakushevich, et al, 2002) investigated interaction between the solitons, their interactions with the chain inhomogeneities and stability of the solitons with respect to thermal oscillations and have shown that three types of topological solitons can occur in the DNA double chain. The composite model for DNA is also based on Y model. The sugar-phosphate group and the base are described by separate degrees of freedom. The composite model fits experimental data better than the simple Y model. DNA nucleotides are represented as two distinct discs, one still centered about the backbone axis and representing the sugar–phosphate group and the second rigidly rotating about a fixed point of the former. The composite model supports solitonic solutions, qualitatively and quantitatively very similar to the Yakushevich solitons. (See [11] by De Leo and Demelio, and [7] by 2008; Cadoni et al, 2008).

Dynamic plane–base rotator model is suitable for study the nonlinear dynamics of the inhomogeneous dDNA especially angular rotation of bases in a plane normal to the helical axis. (See [10] by Daniel and Vasumathi, 2007). This model is also used to study the effect of phonon interaction on base pair opening in the dsDNA. The velocity of the soliton increases or decreases or remains uniform or even the soliton stops depending on the values of the coupling strengths. There is no change in the topological character of the soliton in the asymptotic region. (See [54] by Vasumathi and Daniel, 2008).

DNA model by N. Kovaleva and L. Manevich

In this model, three beads represent each nucleotide with interaction sites corresponding to phosphate group, group of sugar ring, and the base, see Fig 2a and 2b in the main text. (See [41] by Kovaleva et al, 2007). It is soliton-supporting model.

It is planer DNA model in which the chains of the macromolecule from two parallel strait lines place at a distance *h* from each other, the bases can make only rotation motions around their own chain, being all the time perpendicular to it. N. Kovaleva et al. (See Ref [41,42] by Kovaleva et al, 2007; Kovaleva and Manevich, 2005) point out that solitons and breathers play a functional role in DNA chains. They show that a localized excitation (breather) can exist in a double DNA helix. Authors formulated conditions of the breathers' existence and estimate their characteristic parameters describing opening of DNA double helix. They investigated also the stability of breathers.

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

Hedrih and Hedrih, (See Ref [35-38] by Hedrih (Stevanović) and Hedrih, 2010; 2009a, 2009b, 2009c) gave several mechanical models of double DNA. In their models DNA is in a form of homogenous multi-chain/ multi-pendulum system which oscillatory signals can be considered trough a system with fixed and with free ends. See Fig. 3 and 4 in the main text. These figures are for the ideal elastic model and different boundary conditions. The dynamics of oscillatory signals in multi-chain systems are represented in ref [27] (Hedrih (Stevanovic) 2006). Their basic model is linearization of the model propose by Kovaleva and Manevich (See Ref [42] by Kovaleva and Manevich, 2005). System is considered as homogeneous, which means that all the masses are equal; rigidities of the linear-elastic spring elements are equal. The models differ in the way of coupling between the material (mass) particles. If the martial (mass) particles are coupled with standard light hereditary elements the model has viscoelastic properties; if the martial particles are coupled with standard light fractional order elements it has viscoelastic and creep properties. They are several types of these models:

- *Model with ideally elastic properties (linear or nonlinear),*
- *Model with hereditary properties and*
- *Fractional order model*.

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

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

- **Model with ideally linear elastic properties**

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

$$\frac{1}{\omega_0^2}\ddot{\xi}_{\mathbf{k}} - \xi_{\mathbf{k+1}} + 2\xi_{\mathbf{k}}\left[1+\mu-\kappa\right] - \xi_{\mathbf{k-1}} = 0\,,\ k=1,2,3,.....,n \tag{E.2.1}$$

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

$$\frac{1}{\omega_0^2}\ddot{\eta}_{\mathbf{k}} - \eta_{\mathbf{k+1}} + 2\eta_{\mathbf{k}}(1+\mu) - \eta_{\mathbf{k-1}} = 0\,, \qquad k=1,2,3,.....,n \tag{E.2.2}$$

of the n eigen circular frequencies of the second eigen main chain of the homogeneous double DNA chain helix. In the case of forced oscillatory regimes, using the obtained sets of eigen circular frequencies obtained from subsystems (E.2.1)-(E.2.2), it is possible that resonant regimes on the corresponding circular frequencies are present only on one eigen main chain, while in the other eigen main chain forced oscillatory regimes are normal, without resonance. Also, in forced frequency regimes it is possible to identify phenomena of dynamical absorptions, without losing mechanical energy of the double DNA chain helix (for detail see [35] Hedrih (Stevanović) and Hedrih, 2010). Also, we obtained two subsets of the eigen circular frequencies (ω^2_s) of the vibration signal modes of separate eigen main chains *in* the double DNA chain helix using the trigonometric method (See [48,49,27,28] by Rašković and Hedrih (Stevanović)), as well as amplitudes. Two subsets of eigen circular frequencies are obtained in the following forms (for detail see [36,37,35], Hedrih (Stevanović) and Hedrih):

$$\omega_s^2 = 2\omega_0^2\left[2\sin^2\frac{\varphi_s}{2} + (\mu-\kappa)\right],\ \ \omega_r^2 = 2\omega_0^2\left[2\sin^2\frac{\vartheta_r}{2} + \mu\right],\quad s,r=1,2,3,4...,n \tag{E.2.3}$$

where φ_s and ϑ_r are characteristic numbers depending of boundary conditions of the model of the double DNA linear order chain helix. By use corresponding boundary conditions of the obtained eigen main chains of the considered double DNA linear order chain helix it is easy to obtain corresponding values of these characteristic numbers in a case when both ends of the of the double DNA chain helix are free as well as fixed.

- **Model with Hereditary Properties**

This model of double DNA is considered as a homogeneous system containing two coupled multi pendulum subsystems. Corresponding material particles of the corresponding multi-pendulum chains are each two inter coupled by one standard light hereditary element (see [35,38,20,22] by Hedrih (Stevanović) and Hedrih, 2009a, 2009c, Goroško and Hedrih (Stevanović), 2001, 2008). Standard light hereditary element has relaxation time *n.* Biological materials are changing their mechanical properties during aging. Biomaterials during aging may express relaxation properties and delay elasticity. We propose model with hereditary properties because it may be suitable for explaining this behavior.

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

a* first subset:

$$\delta_{0(\xi,s)} = \frac{k}{n}\left[1+\frac{(1-k)k}{n^2\omega_{\xi,s}^2}\right],\quad \delta_{(\xi,s)} = \frac{1-k}{2n}\left[1-k^2\frac{1}{n^2\omega_{\xi,s}^2}\right] \text{ and } \tilde{\omega}_{(\xi,s)}^2 = \omega_{\xi,s}^2\left[1-(1-k)\frac{1+3k}{4}\frac{1}{4n^2\omega_{\xi,s}^2}\right] \tag{E.2.4}$$

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

b* Second subset:

$$\delta_{0(\eta,r)} = \frac{k}{n}\left[1+\frac{(1-k)k}{n^2\omega_{\eta,r}^2}\right],\quad \delta_{(\eta,r)} = \frac{1-k}{2n}\left[1-k^2\frac{1}{n^2\omega_{\eta,r}^2}\right] \text{ and } \tilde{\omega}_{(\eta,r)}^2 = \omega_{\eta,r}^2\left[1-(1-k)\frac{1+3k}{4}\frac{1}{4n^2\omega_{\eta,r}^2}\right] \tag{E.2.5}$$

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

APPENDIX E.3

Expansion of the Laplace transform into series (for details see [19] by Gorenflo and Mainardi (2000); [3] by Bačlić and Atanacković (2000) and [34] by Hedrih (Stevanović) and Filipovski (2002)):

$$\mathsf{L}\{\xi_2\} = \frac{p\varphi_{0i} + \dot{\varphi}_{0i}}{2\left(p^2 + \omega_{0\alpha}^2 p^\alpha + \widetilde{\omega}_0^2 + \omega_{00}^2\right)} \tag{E.3.1}$$

$$\mathsf{L}\{\xi_2(t)\} = \frac{p\varphi_{01} + \dot{\varphi}_{01}}{2p^2\left[1 + \frac{\omega_{0\alpha}^2}{p^2}\left(p^\alpha + \frac{\widetilde{\omega}_0^2 + \omega_{00}^2}{\omega_{0\alpha}^2}\right)\right]} = \left(\varphi_{01} + \frac{\dot{\varphi}_{01}}{p}\right)\frac{1}{2p}\frac{1}{\left[1 + \frac{\omega_{0\alpha}^2}{p^2}\left(p^\alpha + \frac{\widetilde{\omega}_0^2 + \omega_{00}^2}{\omega_{0\alpha}^2}\right)\right]} \tag{E.3.2}$$

$$\mathsf{L}\{\xi_2(t)\} = \left(\varphi_{01} + \frac{\dot{\varphi}_{01}}{p}\right)\frac{1}{2p}\sum_{k=0}^{\infty}\frac{(-1)^k\omega_{0\alpha}^{2k}}{p^{2k}}\left(p^\alpha + \frac{\widetilde{\omega}_0^2 + \omega_{00}^2}{\omega_{0\alpha}^2}\right)^k \tag{E.3.3}$$

$$\mathsf{L}\{\xi_2(t)\} = \left(\varphi_{01} + \frac{\dot{\varphi}_{01}}{p}\right)\frac{1}{2p}\sum_{k=0}^{\infty}\frac{(-1)^k\omega_{0\alpha}^{2k}}{p^{2k}}\sum_{j=0}^{k}\binom{k}{j}\frac{p^{\alpha j}\omega_{0\alpha}^{2(j-k)}}{\left(\widetilde{\omega}_0^2 + \omega_{00}^2\right)^j} \tag{E.3.4}$$

APPENDIX E.4

Solution of a fractional order differential equation of a fractional order creep oscillator with single degree of freedom.The fractional order differential equations obtained and the considered cases of eigen fractional order partial oscillators of the hybrid fractional order multichain system are in mathematical analogy to the same fractional order differential equation with corresponding unknown time-functions. We can use the notation $T(t)$ and all previously derived fractional order differential equations of eigen fractional order partial oscillators with one degree of freedom correspond to the hybrid fractional order multichain system dynamics with sixth degree of freedom, and can be rewritten in the following form:

$$\ddot{T}(t) \pm \omega_\alpha^2 T^{(\alpha)}(t) + \omega_0^2 T(t) = 0 \tag{E.4.1}$$

This fractional order differential equation (E.4.1) on unknown time-function $T(t)$, can be solved applying the Laplace transforms (see [19] by Gorenflo, R., Mainardi, F., (2000); [3] by Bačlić, B. S., Atanacković, T., (2000) or [34] by Hedrih (Stevanović) K. and Filipovski A.,(2002)). Upon that fact, the Laplace transform of solution is in the form:

$$\mathsf{T}(p) = \mathsf{L}[T(t)] = \frac{pT(0) + \dot{T}(0)}{p^2 + \omega_0^2\left[1 \pm \frac{\omega_\alpha^2}{\omega_0^2}\mathbf{R}(p)\right]} \tag{E.4.2}$$

where $\mathsf{L}\left[D_t^\alpha[T(t)]\right] = \mathbf{R}(p)\mathsf{L}[\mathrm{T(t)}]$ is the Laplace transform of a fractional derivative $\frac{d^\alpha T(t)}{dt^\alpha}$ for $0 \le \alpha \le 1$. For creep rheological material those Laplace transforms have the form:

$$\mathsf{L}\left[D_t^\alpha[T(t)]\right] = \mathbf{R}(p)\mathsf{L}[T(t)] - \frac{d^{\alpha-1}}{dt^{\alpha-1}}T(0) = p^\alpha\mathsf{L}[T(t)] - \frac{d^{\alpha-1}}{dt^{\alpha-1}}T(0) \tag{E.4.3}$$

where the initial values are:

$$\left.\frac{d^{\alpha-1}T(t)}{dt^{\alpha-1}}\right|_{t=0} = 0 \tag{E.4.4}$$

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

$$\mathsf{L}\{T(t)\} = \frac{pT_0 + \dot{T}_0}{\left[p^2 \pm \omega_\alpha^2 p^\alpha + \omega_0^2\right]} \tag{E.4.5}$$

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

$$1^*\quad \ddot{T}(t) \pm \widetilde{\omega}_{0\alpha}^2 T^{(0)}(t) + \omega_0^2 T(t) = 0 \text{ for } \alpha = 0 \tag{E.4.6}$$

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

$$2^*\quad \ddot{T}(t) \pm \omega_{1\alpha}^2 T^{(1)}(t) + \omega_0^2 T(t) = 0 \text{ for } \alpha = 1 \tag{E.4.7}$$

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

The solutions to equations (E.4.6) and (E.4.7) are:

$$1^*\ T(t)=T_0\cos t\sqrt{\omega_0^2\pm\widetilde{\omega}_{0\alpha}^2}+\frac{\dot{T}_0}{\sqrt{\omega_0^2\pm\widetilde{\omega}_{0\alpha}^2}}\sin t\sqrt{\omega_0^2\pm\widetilde{\omega}_{0\alpha}^2} \tag{E.4.8}$$

for $\alpha=0$.

2* a.

$$T(t)=e^{\mp\frac{\omega_1^2}{2}t}\left\{T_0\cos t\sqrt{\omega_0^2-\frac{\omega_{1\alpha}^4}{4}}+\frac{\dot{T}_0}{\sqrt{\omega_0^2-\frac{\omega_{1\alpha}^4}{4}}}\sin t\sqrt{\omega_0^2-\frac{\omega_{1\alpha}^4}{4}}\right\} \tag{E.4.9}$$

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

2* b.

$$T(t)=e^{\mp\frac{\omega_{1\alpha}^2}{2}t}\left\{T_0 Ch\, t\sqrt{\frac{\omega_{1\alpha}^4}{4}-\omega_0^2}+\frac{\dot{T}_0}{\sqrt{\frac{\omega_{1\alpha}^4}{4}-\omega_0^2}}Sh\, t\sqrt{\frac{\omega_{1\alpha}^4}{4}-\omega_0^2}\right\} \tag{E.4.10}$$

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

For the critical case:

$$2^*\text{ c.}\qquad T(t)=e^{\mp\frac{\omega_{1\alpha}^2}{2}t}\left\{T_0+\frac{2\dot{T}_0}{\omega_{1\alpha}^2}t\right\}\text{ for }\alpha=1\quad\text{and}\quad\omega_0=\frac{1}{2}\omega_{1\alpha}^2. \tag{E.4.11}$$

Fractional-differential equation (E.1.1) for the general case, when α is real number from the interval $0<\alpha<1$ can be solved by using Laplace's transformation. Using:

$$\mathsf{L}\left\{\frac{d^\alpha T(t)}{dt^\alpha}\right\}=p^\alpha\mathsf{L}\{T(t)\}-\left.\frac{d^{\alpha-1}T(t)}{dt^{\alpha-1}}\right|_{t=0}=p^\alpha\mathsf{L}\{T(t)\} \tag{E.4.12}$$

and introducing for initial conditions of fractional derivatives in the form (E.4.3), and after taking Laplace's transform of the equation (E.4.1), we obtain a corresponding equation. *Analyzing the previous Laplace transform (E.4.12) of solution we can conclude that two cases can be considered.*

For the case when $\omega_0^2\neq0$, the Laplace transform solution can be developed into series in the following way:

$$\mathsf{L}\{T(t)\}=\frac{pT_0+\dot{T}_0}{p^2\left[1+\frac{\omega_\alpha^2}{p^2}\left(\pm p^\alpha+\frac{\omega_0^2}{\omega_\alpha^2}\right)\right]}=\left(T_0+\frac{\dot{T}_0}{p}\right)\frac{1}{p}\frac{1}{1+\frac{\omega_\alpha^2}{p^2}\left(\pm p^\alpha+\frac{\omega_0^2}{\omega_\alpha^2}\right)} \tag{E.4.13}$$

$$\mathsf{L}\{T(t)\}=\left(T_0+\frac{\dot{T}_0}{p}\right)\frac{1}{p}\sum_{k=0}^{\infty}\frac{(-1)^k\omega_\alpha^{2k}}{p^{2k}}\left(\pm p^\alpha+\frac{\omega_0^2}{\omega_\alpha^2}\right)^k \tag{E.4.14}$$

$$\mathsf{L}\{T(t)\}=\left(T_0+\frac{\dot{T}_0}{p}\right)\frac{1}{p}\sum_{k=0}^{\infty}\frac{(-1)^k\omega_\alpha^{2k}}{p^{2k}}\sum_{j=0}^{k}\binom{k}{j}\frac{(\mp1)^j p^{\alpha j}\omega_\alpha^{2(j-k)}}{\omega_o^{2j}} \tag{E.4.15}$$

In writing (E.4.15) it is assumed that expansion leads to convergent series. The inverse Laplace transform of previous Laplace transform of the solution (E.4.15) in term-by-term steps is based on known theorem, and yields the following solution of differential equation (E.4.1) of time function in the following form of time series: (E.4.16)

$$T(t)=\mathsf{L}^{-1}\mathsf{L}\{T(t)\}=T_0\sum_{k=0}^{\infty}(-1)^k\omega_\alpha^{2k}t^{2k}\sum_{j=0}^{k}\binom{k}{j}\frac{(\mp1)^j\omega_\alpha^{2j}t^{-\alpha j}}{\omega_o^{2j}\Gamma(2k+1-\alpha j)}+\dot{T}_0\sum_{k=0}^{\infty}(-1)^k\omega_\alpha^{2k}t^{2k+1}\sum_{j=0}^{k}\binom{k}{j}\frac{(\mp1)^j\omega_\alpha^{-2j}t^{-\alpha j}}{\omega_o^{2j}\Gamma(2k+2-\alpha j)}$$

SUBJECT INDEX