Recurrent sequences and the harmonic progression in genetic biomechanics

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Abstract. The article is devoted to the study of new approaches to the development of mathematical models in genetic biomechanics, which studies the structural relationships of the genetic coding system with genetically inherited biological forms. More specifically, we are talking about models based on the recurrent harmonic progression known in science, the universal connection of which with the information sequences of DNA heredity molecules in the genomes of higher and lower organisms was revealed in the laboratory of biomechanical systems research at the IMASH RAS. This progression is associated with fundamental hyperbolic rules for organizing DNA nucleotide sequences of genomes and is represented on a two-dimensional Cartesian plane by a hyperbolic sequence associated with natural logarithms. The latter have long been used in science to adequately model many inherited biological phenomena. The article describes previously unknown connections of natural logarithms with the structure of the molecular genetic system. The problems of modeling biological phenomena in connection with the revealed structural properties of the molecular genetic system are discussed.

1. Introduction

Investigations of symmetries in inherited biological structures are an important component of biomechanics, biophysics, biochemistry, and other sciences of living matter. Many monographs, international forums, including the Nobel Symposium on Symmetries, etc. are devoted to them. The continuation of these studies is an urgent task, which is associated with the disclosure of many secrets of living nature and the creation of new biotechnologies.

In particular, these studies have long drawn attention to the recurrent structure of many inherited biological configurations, which consist of recurrently repeating blocks related, for example, by similarity symmetries; these configurations are abundant in flowers, shells of mollusks, metameric bodies of animal organisms, etc. [1]. The inheritance of configurations relies on the work of the genetic coding system, which allows the reproduction of such forms in a series of generations. Recently, in the genomes of higher and lower organisms, an important rule for the recurrent organization of DNA nucleotide sequences was discovered; these sequences serve for the transferring genetic information [2, 3]. This hyperbolic rule for the relationship of oligomeric sums is associated with a long-known harmonic progression (1):
Below we consider the use of a number of properties of this progression to build new models in genetic biomechanics and algebraic biology.

2. Computational approaches and models

Our computational approaches and models of biological structures are based on the mathematical properties of harmonic progression (1). Its historically renowned name - "harmonic progression" - derives from its association with a series of harmonics in music (or with a series of standing wavelengths in a vibrating string). It is also indirectly associated with a set of trigonometric functions in the Fourier series. Pythagoras, Orem, Leibniz, Newton, Euler, Fourier, Dirichlet, Riemann and many others were engaged in research of mathematical properties, generalizations and applications of the harmonic progression in various problems. The unexpected discovery of this recurrent harmonic progression in genomes, which are the genetic information basis of living organisms, entails many new scientific issues. The aim and objectives of this study are to study how the mathematical properties of this recurrent genetic progression (1) are able to influence the inherited biomechanical structures bearing the stamp of the structural features of genetic coding. This study leads to the emergence of new model approaches in genetic biomechanics, developing the theme of structural relationships between genetic coding and inherited biomechanical phenomena.

Organisms are cooperative aggregates of a huge number of various molecules that have the ability to reproduce themselves in their descendants. Gr. Mendel in experiments on crossing organisms showed that the inheritance of traits to descendants obeys certain algebraic rules. Thus, he actually became the founder of algebraic biology, which uses algebraic methods to model inherited biological phenomena. At present, in this regard, an international interdisciplinary seminar "Algebraic biology and systems theory" ([4]) is functioning in Moscow. According to Mendel's law of independent inheritance of traits, information from the level of genetic DNA molecules dictates the macrostructure of living bodies through many independent channels, despite strong noises and interference. For example, hair, eye, and skin colors are inherited independently of each other. This determinism is provided by unknown algorithms of multichannel noise-immune coding. Accordingly, each organism is a multichannel noise-immune coding machine. Our studies of the properties of genetic inheritance of biological structures and the possibilities of their algebraic modeling are based on the well-known mathematical formalisms of matrix and tensor analysis, recurrent sequences, the theory of information noise-immune coding, as well as on known academic information about genetic and other biological structures.

3. Results and discussion

Let us present some of the possibilities we have studied of using the mathematical properties of harmonic progression (1), which is associated with the organization of genomes of higher and lower organisms, for modeling inherited biological structures and processes.

Harmonic progression is related to the well-known concept of harmonic mean and is a recurrent sequence based on it: knowing two adjacent members of this progression, you can build the entire given progression. Indeed, the harmonic mean \( x_{n+1} \) for two numbers \( x_n \) and \( x_{n+2} \) is expressed by the relation (2):

\[
x_{n+1} = \frac{2}{\frac{1}{x_n} + \frac{1}{x_{n+2}}} \Rightarrow x_{n+1} = \frac{2x_n x_{n+2}}{x_n + x_{n+2}}
\]

Knowing two neighboring numbers \( x_n \) and \( x_{n+1} \) in this triplet of numbers, the third number \( x_{n+2} \) is determined, respectively, by the relation (3):

\[
x_{n+2} = \frac{x_n x_{n+1}}{2x_n - x_{n+1}}
\]
Successively applying this recurrence relation (3) to the first terms \( x_1 = 1 \) and \( x_2 = 1/2 \) of the harmonic progression (1), we obtain the entire series of its terms. It seems interesting and useful to investigate in the future the harmonic mean ratios in inherited biological structures and processes.

Pairs of numbers \( n \) and \( 1/n \) define points on the plane with coordinates \([n, 1/n]\) in the Cartesian coordinate system belonging to the hyperbola \( y = 1/n \), which is closely related to the natural logarithm function \( \ln x \). As you know, the natural logarithm can be defined for any positive real number "a" as the area under the hyperbola \( y = 1/x \) from 1 to \( a \) (figure 1 (a)) [5]. In the polar coordinate system \([\theta, r]\), the natural logarithm \( \ln x \) - as a function of the variable \( x \) - is represented by a spiral if \( x \) plays the role of the angular coordinate \( \theta \), and \( \ln x \) plays the role of the radius vector \( r \) (figure 1 (b)).

![Figure 1](image)

*Figure 1.* (a) Illustration of the natural logarithm \( \ln x \) as the area under the hyperbola \( y = 1/x \). (b) Natural logarithm function in polar coordinates.

This analysis gives evidences that our sensory perception obeys the same structural principles as morphogenesis with its phyllotaxis laws and that these principles can be effectively modelling on the basis of hyperbolic numbers.

The natural logarithm function is widely used in mathematical biology to model inherited biological phenomena. For example, various types of inherited sensory perceptions - sight, hearing, smell, tactile sense, taste - are subject to the basic psychophysical Weber-Fechner law, which is logarithmic. This law states that the intensity of perception is proportional to the logarithm of the intensity of the stimulus. By virtue of this law, for example, the power of sound in engineering is expressed in a logarithmic decibel scale. The logarithmic nature of perception provides the body with a huge expansion of the range of perceived stimuli, which can differ in intensity by many millions or even billions of times: for example, hammer strikes on a steel plate generate noise that is a hundred billion times louder than the quiet rustle of leaves, and the brightness of a volt arc trillions of times the brightness of a faint star, barely visible in the night sky [6]. It can be assumed that organisms use natural logarithms as the basis for their internal counting.

Taking into account the named connection of the natural logarithm function with the hyperbola \( y = 1/x \), we note that the recurrent harmonic progression (1) is conjugate, respectively, with a recurrent sequence of natural logarithms (4):

\[
\ln 1, \ln 2, \ln 3, ..., \ln n
\]

(4)

Figure 2 shows this recurrent sequence (4) in graphical form in a polar coordinate system, where an integer positive variable \( n \) plays the role of the angular coordinate \( \theta \), and \( \ln n \) plays the role of the radius vector \( r \).

Turning to discrete values of functions in modeling biological phenomena seems to be fundamentally important due to the discrete nature of the organization of both the genetic coding system (discrete DNA alphabets, etc.) and a variety of biomechanical processes (for example, the seemingly continuous movement of a human hand is provided due to the total effect of discrete contractions of a huge variety of muscle units, each of which has its own threshold of excitability and
is contracted out of step with the rest). As is known, for all excitable cells of the body, the genetically inherited universal law of "all or nothing" of a discrete nature is valid: the cell does not respond at all to stimuli of a subthreshold value, but reacts to above-threshold stimuli with full amplitude. These facts indicate that biomechanics, if it takes into account these fundamental features of living tissue, should be developed as the mechanics of discrete sequences and processes, taking into account their relationship with discrete genetic coding.

Figure 2. Graphic representation of a sequence of discrete values of the natural logarithm \( \ln n \) in a polar coordinate system for \( n = 1, 2, \ldots, 30 \).

The use of a polar coordinate system for the graphic representation of biological structures as configurations of a spiral type is justified by the fact that spirals have long been considered as "the curves of life" [7, 8]: spiral and helical configurations are characteristic of DNA molecules, proteins, bones, tendons, muscles, etc. For example, the heart is a holistic spiral muscle that pushes blood by its action of twisting and untwisting, similar to how a washerwoman squeezes water out of laundry by twisting it.

The natural logarithm function \( y = \ln x \), which is important for modeling inherited biological phenomena, is mutually inverse to the exponent function \( x = e^y \), which are also used for a long time to model morphogenetic and other bio-phenomena. Accordingly, the recurrent sequence (4) is mutually inverse to the recurrent sequence (5) of exponentials \( e^n \):

\[
e^1, e^2, e^3, \ldots, e^n
\]  

(5)

Figure 3 shows a continuous exponential function \( e^x \) and a discrete recurrent exponential sequence in a polar coordinate system. These graphs correspond to continuous and discrete logarithmic spirals.

Figure 3. (a) Graphical representation of a continuous exponential function \( e^{0.1x} \) in a polar coordinate system. (b) Discrete sequence \( e^{0.1n} \) for \( n = 1, 2, \ldots, 30 \) in a polar coordinate system.

Logarithmic functions and logarithmic spirals model many genetically inherited biological phenomena, including morphogenetic configurations of phyllotaxis laws [9], which are associated with another recurrent sequence - a series of Fibonacci numbers related to the golden ratio. Figure 4 shows examples of logarithmic spirals in inherited morphological structures.
Let us add that many cases of biomechanical movements - growth and motor - of living bodies can be modeled as a transition from one discrete recurrent logarithmic spiral to another. This corresponds to the statement of the classic of biomechanics N.A. Bernstein: “The idea that movement is in many respects like an organ seems extremely fruitful” [10].

![Figure 4](image-url)

**Figure 4.** Examples of logarithmic spirals in morphogenetic configurations: (a) sunflower head, (b) two clamshells, (c) aloe.

### 4. Some concluding remarks

The work of the laboratory for the research of biomechanical systems of the IMASH RAS revealed fundamental hyperbolic rules for the organization of DNA information texts in the genomes of higher and lower organisms (eukaryotes and prokaryotes), associated with harmonic progression (1), which is well-known in science in connection with various mathematical and physical problems. The discovery of the important role of the harmonic progression in genetic informatics leads to the development of new mathematical models in genetic biomechanics, which studies the relationship of inherited biomechanical structures with genetic DNA texts, since DNA molecules play a dictatorial role in living organisms, determining their genetically inherited physiological structures [11]. Additionally, we note that harmonic progression plays a prominent role in aesthetics. This progression (1) is important not only for music with its systems of musical harmony and musical overtones. At least since the time of the Pythagorean doctrine of the aesthetics of proportions, there has been an idea that the composer R. Schumann expressed as follows: “The aesthetics of one art is at the same time the aesthetics of another art; only the material is different” [12]. In light of this, architecture has long been interpreted as frozen music and music as dynamic architecture. In connection with our research, assumptions arise about the genetic basis of a number of aesthetic parallels in various arts.

The above features of harmonic progression (1) do not exhaust its rich mathematical features, which can serve to create new approaches to the construction and substantiation of models in genetic biomechanics, as well as contribute to the development of algebraic and quantum biology [13].

### References

[1] Shubnikov A V and Koptskik V A 2004 *Symmetry in Science and Art* (Moscow: RCHD)
[2] Petoukhov S V 2020 Hyperbolic rules of the oligomer cooperative organization of eukaryotic and prokaryotic genomes *Preprints* 2020050471
[3] Petoukhov S V 2020 *Symmetry: Culture and Science* 31(2) pp 222-3
[4] Conway J H and Guy R K 1995 *The Book of Number* (New-York: Copernicus)
[5] Available at: https://www.youtube.com/channel/UC8JLsuRzzPsRiHwrmEjMCTw
[6] Vilenkin N Ya 1985 *Functions in nature and technology* (Moscow: Prosveschenie)
[7] Cook T A 1914 *The Curves of Life* (London: Constable and Co)
[8] Petoukhov S V, Svirin V I and Khazina L V 2015 Bionics of spiral structures *J. of Machinery Manufacture and Reliability* 44(3) pp 249–53
[9] Jean R V 1994 *Phyllotaxis: A Systematic Study in Plant Morphogenesis* (Cambridge: Cambridge University Press)
[10] Bernstein N A 1966 *Essays on the physiology of movements and the physiology of activity* (Moscow: Medicine)
[11] McFadden J and Al-Khalili J 2018 *Proc. R. Soc. A* 474(2220) 20180674
[12] Schumann R 1969 On Music and Musicians ed Konrad Wolff (New York: Norton)
[13] Petoukhov S V and He M 2010 Symmetrical Analysis Techniques for Genetic Systems and Bioinformatics: Advanced Patterns and Applications (USA: IGI Global)