Algebraic harmony in genoms of higher and lower organisms. Non-euclidean biosymmetries

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Abstract. The article is devoted to the study of the relationship between non-Euclidean symmetries in inherited morphogenetic and other bio-structures with algebraic features of information sequences of nucleotides in DNA heredity molecules in the genomes of eukaryotes and prokaryotes. These genomic sequences obey the universal hyperbolic rules of the oligomer cooperative organization, which are associated with the harmonic progression of 1/1, 1/2, 1/3, ..., 1/n. This progression has long been known and studied in various branches of mathematics and physics, and has now manifested itself in genetic informatics. The performed analysis of the harmonic progression revealed its connection with the double ratio known in geometry, which is the main invariant of projective geometry. This connection consists in the fact that the magnitude of the double ratio is the same and is equal to 4/3 for any four adjacent members of this progression. This fact of the connection of genetic informatics with the main invariant of projective geometry can be used to explain the implementation of non-Euclidean symmetries in genetically inherited structures of living bodies.

1. Introduction

The phenomena of the symmetric inherited structure of biological bodies have been the subject of research since ancient times. The importance of studying these phenomena is described, for example, in classic books [1, 2]. At the same time, until recently, all attention was paid to the biosymmetries of similarity, which are described using a group of geometric similarity transformations. According to F. Klein's Erlangen program, this group of transformations underlies Euclidean geometry and includes transformations of translations, rotations, specular reflections and scaling. At the same time, the hypothesis by V.I. Vernadsky on the possible important morphological significance of non-Euclidean symmetries in living bodies is widely known.

Clarification of the geometric foundations of morphology entails shifts in various areas of biomechanics and physiology: biomechanics of postures, biomechanics of growth and motor movements, psychophysics, etc. In the variety of organic forms, multiblock structures are of particular interest, the components of which are mutually conjugated on the basis of certain algorithms, repeated on the most diverse lines and branches of biological evolution. The general rule of such varieties, consisting of blocks or motivic units, is that the previous motivic unit is translated into the subsequent one by some fixed Euclidean or non-Euclidean transformation. In other words, so organized
segmented varieties have a cyclic group of automorphisms, and their motivic units are arranged along the orbit of the corresponding cyclic group. Earlier, in the works of the Institute of Mechanical Engineering Research Institute of the Russian Academy of Sciences, a wide representation in the inherited configurations of the set of living bodies of non-Euclidean symmetries was revealed, which are based on the groups of projective and Möbius transformations, which generalize the group of similarity transformations and contain it as their subgroup [3, 4].

Genetically inherited morphological structures must be structurally linked to the molecular genetic system for their genetically coding and transmission along the chain of generations. Therefore, it is important to look for traces of symmetries and invariants of non-Euclidean transformations in the genetic informatics of living bodies, including in the information texts of DNA heredity molecules carrying genetic information in the form of long nucleotide sequences. As a result of the work of the laboratory for research of biomechanical systems of the Institute of Mechanical Engineering of the Russian Academy of Sciences in 2020, universal hyperbolic rules for the cooperative organization of genomes of higher and lower organisms were discovered [5]. These rules are associated with harmonic progression (1), which has long been known in various fields of science and has now received the status of an important participant in genetic informatics, capable of influencing the characteristics of inherited biosymmetries:

\[
\frac{1}{1}, \frac{1}{2}, \frac{1}{3}, \frac{1}{4}, \ldots, \frac{1}{n}
\]  

(1)

In this article, we consider the mathematical connections of this progression with the groups of projective and Möbius transformations, on which non-Euclidean symmetries are based.

2. Computational approaches and models

Our computational approaches and models of biological structures are based on the mathematical properties of harmonic progression (1), which were studied by Pythagoras, Orem, Leibniz, Newton, Euler, Fourier, Dirichlet, Riemann and many other researchers in connection with various problems of physics and mathematics. Nowadays this list is supplemented with the tasks of studying its role in the genetic information fundamentals of living matter and the structuring of inherited biological systems. Its historically known name - "harmonic progression" - sequence (1) was received due to its connection with a number of harmonics in music (or a number of lengths of standing waves when vibrating a stretched string). This article presents the results of an analysis of the conjugation of this progression with the main invariant of projective geometry, called the double ratio (as well as the wurf and anharmonic ratio). In the one-dimensional case, the group of projective transformations and the group of Möbius transformations coincide, and the double relation is simultaneously an invariant of both projective and Möbius transformations. In our research on non-Euclidean biosymmetries, we actively use the provisions of the famous Erlangen program of F. Klein, which defined geometry as the science of invariants of the transformation group. In accordance with this program, each group of transformations has its own geometry, which has its own individual set of invariants. In particular, the groups of projective and Möbius transformations define projective and Möbius geometries (the latter is also called the geometry of reciprocal radii or conformal geometry).

The cross-ratio (or double ratio or wurf) of the four numbers \(a, b, c, d\) is determined by the expression (2):

\[
(ab, cd) = \frac{c-a}{c-b} \frac{d-b}{d-a}
\]  

(2)

If the four numbers \(a, b, c, d\) correspond to the coordinates of four points on the number line, then expression (2) consists of the lengths of the corresponding segments between the indicated pairs of points. Under projective transformations of such a straight line, the lengths of the segments and the simple relations between them change, but the value of the cross-ratio remains unchanged.
3. Results and discussions

One of the properties of the harmonic progression (1) is that the value of the cross-ratio of any of its four neighboring numbers is equal to $4/3$. Any four adjacent numbers in a series of natural numbers $1, 2, 3, \ldots, n$ also have the same value of the cross-ratio. This means that the harmonic progression (1) and the natural series of numbers are projectively equivalent to each other (figure 1).

![Figure 1](image)

**Figure 1.** Examples of projective transformation. (a) A central projective transformation changes the lengths of the line segments and their simple ratios, but retains the magnitude of the cross-ratio. (b) The location of the numbers of the harmonic progression (1) and a series of natural numbers on the number line.

The connection of the harmonic progression (1) with the cross-ratio leads to the following conclusions:

1) various fragments of a harmonic progression can be considered as projectively symmetric to each other;

2) in the genomes of eukaryotes and prokaryotes, various hyperbolic sequences of oligomeric sums corresponding to the classes of A-, T-, C- and G-oligomers [5] are projectively similar to each other with the high accuracy with which hyperbolic rules are fulfilled in them;

3) all investigated genomes of eukaryotes and prokaryotes with respect to their sequences of oligomeric sums are projectively similar to each other (with the high accuracy, with which hyperbolic rules are fulfilled in them).

Similar hyperbolic rules associated with harmonic progression (1) are fulfilled not only in genomic DNA sequences of nucleotides, but also in the studied long proteins (such as the Titin protein containing 33423 amino acids and presented at https://www.ncbi.nlm.nih.gov/protein/ACN81321.1) in relation to oligomer sums in their 20 classes of amino acids. The point is that in the case of protein sequences of 20 types of amino acids, 20 equivalence classes can be analyzed, each of which is determined by the corresponding type of amino acid and combines all $n$-oligomers (fragments of length $n$) of a given protein that begin with a given amino acid. For example, the amino acid Ala defines a class of Ala-oligomers, which includes all $n$-oligomers starting with this amino acid: the subset of Ala-doublets contains all 20 doublets that start with Ala (AlaAla, AlaArg, AlaAsn, ...), AlaCys); the subset of Ala-triplets contains all 400 triplets that start with Ala (AlaAlaAla, AlaAlaArg, ...), AlaCysCys), and so on. The quantitative compositions of these subsets of $n$-oligomers of each of these amino acid classes for different $n = 1, 2, 3, \ldots$ (here $n$ is much less than the protein length) are mutually related with high accuracy and obey hyperbolic rules associated with harmonic progression (1). Accordingly, taking into account the mentioned connection of this progression with the cross-ratio, we can talk about the projective-geometric (as well as the Möbius-geometric) similarity of the named quantitative characteristics of the structure of long proteins such as the Titin protein [5].
Taking into account that the numerical characteristics of genetic sequences are associated with the main invariant of projective geometry, then it can be expected that projective-geometric and Möbius-geometric symmetries will appear in genetically inherited physiological structures. This allows us to consider in a new light the existence of the non-Euclidean symmetries previously established in the works of the IMASH RAS in a wide variety of morphogenetic structures and growth processes in living bodies [3, 4].

For example, the cross-ratio was applied to the analysis of growth changes in the longitudinal proportions of three-membered kinematic blocks in the human body: three-phalangeal fingers, three-membered limbs (shoulder-forearm-hand and thigh-calf-foot) and the entire three-membered body (in anthropology, the body is subdivided into the upper, trunk and lower segments). The value of the cross-ratio of the lengths of the three members in all these trebled blocks, at least during the entire postnatal period, is grouped around the reference value of 1.3. This is all the more interesting because the growth of the human body is essentially non-linear (figure 2): for example, during a person's life from birth, the upper part of the body grows 2.4 times, the trunk - 2.8 times, and the lower part - 3.8 times. This invariance of the cross-ratio value turns out to be largely true not only for normally developed people, but also for dwarfs and giants. This is also true for a wide range of highly organized animals.

![Figure 2](image)

**Figure 2.** Age-related changes in the proportions of the human body (from [6]). (a), (b) - antenatal and postnatal stages: (a) - in the lunar months; (b) - in years (first newborn on the left); (c) - examples of projectively equivalent three-term segments, the cross-ratio values of which are equal to 1.3.

We note additionally that projective-geometric transformations and the cross-ratio as their main invariant are mathematical tools, on which the study of visual perception and the creation of methods of computer vision, pattern recognition, and artificial intelligence are largely based. A huge number of publications are devoted to this topic (see, for example, [7, 8]). The study of the relationship between the genetic system and genetically inherited biological structures, which are connected with non-Euclidean symmetries and harmonic progression, continues, including for the development of genetic biomechanics and algebraic biology. These issues, in particular, are considered at the International Interdisciplinary Seminar "Algebraic Biology and Systems Theory" [9].

The creators of quantum mechanics P. Jordan and (later) E. Schrödinger pointed out the key difference between living bodies and inanimate ones: inanimate objects are controlled by the average random motion of their millions of particles and the motion of an individual particle is not essential for the whole; on the contrary, in a living organism the chosen - genetic - molecules have a dictatorial (!) influence on the entire organism (see the history of quantum biology [10]). In accordance with this statement, in our research we focus on the properties of DNA information sequences and study their influence on inherited biological structures.
4. Conclusions
Studies of nucleotide DNA sequences in the genomes of higher and lower organisms reveal the existence in them of a system of quantitative hyperbolic rules of a universal nature, which are related to the harmonic progression (1).

The mathematical properties of this historically known progression, used in various fields of science and now found in the quantitative characteristics of molecular genetic informatics, indicate that the algebraic structures of genetic informatics can be a basis of non-Euclidean symmetries in the inherited morphology and biomechanics of movements [11]. On this path, new classes of models in biomechanics, psychophysics of sensory perception and algebraic biology, as well as new approaches in biotechnology and biotechnical systems, including artificial intelligence systems, are being developed.

Additional materials were obtained to the well-known statement based on the achievements of molecular biology: life is a partnership between genes and mathematics [12].

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