

# The Structure of the Polytope of Hereditary Information

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## ABSTRACT

The representations of the sugar molecule and the residue of phosphoric acid in the form of polytopes of higher dimension are used. Based on these ideas and their simplified three-dimensional images, a three-dimensional image of nucleic acids is constructed. The geometry of the neighborhood of the compound of two nucleic acid helices with nitrogen bases has been investigated in detail. It is proved that this neighborhood is a cross-polytope of dimension 13 (polytope of hereditary information), in the coordinate planes of which there are complementary hydrogen bonds of nitrogenous bases. The structure of this polytope is defined, and its image is given. The total incident flows from the low-dimensional elements to the higher-dimensional elements and vice versa of the hereditary information polytope are calculated equal to each other. High values of these flows indicate a high intensity of information exchange in the polytope of hereditary information that ensures the transfer of this information.

## KEYWORDS

Dimension, Hereditary Information, N-Cross-Polytope, N-Simplex, Polytope, Space, Structure

## INTRODUCTION

In 1953, James Watson and Francis Crick based on the analysis of diffractograms proposed a three-dimensional model of a DNA molecule consisting of two chains twisted into a spiral (Watson, & Crick, 1953a, 1953b). At the same time, sugar molecules and phosphoric acid residues included in the DNA molecule were also considered three-dimensional. However, it was not indicated which three-dimensional figures correspond to sugar molecules and phosphoric acid residues. According to this model, flat nitrogenous bases, being in different chains, using two complementary hydrogen bonds connected two spirals into a single whole. But how exactly the flat nitrogenous bases are located in space remained unknown. And this is despite the fact that it is these relations that determine the most important issue of the transmission of hereditary information. Recently, it was proved that sugar molecules and phosphoric acid residues have the highest dimension (Zhizhin, 2016, 2018a, 2018b). The phosphoric acid residue has a dimension of 4, and the sugar molecule has a dimension of 12. In this regard, the geometry of nucleic acids was considered taking into account the highest dimension of the components (Zhizhin, 2018b, 2019a, 2019b, 2020). In addition, for the convenience of images, a simplified three-dimensional model of a sugar molecule was built on the basis of a full twelve-dimensional model of a sugar molecule (Zhizhin, 2019c). This model can be used in further

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constructions, not forgetting the dimension of its complete model. This model was used to construct images of single nucleic acid helices. When passing to the analysis of nucleic acids consisting of two linked helices, it is necessary to take into account the emerging anti-parallelism of geometric elements in linked spirals (Zhizhin, 2019c). In this article, continuing the research begun in the works (Zhizhin, 2018b, 2019d), it will be shown that sugar molecules located in linked nucleic acid helices form a polytope of dimension 13 of the type of cross-polytope in which there are exactly 12 coordinate planes. In these coordinate planes outlined by rectangles with antiparallel edges, exactly 12 compounds of nitrogen bases currently known can be located (Spirin, 2019). The image of the polytope and its coordinate planes is obtained, its structure is determined. This polytope can be called the polytope of hereditary information, since it transmits hereditary information from one spiral to another using a sequential alternation of nitrogenous bases.

It has been shown that the polytopic of hereditary information is characterized by a powerful stream of incidents between geometric elements of different dimensions (Zhizhin, 2019c), providing an extremely intense exchange of information between the components of nucleic acids. The evidence of the existence of such an exchange of information can be found in the recently discovered inheritance of changes not related to the modification of sequences in DNA, i.e. with methylation - the binding of a methyl group  $CH_3$  to the nitrogenous base of DNA (Mancuso, 2017; Lindquist et al., 2016; Sanbonmatsu et al., 2016).

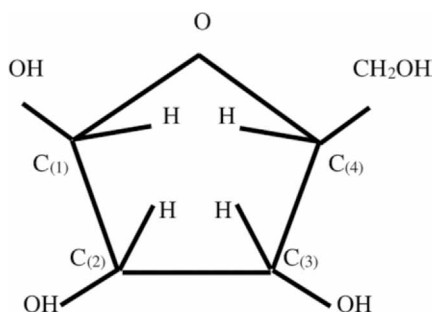
## SPATIAL MODES OF SUGAR MOLECULE AND NUCLEIC ACID HELICES

From a sugar molecule with five carbon atoms in the Fischer form (Lehninger, 1982), we can move on to representing the molecule as a closed chain. Having chosen, for example, Form B from the two enantiomorphic forms A and B, the closed chain of the sugar molecule has the form in Figure 1 (Zhizhin, 2016, 2019a, 2019b, 2019c).

To obtain a spatial figure of a sugar molecule (B-ribose), considering the atoms and functional groups shown in the projection onto the plane in Figure 1 as the vertices of the corresponding spatial figure, it is necessary to introduce additional edges in addition to the edges shown in Figure 1 (Zhizhin, 2019c). These edges will have only spatial significance, unlike the edges in Figure 1, which also depict chemical covalent bonds. To distinguish between edges, we will depict edges corresponding to chemical covalent bonds with thick solid black lines. Edges that have only spatial significance in the images of the figures will be indicated by thin dashed black lines.

Since the number of atoms and functional groups is 13, the closest convex closed figure that can be obtained from Figure 1 is a simplex of dimension 12. The dimension of the simplex is  $n - 1$ , where  $n$  is the number of vertices (Zhizhin, 2016). Moreover, each vertex is connected to all other vertices by edges, i.e. 12 edges emanate from each vertex. A spatial image of the B-ribose molecule is given in the article (Zhizhin, 2016). If, as a simplification, we leave, in addition to the edges corresponding

Figure 1. Closed chain sugar molecule (form B)



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