



# The Properties of Biomaterials Hidden in the Spaces of Higher Dimension

Zhizhin G\*

Professor, Academician of Russian Academy of Natural Sciences, Russia

\*Corresponding author: Gennadiy Zhizhin, Professor, Academician of Russian Academy of Natural Sciences, Russia, Tel: +7 905 289 57 75; Email: genzhizhin@gmail.com

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## Abstract

The influence of the higher dimension of biomolecules on processes in biomaterials is investigated. It has been proved that the optical activity of organic compounds is a consequence of the higher dimensionality of molecules in solution, and not a consequence of the three-dimensional shape of solid crystals, as Pasteur suggested. It is shown that glucose and ribose molecules have dimensions of 15 and 12, respectively. Helical chains of glucose molecules are characterized by the rotation of molecules in perpendicular planes in the opposite directions. A hidden order of interaction of nucleic acids in a space of higher dimension was discovered, leading to a one-to-one correspondence between the number of pair of bound nitrogenous based and the number of amino acids.

**Keywords:** Genetic Code; Glucose Molecules; Nucleic Acids; Polytopes; Sugar Molecules

## Introduction

The study of the structure of biomaterials is the subject of many studies. All these studies suggest that the dimension of biomolecules is no more than three. However, recent studies by the author Zhizhin, 2014-2022 [1-14] convincingly prove that almost all molecules of inorganic and organic chemistry, especially biomolecules, have a higher dimension. Ignoring the higher dimensionality of the molecules that form biomaterials does not allow one to explain many observed phenomena and leads to incorrect conclusions regarding the properties of biomaterials. In this paper, this is illustrated by three important examples: studies of tartaric acid, the properties of glucose, and the interaction of nucleic acids.

### The Studies of Tartaric Acid

The study of tartaric acid played an important role in the development of biology, beginning with the well-known

work of Pasteur (1848) Pasteur [15] on the rotation of the plane of polarization of light by tartaric acid. In the Fischer form, tartaric acid has two enantiomeric forms D and L (Figures 1 & 2).

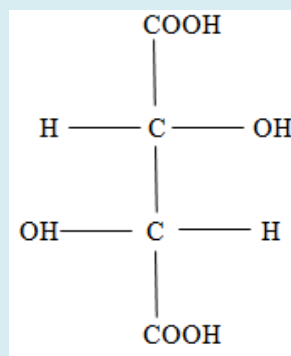
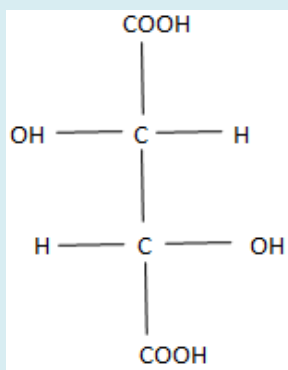
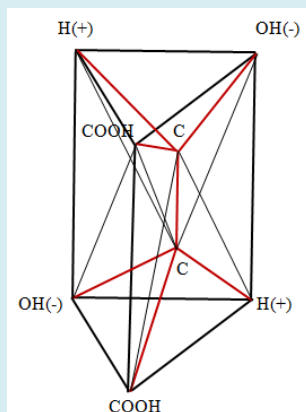


Figure 1: Shema of the molecules D-wine acid.

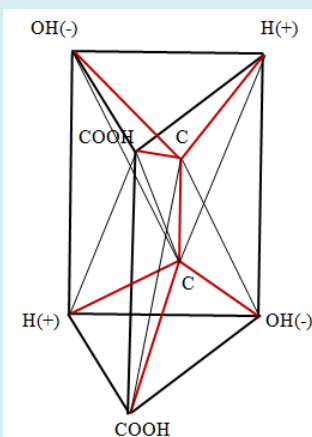


**Figure 2:** Shema of the molecules L-wine acid.

Fischer forms are flat and do not reflect the spatial shape of the molecule. From Figures 1, 2 it follows that in the spatial image both forms D and L have two tetrahedrons with a center. Moreover, the center of one of them is the top of the other, and the center of the other is the top of the first. These spatial images are shown in Figure 3 (D) and Figure 4 (L), respectively.



**Figure 3:** Spatial structure of the D-wine acid.



**Figure 4:** Spatial structure of the L-wine acid.

Here, the edges corresponding to chemical bonds are depicted in red, and the edges, which are necessary only to represent the spatial images of molecules, are marked in black. In Figure 3, along with the indication of the functional group located at the vertex, the symbol of the vertex is indicated by a small Latin letter. It is necessary to determine the dimension of the polytope  $bcdahgo$ . The polytope in Figure 3 has 8 vertices ( $f_0 = 8$ ), 22 edges ( $ab, ag, af, ao, ah, gh, gf, go, gd, bf, bo, bd, bc, df, do, dc, hc, hf, ho, cf, co, fo$ ). Therefore,  $f_1 = 22$ . The polytope in Figure 3 has 29 planar faces, of which 26 are the triangles ( $aho, afo, ahf, afg, ahg, aog, aob, afb, bfo, bco, bod, bfd, bfc, bcd, ghf, gho, gfo, god, gfd, dfo, dco, dfc, cof, chf, cho, hfo$ ) and 3 quadrangles ( $abdg, hcgd, abhc$ ). Therefore,  $f_2 = 29$ . The polytope in Figure 3 has 20 three-dimensional figures, of which 13 are tetrahedrons ( $bctd, ahog, dcfo, bcdo, bfdo, cfdo, ahof, ahgf, hogf, aogf, fgod, foah, foab$ ), 6 pyramids ( $agbdo, ahbcf, ahbco, agbdf, Chgdf, chgdo$ ) and one ( $ahgbcd$ ) prism. Therefore,  $f_3 = 20$ . It follows from the construction of the polytope in Figure 3 that it includes two tetrahedrons with the center  $bctfo$  and  $oahgf$ . In addition to these two polytopes with dimension 4, five 4-polytopes also appear in the polytope in Figure 3. Three of these polytopes have as their base three rectangular faces of the prism  $ahgbcd$ , whose vertices are connected with the vertices  $f, o$  located inside the prism. To prove their 4-dimensionality, consider one of these polytopes  $ahbcfo$ , since the proofs for the other two polytopes are similar. This polytope has 6 vertices ( $f_0 = 6$ ); 13 edges ( $ab, ah, hc, bc, af, hf, bf, cf, ho, ao, bo, co, fo$ ),  $f_1 = 13$ ; 13 two-dimensional faces ( $ahf, aho, abo, abf, afo, bfo, boc, ahbc$ ),  $f_2 = 13$ ; 6 three-dimensional faces ( $hfoc, abof, bfoc, afho, ahcbf, ahcbo$ ),  $f_3 = 6$ . Define dimension polytope in Figure 3 on the Euler-Poincare equation Poincare [16].

$$\sum_{i=0}^{n-1} (-1)^i f_i(P) = 1 - (-1)^n, \quad (1)$$

is the number of the elements with the dimension  $i$  at polytope  $P$ ;  $n$  is dimension of the polytope  $P$ .

Substituting the obtained values of the numbers of faces of different dimensions into equation (1), can find that equation (1) is satisfied for  $n=4$   
 $6 - 13 + 13 - 6 = 0$ .

It is proved by the 4-dimensionality of the polytope  $ahbcfo$ .

The two polytopes of dimension 4 there are formed by the  $ahgbcd$  prism with the vertex  $f$  or  $o$  inside its. Consider the prism  $ahgbcd$  with the vertex  $f$  (the proof for the prism with vertex  $o$  is similar). The polytope  $ahgbcdf$  has 7 vertices,  $f_0 = 7$ ; 15 edges ( $ah, hg, ag, bd, bc, cd, ab, hc, gd, af, fh, fg, bf, fc, fd$ ),  $f_1 = 15$ ; 14 two-dimensional faces ( $ahg, bdc, ahf, hfg, afg, bfc, fcd, bfd, fhc, afb, fgd, ahbc, hcgd, agbd$ ),  $f_2 = 14$ ; 6 three-dimensional faces ( $ahgbcd, ahgf, bctd, abdgf, hgdf, ahbcf$ ),  $f_3 = 6$ . Substituting the values of the numbers of faces

of various dimensions obtained for the polytope  $ahgbcdf$  into equation (1), can find that it is satisfied for  $n=4$

$$7 - 15 + 14 - 6 = 0.$$

This proves that the polytope  $ahgbcdf$  has a dimension of 4.

Thus, for the polytope in Figure 3 are  $f_0=8$ ,  $f_1=22$ ,  $f_2=29$ ,  $f_3=20$ ,  $f_4=7$ . Substituting these values into equation (1), can find that it is satisfied for  $n=5$

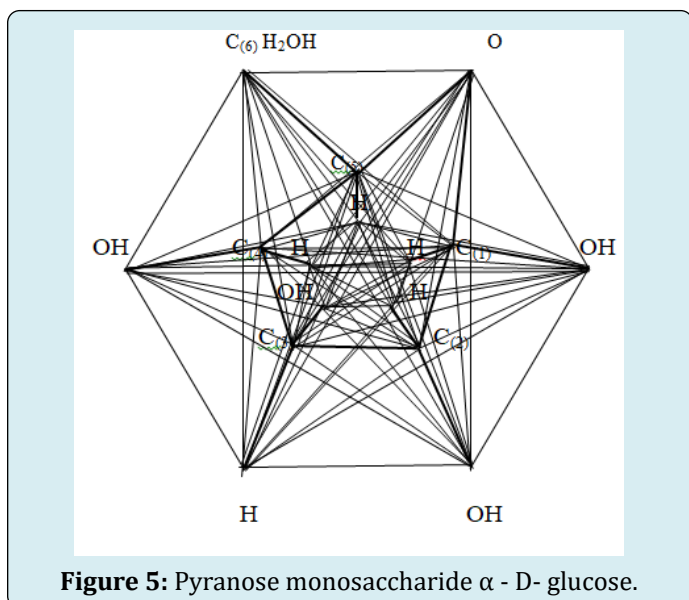
$$8 - 22 + 29 - 20 + 7 = 2.$$

This proves that the polytope in Figure 3 has dimension 5.

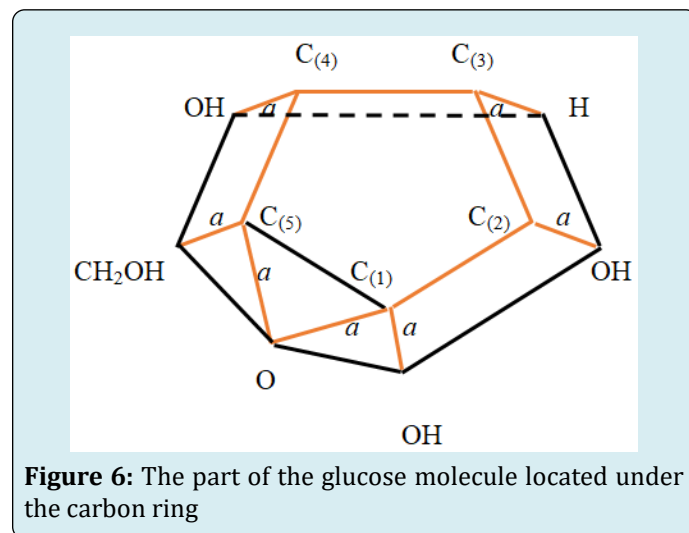
The images obtained make it possible to explain the main property of tartaric acid - rotation of the plane of polarization of the incident light in different directions: in the case of the D form to the right, in the case of the L form to the left. It is known devices for rotating the plane of polarization of light, having the appearance of two folded triangular prisms, the boundary between which serves to reflect light Wood [17]. Can say that the molecule of tartaric acid is a natural device for rotating the plane of light polarization. Two carbon atoms play the role of the reflecting partition in the molecule. The rotation occurs in the forms D and L in different directions because of the opposite arrangement of the charges of the hydrogen ions (+) and the hydroxyl group (-) in these forms.

### The Chains of Molecules $\alpha$ - D - Glucose

Back in 2016 [4], a spatial model of the  $\alpha$  - D-glucose molecule was built and it was proved that the molecule has the type of a simplex, and its dimension is 15. In this work, based on this model, a simplified three-dimensional model of this molecule was built, taking into account the features of the full model. Figure 5 shows the complete model of the molecule.

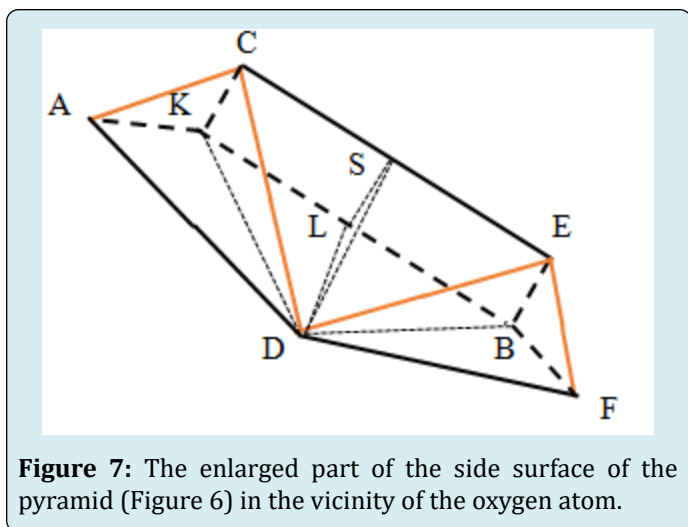


Now, based on the image of the higher dimensional image of the pyranose glucose molecule (Figure 5), we can begin to obtain a three - dimensional simplified image of this molecule and then compare this image with known common images. To obtain a three - dimensional simplified model of the molecule  $\alpha$  - D - glucose, in Figure 5 we leave only the edges corresponding to chemical covalent bonds, the edges of the external contour, and the edge connecting the  $C_{(1)}$ ,  $C_{(5)}$  atoms. We assume as a first approximation that the ring of carbon atoms  $C_{(1)} \div C_{(5)}$  is a regular pentagon with a side length of 0.15 nm (the standard length of the carbon - carbon chemical bond). Since carbon atoms exhibit tetrahedral coordination, other valence bonds of carbon atoms must be located either above the plane of the ring or below the plane of the ring. It is convenient to assume for further geometric analysis that the atoms of hydrogen and the hydroxyl group located in Figure 5 inside the carbon ring are in space above the plane of the carbon ring. While the oxygen atom and the functional groups of the outer contour (larger) are under the plane of the carbon ring. A part of this spatial structure located under the plane of the carbon ring is shown in Figure 6.



The length of the carbon - hydrogen and carbon - oxygen bonds is denoted by the letter  $a = 0.1$  nm. Then the carbon - carbon bond length takes the form  $1.5a$ . Thus, the part of the construction of the  $\alpha$  - D - glucose molecule under the carbon ring is a pyramid with a lower base in the form of an irregular hexagon and an upper base in the form of a regular pentagon.

To determine the yet unknown geometric characteristics of the figures, it is first necessary to find the value of the angle of inclination of the side edges of the pyramid to its base. For this, we consider separately the flat lateral faces of the pyramid in the vicinity of the oxygen atom. We double these faces and designate the vertices and some characteristic points of this structure in separate letters (Figure 7).



**Figure 7:** The enlarged part of the side surface of the pyramid (Figure 6) in the vicinity of the oxygen atom.

We denote the angle  $\angle CAK$  by the letter  $\varphi$ . Given that  $\angle AKC = \pi/2$  we have  $CK = LS = BE = a \sin \varphi$ , so

$AC=CD=DE=EF=a$ ,  $AK=a \cos \varphi$ . Since the carbon cycle is a regular pentagon, then  $\angle AKL = \pi/2 - 54 = 126^\circ$ . Since

$CE=1.5a$  and point  $S$  is middle of segment  $CE$  then  $DS = \sqrt{a^2 - (3/4)^2 a^2} = a\sqrt{7}/4$ . From triangle  $DSL$  we have

$DL = \sqrt{DS^2 - SL^2} = \frac{a}{4}\sqrt{7-16\sin^2 \varphi}$ . Therefore, from the

triangle  $KLD$  we obtain  $KD = \sqrt{DK^2 + KL^2} = a \cos \varphi = AK$ .

Then  $\angle KDC = \varphi$ .

Besides,

$$\sin \angle DKL = \frac{DL}{KD} = \frac{\sqrt{7-16\sin^2 \varphi}}{4 \cos \varphi}.$$

Therefore,

$$\angle AKD = \angle AKL - \angle DKL = 126^\circ - \arcsin \frac{\sqrt{7-16\sin^2 \varphi}}{4 \cos \varphi}.$$

From the triangle  $KAD$  we obtain  $\frac{AD}{2a \cos \varphi} = \sin \frac{\angle AKD}{2}$ .  
From here we find

$$AD = 2 \cos \varphi \sin \left( 63^\circ - \frac{1}{2} \arcsin \frac{\sqrt{7-16\sin^2 \varphi}}{4 \cos \varphi} \right). \quad (2)$$

Besides, from four - angle  $AKLD$  we have  $KN/AK = \cos (126^\circ - 90^\circ)$ . Then,

Therefore,

$$KN = a \cos \varphi \cos 36^\circ = LM. AM = AN + NM = a \cos \varphi \sin 36^\circ + \frac{3}{4} a.$$

$$MD = DL - LM = \frac{a}{4} \sqrt{7-16\sin^2 \varphi} - a \cos \varphi \cos 36^\circ.$$

Thus, we find also one express for segment  $AD$

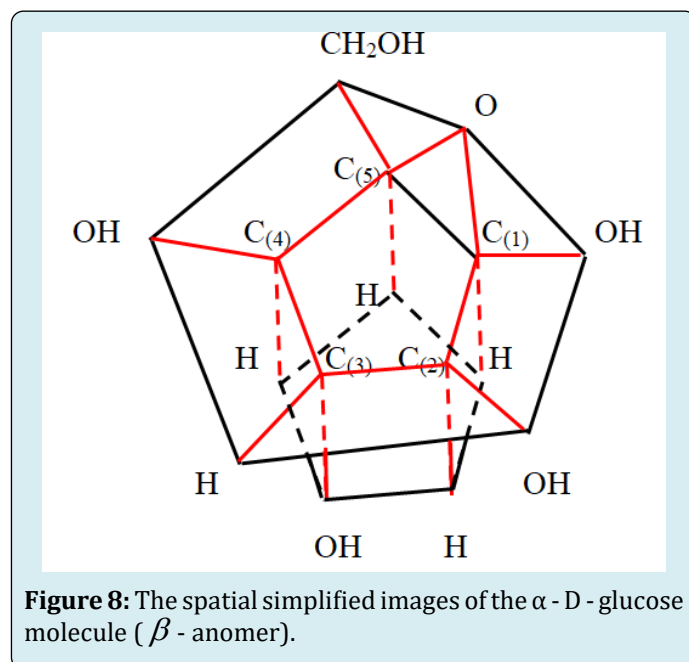
$$AD = \sqrt{MD^2 + AM^2} = \left[ \left( \frac{a}{4} \sqrt{7-16\sin^2 \varphi} - a \cos \varphi \cos 36^\circ \right)^2 + \left( a \cos \varphi \sin 36^\circ + \frac{3}{4} a \right)^2 \right]^{1/2} \quad (3)$$

Comparing (2) and (3) after transformations, we obtain the equation for finding the angle  $\varphi$  for any  $a$

$$\sin \left( 63^\circ - \frac{1}{2} \arcsin \frac{\sqrt{7-16\sin^2 \varphi}}{4 \cos \varphi} \right) = \left[ \frac{1}{2} + \frac{3 \sin 36^\circ}{8 \cos \varphi} - \cos 36^\circ \frac{\sqrt{7-16\sin^2 \varphi}}{8 \cos \varphi} \right]^{1/2} \quad (4)$$

Solving equation (4) numerically, we find that the angle  $\varphi = 36^\circ$ . Thus, the height of the lower part of the  $\alpha$ -D - glucose molecule is  $a \sin \varphi = 0.058778$  nm, the characteristic size of the upper base is 0.243 nm, and the characteristic size of the lower base is  $0.243 + 2a \cos \varphi = 0.405$  nm.

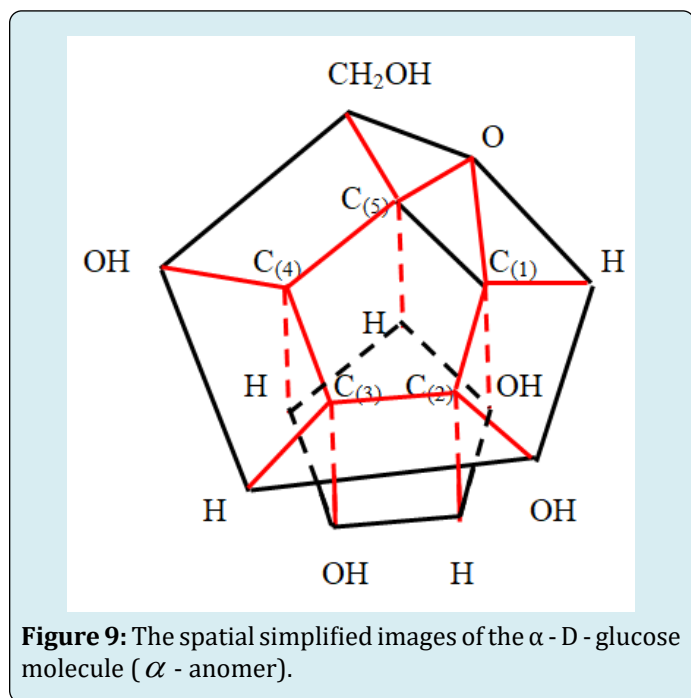
The angle of inclination of the side edges of the lower part of the model, as follows from the solution, is different from 90. This reflects in averaged form the presence of atoms in the conformations of the  $\alpha$ -D - glucose molecule located quite close to the equatorial plane of the molecule [18-20].



**Figure 8:** The spatial simplified images of the  $\alpha$ -D - glucose molecule ( $\beta$ -anomer).

The upper part of the  $\alpha$ -D - glucose molecule above the carbon cycle should be depicted in the form of a pentagonal prism, directing the volatile bonds from the carbon atoms of the cycle vertically upward. This is consistent with the

tetrahedral coordination of atoms around a carbon atom. Thus, the  $\alpha$ -D-glucose molecule in a simplified three-dimensional form is a pyramid in contact with the carbon cycle with hexagonal and pentagonal bases and a straight pentagonal prism. However, in order to compare the obtained image with the known images of the  $\alpha$ -D-glucose molecule in the Haworth projection [20], it is necessary to expand so that the pentagonal prism is at the bottom and the arrangement of other atoms and functional groups is consistent. In this case, it is necessary to take into account the possibility of changing the position of the hydroxyl group at the carbon atom  $C_{(1)}$ . In this way, two spatial simplified images of the glucose molecule are obtained, shown in Figure 8 ( $\beta$ -anomer) and Figure 9 ( $\alpha$ -anomer).



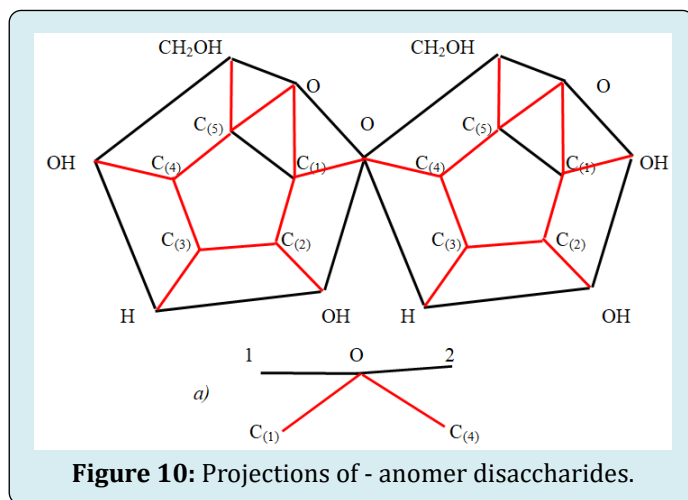
In the molecules of other pyranoses, the atoms or functional groups partially connected to the carbon atoms of the carbon cycle partially change. In this case, the structure of the molecules, up to functional groups, remains the same for glucose molecules in the pyranose cycle carbon atoms. Therefore, the dimension of molecules such as D-mannose, D-galactose, L-fucose is also equal to 15.

Thus, we see that a simplified three-dimensional image of a pyranose monosaccharide molecule has the form of two three-dimensional polytopes stacked on top of each other. The lower figure is cylindrical prism with a regular pentagonal base. The top figure is a pyramid with pentagonal and hexagonal bases. These figures are connected by a carbon cycle. We emphasize that this image was obtained as a result of the analysis of the image in the space of higher dimension and numerical research. The resulting image does

not in any way resemble an armchair, which is widely used in the literature as an image of a pyranose monosaccharide molecule.

Representations of the saccharide molecules in the form of polytope simplifies the understanding of the formation of polysaccharides.

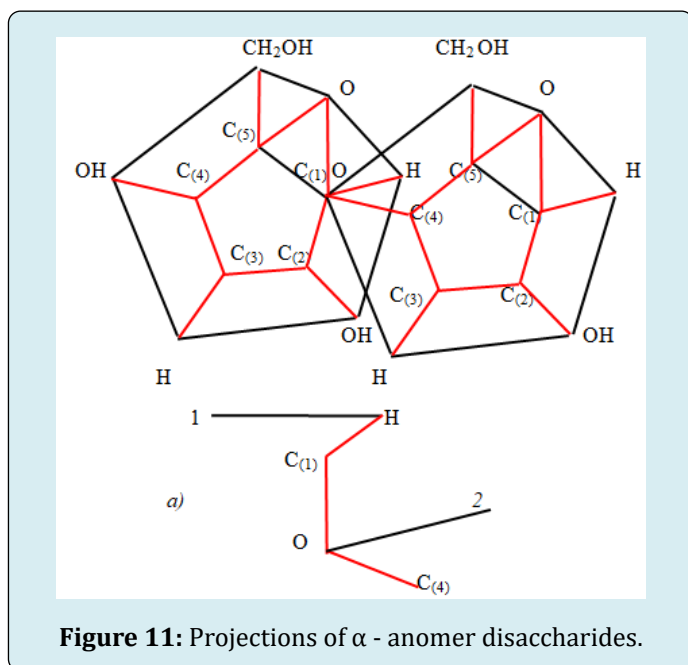
Monosaccharide molecules combine with each other thanks to the combination of two hydroxyl groups with the release of a water molecule. The remaining oxygen atom connects the remaining part of the monosaccharides. The most common chains of  $\alpha$ -D-glucose monosaccharide residues. Here, residual  $\alpha$ -D-glucose molecules can be joined through an oxygen atom, connecting carbon atoms 1-1, 1-4, 4-4, 4-1. In some cases, the carbon atom  $C_{(2)}$  in the cycle will be involved in the compound. Branching chains of glucose molecules occurs at the sixth carbon atom in the functional group  $CH_2OH$ . Monosaccharide chains have different forms depending on the type of these molecules, i. e. depending on whether these molecules are  $\beta$ -anomers or  $\alpha$ -anomers. Using the obtained simplified three-dimensional models of  $\alpha$ -D-glucose molecules, we consider in more detail these compounds in a metric image, taking into account the angles between the valence bonds. Let two  $\beta$ -anomers of the  $\alpha$ -D-glucose molecule join together, linking the carbon atom  $C_{(1)}$  of the first  $\alpha$ -D-molecule to the carbon atom  $C_{(4)}$  of the second  $\alpha$ -D-molecule (lactose). Based on the geometric image in Figure 10, you can imagine a top view of this connection (Figure 10).



It is easy to see that the same attachment of the third  $\alpha$ -D-glucose molecule leads to a linear arrangement of molecules when viewed from above on this compound. Linearity will not change with the following similar connections. However, given the three-dimensionality of the image, you should look at this connection from a different view. Figure 10a) shows an image of the junction of two  $\alpha$ -D

- glucose molecules when viewed from the front. The black segments in Figure 10 a) are the traces of the intersection of the upper bases of the prism with a plane passing through the valence bonds of the oxygen atom and carbon atoms. According to the obtained solution of equation (3), the angle between the base of the prism and the valence bond is 36 degrees. both the first  $\alpha$ -D - glucose molecule and the second  $\alpha$ -D - glucose molecule. The valence angle at the oxygen atom in compounds with two carbon atoms in the chain of  $\alpha$ -D - glucose molecules, as you know, is slightly larger than the normal valence angle and is about 112 degrees. Thus, the angle 102 in Figure 10a) is 176 degrees. This means that the base of the second  $\alpha$ -D - glucose molecule has a slope to the base of the first  $\alpha$ -D - glucose molecule other than zero. More precisely, this slope is 4 degrees, therefore the second  $\alpha$ -D - glucose molecule, when viewed in full view, turns to the left relative to the first  $\alpha$ -D - glucose molecule. It is clear that such an addition of a third  $\alpha$ -D - glucose molecule will increase the angle of inclination of this molecule relative to the first molecule. Thus, the statement about the linearity of the chain of  $\alpha$ -D - glucose molecules when connecting them in the case of anomers is not entirely accurate. One can say that this statement is somewhat one - sided.

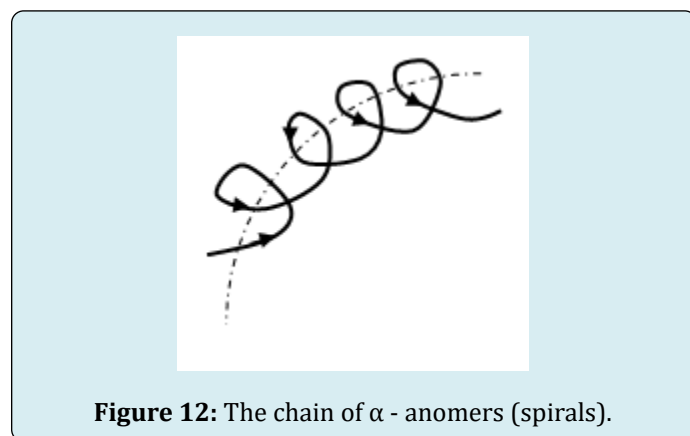
Let two  $\alpha$ - anomers of the  $\alpha$ -D - glucose molecule join together, linking the carbon atom  $C_{(1)}$  of the first  $\alpha$ -D - molecule to the carbon atom  $C_{(4)}$  of the second  $\alpha$ -D - molecule (maltose). Based on the geometric image in Figure 9, you can imagine a top view of this connection Figure 11.



**Figure 11:** Projections of  $\alpha$ - anomer disaccharides.

It is easy to see that the same attachment of the third  $\alpha$ -D - glucose molecule leads to a nonlinear arrangement of molecules when viewed from above on this compound.

Nonlinearity will save with the following similar connections. Thus, the chain of molecules turns to the right. However, given the three - dimensionality of the image, you should look at this connection from a different view. Figure 11a) shows an image of the junction of two  $\alpha$ -D - glucose molecules when viewed from the front. The black segments in Figure 11 a) are the traces of the intersection of the upper bases of the prism with a plane passing through the valence bonds of the oxygen atom and carbon atoms. According to the obtained solution of equation (3), the angle between the base of the prism and the valence bond is 36 degrees both the first  $\alpha$ -D - glucose molecule and the second  $\alpha$ -D - glucose molecule. Thus, on the Figure 11a the angle  $1H C_{(1)}$  is 36 degrees and the angle  $C_{(1)}OC_{(4)}$  is 112 degrees. Since, the angle  $C_{(4)}O_2$  is 36 degrees too, so the angle between bases  $1H$  and  $O_2$  is 14 degrees. This means that the base of the second  $\alpha$ -D - glucose molecule has a consequently slope to the base of the first  $\alpha$ -D - glucose molecule to the left. It is clear that such an addition of a third  $\alpha$ -D - glucose molecule will increase the angle of inclination of this molecule relative to the first molecule. In the chains of  $\alpha$ - anomers, one of the projections is linearly transmitted along the chain, and the projection perpendicular to it along the chain along a curved line. In chains of  $\alpha$ - anomers (spirals), it is observed that when moving along a chain of projections in mutually perpendicular planes, the pyranose molecules rotate in opposite directions (Figure 12).



**Figure 12:** The chain of  $\alpha$ - anomers (spirals).

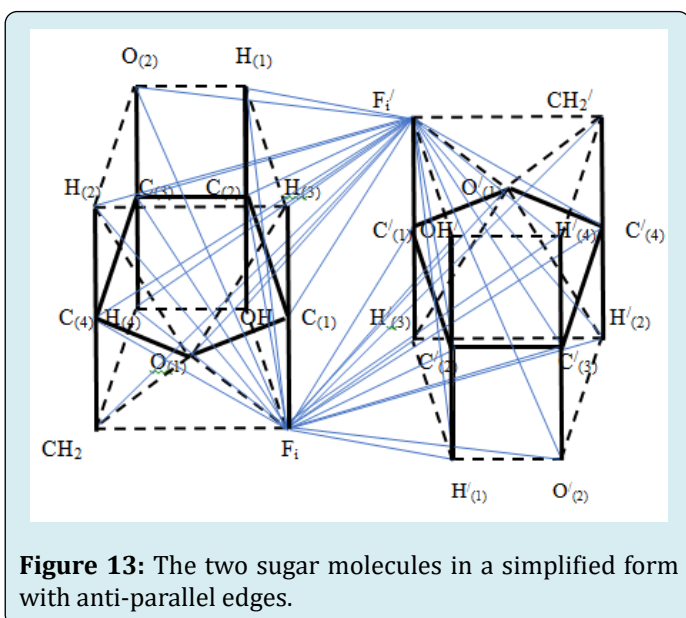
Thus, chains of  $\alpha$ - anomers of  $\alpha$ -D - glucose molecules rotate simultaneously in opposite directions in perpendicular planes.

The study of furanose chains using simplified three - dimensional models was carried out using nucleic acids as an example, in which furanose models were connected to each other using phosphoric acid residues. These studies showed that, when nucleic acids bound by nitrogen bases interact, there is a latent degree of freedom of arrangement of nitrogen bases in higher dimensional space, leading to an unambiguous corresponding number of nucleotides taking into account their possible location in space and the number

of amino acids [11-13].

### Hidden Order of Interacting Nucleic Acids

Recently, the question was raised about the existence of a hidden order in nucleic acids in the space of the highest dimension of models of nucleic acids [11,12]. In particular, the existence of a polytope of hereditary information of dimension 13 in the local region of interaction of two sugar molecules with antiparallel edges was established [7,9]. This polytope has 12 coordinate planes (Figure 13).



Exactly as many as there are different pairs of bonds of nitrogenous bases [8,21]. In Figure 14, the symbols  $F_i$ ,  $F_i'$ , denotes the vertices of the polytope, to which nitrogenous bases are attached. However, from the geometric conditions for filling the polytope space it follows that out of 12 coordinate planes, only five (5) coordinate planes can contain nitrogenous bases

$$\begin{aligned} &F_i' H_{(1)} \quad F_i' C_{(2)} \quad F_i' H_{(3)} \quad F_i' C_{(1)} \quad F_i' OH \\ &H_{(1)} F_i \quad C_{(2)} F_i \quad H_{(3)} F_i \quad C_{(1)} F_i \quad (OH) F_i \end{aligned} \quad (5)$$

Since there are only 4 canonical pairs of linked nitrogenous bases for DNA molecules [21-23]

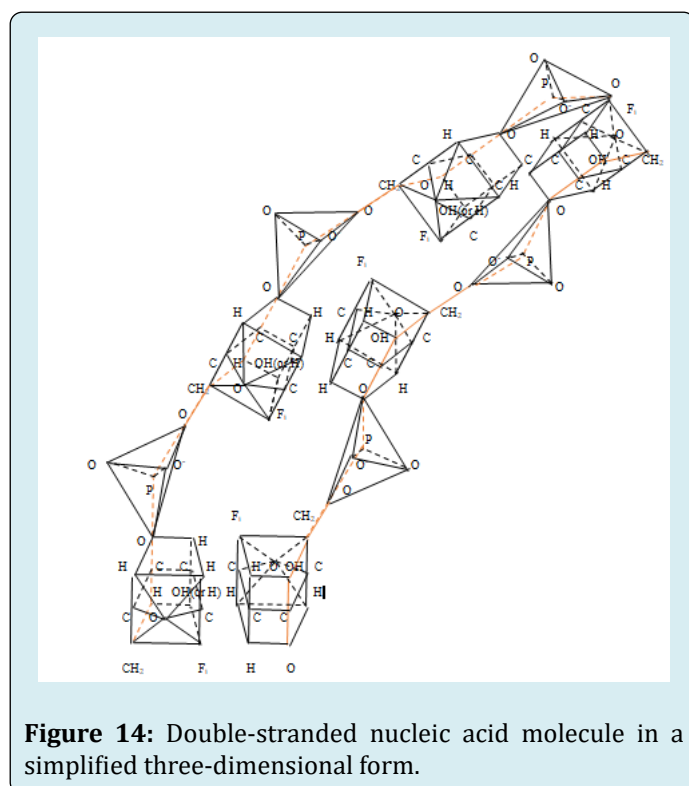
$$A:U, G:C, C:G, U:A, \quad (6)$$

then 20 base pairs are possible, which can alternatively be located in the local area of the hereditary information polytope. This number is equal to the number of possible amino acids required for protein formation. Thus, the uncertainty in the accepted description of the interaction

of nucleic acids, in which the number of nucleotides is less than the number of amino acids, has disappeared. It was this uncertainty that at one time required the introduction of a genetic code to match the number of nucleotides and amino acids [19,20,24]. In this work, geometrical research methods, starting from the research carried out in the local area, are applied to the chain of polytopes of hereditary information connected by sugar molecules and phosphoric acid residues.

### 3D Model of Two Linked Nucleic Acid Molecules

Based on the study of the geometry of sugar molecules, phosphoric acid residues, as objects of the highest dimension, a three-dimensional model of a nucleic acid molecule was built [6,13]. Let us now construct a simplified three-dimensional model of two interacting nucleic acid molecules in helices with antiparallel ribs (Figure 14).



Each nucleotide of any nucleic acid includes a nitrogenous bases, residues of a sugar molecule and phosphoric acid. The nucleotides differ from each other in the nitrogenous base included in them. Therefore, nucleotides are often designated precisely by the designation of the nitrogenous base in their composition. Since there are 5 types of canonical nitrogenous bases included in nucleic acids  $A, U, C, G, T$ , it should be assumed that in each nucleotide from a pair of interacting nucleotides, one of the five nitrogenous bases is located in one of the coordinate planes (5). In another nucleotide from

an interacting pair, another base is located in the same plane in accordance with (6). Thus, the alternation of nucleotides in each helix leads to an alternation of the planes in which the nitrogenous bases are located. It should be remembered that these planes in the complete model are coordinate planes in the 13-dimensional polytope of hereditary information. Therefore, the alternation of nucleotides in the nucleotide chain corresponds to the transition from one coordinate plane of the space of the highest dimension to another coordinate plane of the space of the highest dimension. In this regard, the simplified representation of the nucleotide sequence in the form of a linear chain of symbols of nitrogenous bases is very far from reality.

Considering that in a double helix all the edges of the polytopes of one and the other helix are located antiparallel, then if in one helix (for example, DNA) there is a sequence of nucleotides *A, C, G, U* in one of the two directions, then in the other helix this sequence has the opposite view of *U, G, C, A*. This automatically explains the experimental rule of Chargaff, indicating the order of interaction of nitrogenous bases. In the case of an RNA molecule, instead of base *U*, base *T* should be used. Existence of five different planes of distribution of nitrogenous bases is confirmed to a certain extent by experimental data on the correspondence of triplets of nitrogenous bases to amino acids [21]. If, in accordance with the previous one, we assume that the middle nucleotide in the triplet plays the main role, then the nucleotide *U* corresponds to five amino acids: *Phe, Leu, Ile, Met, Val*. Average nucleotide *C* in a triplet corresponds to amino acids: *Ser, Pro, Thr, Ala, Cys*. Average nucleotide *G* in a triplet corresponds to amino acids: *Ser, Cys, Tyr, Arg, Gly*. Average nucleotide *A* corresponds to amino acids: *Tyr, His, Glu, Asn, Lys, Gln, Asp*. Some violations of the unambiguous equality of five amino acids to each nucleotide can be explained by the influence of literal nucleotides in triplets and non-canonical parasitic bases.

As you know, the genetic code, determined by the correspondence of nucleotides and amino acids, has various cases of degeneration, in which this correspondence is violated [19,20]. Relatively recently, the effect on the transmission of hereditary information of adding a methyl group to the nitrogenous bases with an unchanged nucleotide sequence in helical nucleic acids [14,25-27] on the transmission of hereditary information was experimentally discovered. The existing facts of influence on the transmission of hereditary information can be described within the framework of the law of the conservation of incidents in the polytope of hereditary information (Zhizhin, 2019 b, d) [8,10]. This law takes into account the influence of all atoms in the polytope of hereditary information on the flow of hereditary information.

## Conclusion

Thus, the reason for the different rotation of the plane of polarization of light lies not in the different forms of the crystals of D - tartaric acid and L-tartaric acid, as Pasteur suggested, but in different forms of molecules, clearly visible in the image in the space 5D.

Three-dimensional geometric models of the pyranose molecule and chains of these molecules, constructed on the bases of simplification of complete higher-dimensional models of such molecules, are studied in detail. It is shown that a simplified three-dimensional model of the pyranose molecule consists of two parts of a straight pentagonal prism and a pyramid with pentagonal and to the difference in the geometric three-dimensional figures that form the sugar molecule, the spiral chains of these molecules are characterized by a seemingly paradoxical property: rotation of the figures in two perpendicular planes in opposite directions.

A simplified three-dimensional model of a double-stranded nucleic acid with antiparallel edges has been constructed. It was found that the existence of five different nucleotides *A, U, C, G, T* allows each of the five planar nitrogenous bases to be located in the accessible coordinate planes of the polytope of hereditary information of dimension 13. This leads to the Chargaff's rule of the order of interaction of nitrogenous bases. The existence of five coordinate planes in the polytope of hereditary information and four types of nucleotides for each nucleic acid correlates the number of possible locations of nitrogenous bases in the polytope of hereditary information and the number of possible types of amino acids, without requiring the introduction of three-membered codons. The general flow of transmission of hereditary information in a polytope of hereditary information is determined by the flow of incidents of geometric elements of various dimensions in this polytope.

It should be noted that the widespread algebraic (linear or matrix) description of the genetic code [28] does not take into account the hidden geometric order of nucleic acids and the biological features of their interaction.

## References

1. Zhizhin GV (2014a) On the higher dimension in nature. *Biosphere* 6(4): 313-318.
2. Zhizhin GV (2014b) *World-4D*. St.-Petersburg: Polytechnic Service.
3. Zhizhin GV (2015) Polytopic prismahedrons-fundamental regions of the n-dimension nanostructures.



- Paper presented at The International conference "Nanoscience in Chemistry, Physics, Biology and Mathematics. Cluj-Napoca, Romania.
4. Zhizhin GV (2016) The structure, topological and functional dimension of biomolecules. *J Chemoinformatics and Chemical Engineering* 5(2): 44-58.
  5. Zhizhin GV, Diudea MV (2016) Space of Nanoworld. In: Putz MV & Mirica MC (Eds.), *Sustainable Nanosystems, Development, Properties, and Applications*, New York: IGI Global, pp: 214-236.
  6. Zhizhin, GV (2018) The Metric Structure of Nucleic Acids and the Higher Dimension of Their Constituents. *International Journal of Chemoinformatics and Chemical Engineering* 7(2): 1-15.
  7. Zhizhin GV (2019) The Structure of the Polytope of Hereditary Information. *International Journal of Chemoinformatics and Chemical Engineering* 8(2): 7-22.
  8. Zhizhin GV (2019) Attractors and Higher Dimensions in Population and Molecular Biology: Emerging Research and Opportunities. Hershey, PA: IGI Global.
  9. Zhizhin GV (2019) The Polytope of Hereditary Information: Structure, Location, Signification.
  10. Zhizhin GV (2019) The Law of Conservation of Incidents of the Space of Nanoworld. *International Journal of Chemoinformatics and Chemical Engineering* 8(1): 25-46.
  11. Zhizhin GV (2020) Hidden Nucleic Acid Bond Order? *Acta Scientific Biotechnology* 1(4): 34-36.
  12. Zhizhin GV (2021) Interaction of Nucleic Acids: Hidden Order of Interaction. *International Journal of Applied Research in Bioinformatics* 11(2): 1-8.
  13. Zhizhin GV (2021) The Structures of DNA taking into account the Higher Dimension of its Components. In: Kosrapohr (Eds.), *Encyclopedia of Organizational Knowledge, Administration, and Technologies*. Hershey, PA: IGI Global, pp: 730-745.
  14. Zhizhin GV (2021) Methylated Polytope of Hereditary Information. *International Journal of Applied Research on Public Health Management* 6(2): 49-60.
  15. Pasteur L (1960) *Selected works*. Moscow: Publishing House of the Academy of Sciences of the USSR.
  16. Poincare A (1895) *Analysis situs*. *J de é Ecole Polytechnique* 1: 1-121.
  17. Wood R (1936) *Research in physical optics*. Wentworth Press.
  18. Metzler DE (1980) *Biochemistry the Chemical Reactions of Living Cells*, New York: Academic Press, pp: 1-3.
  19. Lehninger AL (1982) *Principles of Biochemistry*. The Jons Hopkins University: Worth Publishers, Inc.
  20. Koolman J, Roehm KH (2020) *Coloratlas of Biochemistry*. Stuttgart, New York: Thieme.
  21. Spirin AS (2019) *Molecular biology. The ribosomes and protein biosynthesis*. Moscow: Knowledge Lab.
  22. Watson JD, Crick FHC (1953) Molecular structure of nucleic acids. *Nature* 171: 738-740.
  23. Watson JD, Crick FHC (1953) Genetical implications of the structure of deoxyribose nucleic acid. *Nature* 171: 964-967.
  24. Crick FHC (1959) The present position of the coding problem. *Brokhaven Symp. Biol* 12: 35-39.
  25. Mancuso S (2017) *Plant Revolution. Le piante hanno gia inventato it nostro future*. Guiuti Editore.
  26. Lindquist S, Chakrabortee S, Kayatekin C, Newby GA (2016) *Luminidependens (LD) is an arabidopsis protein with prion behavior*. *Proceedings of the National academy of sciences of the United States of America* 113(21): 6065- 6070.
  27. Hawkes EJ, Hennelly SP, Novikova IV, Irwin JA, Sanbonmatsu KY, et al. (2016) COOLAIR antisense RNAs from evolutionary conserved elaborate secondary structures. *Cell Rep* 16(12): 3087-3096.
  28. Petoukhov SV (2006) Metaphysical aspects of matrix analysis of genetic coding and the golden ratio. In *Metaphysics. Century 21*, In: Vladimirov YS (Eds.), Moscow: BINOM, Knowledge laboratory, pp: 250.

