On the Question of the Geometry of Nucleic Acids Structure

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Abstract. The analysis of various forms of nucleic acids known from experiments is carried out using the metric and topological geometry of their components and the possibility of connecting the components into a chain. The shape and dimension of the components, defined in our previous works, with the involvement of the geometry of spaces of higher dimension is enriched. The geometrical cause of the formation of different DNA molecules (right and left spirals with different number of deoxyribose and ribose molecules in the period, closed chains included) has been determined. This is connected with the mutual arrangement of polytopes of phosphoric acid residues and deoxyribose or ribose molecules. It has been shown that the two carbohydrate molecules located in two helices of nucleic acids linked by a hydrogen bond with nitrogen bases form a cross – polytope of 13th dimension. It was determined that the 12 coordinate planes of this cross - polytope can accommodate the known 12 possible complementary compounds of nitrogen bases.

Keywords: *atom, molecule, covalent bond, Hydrogen bond, cross-polytope, polymer, simplex.*

1. Introduction

The structure of the double helix DNA was proposed by Francis Crick and James Watson in 1953, on the groung of X-ray structural data obtained by Maurice Wilkins and Rosalind Franklin and the "Chargaff rules" according to which, in each DNA molecule the strict relationships connecting the quantity of nitrogenous bases is different (Watson, & Crick, 1953a, b). For this outstanding contribution to the science, Francis Crick, James Watson and Maurice Wilkins were awarded the 1962 Nobel Prize in Physiology or Medicine.

Deoxyribonucleic acid (DNA) is a biopolymer, the monomer of which is a nucleotide (Albert, et al., 2002; Butler, 2005). Each nucleotide consists of a phosphoric acid residue attached to sugar deoxyribose, to which one of the four nitrogen bases is also attached. The bases that make up the nucleotides are either purines (adenine [A] and guanine [G]) or pyrimidines (cytosine [C] and thymine [T]); they are formed by combining five - and six - membered heterocycles.

In 1986, Frank-Kamenetskiy in Moscow had shown how a double-stranded DNA folds into a so-called H-shape, composed not of two but three strands of DNA (Frank – Kamenetskiy, 1986, 1988).

Complementarity of the double helix means that the information contained in one chain is also contained in another chain. Different base pairs form a different number of hydrogen bonds. Further, the existence of nucleic acids differing in the length of the period and shape with rotation of the spiral both to the right and to the left was experimentally established (Ha, et al., 2005; Cantor, & Schimmel, 1980; Frank – Kamenetskiy, 2010).

Watson and Crick postulated the spiral form of the DNA molecule, but they did not discuss the reasons for the formation of such a DNA molecule. Until now, there were no works explaining the existence of a spiral in the DNA molecule.

Another nucleic acid, RNA, essential for protein sieve, in the transfer of genetic information from DNA to protein, is chemically similar to DNA. There are two differences in the RNA chain vs. a single DNA chain: 1) the five - carbon sugar (pentose) is the ribose in RNA while in DNA is the deoxy- , D-ribose; 2) one of the two pyrimidine nucleotides in RNA is the uracyl, U, instead of its methylated derivative, the timine, T, in DNA. RNA is formed as a flexible single - stranded polymer, in contrast to the rigid double helix DNA. By the second half of the 1950 it has already been established (Spirin,

2019) that the synthesis of proteins in living cells is carried out by the ribosomes and that RNA represents the main part of the ribosomes. At the same time, the interaction of nitrogenous bases leads to the fact that the single - stranded RNA polymer coagulates onto itself, by forming short double - helix regions, where the paired nitrogenous bases are antiparallel. Some essential low molecular weight components of ribosomes are divalent metal ions, mainly magnesium ions (Spirin, Gavrilova, 1971). It is supposed they ensure the stability of the ribosomes by balancing the negative charges of phosphoric acid residues in RNA.

In a previous book (Zhizhin, 2017), I was shown that, practically all the elements of the periodic system, magnesium and calcium included, form compounds of higher dimension (see also Zhizhin, 2015 a, b; Zhizhin, & Diudea, 2016; Zhizhin, Khalaj, & Diudea, 2016). In the works (Zhizhin, 2016; Zhizhin, 2017), structures of biomolecules, also forming compounds of higher dimension, were also studied. It is shown that the molecule of five - carbon sugar in nucleic acids has the shape of a polytope of the type "simplex", of dimension 12. Its image was presented as the projection on a two - dimensional plane. A simplified image of this projection was used to construct the nucleotide chain. It was found that the alternation of this projection with the image of a phosphoric acid residue in the form of a polytope of dimension 4 leads to a geometric proof of the need to form a helix in the nucleotide chain. Moreover, depending on the possible location of the phosphoric acid residue relative to the ribose molecule (or D - ribose), right - or left - twisted spirals are formed. Given the extreme importance of nucleic acids in the processes of heredity and the clarity of three - dimensional images of geometric formations, it would be useful for further research to obtain three - dimensional images of nucleic acids. As noted in a recent monography, (Spirin, 2019), until now, there was no attempt to build a three - dimensional 3D-image of nucleic acid molecules, that's why the building of such an image was undertaken in this work. Note that, any n-polytope, surrounded by the 3D-space (Zhizhin, 2018), will be bounded by facets of 3D- and finally of 2D-dimensionality, irrespective of n; also note that that the existence of polytopes of higher dimension inside a 3D-space does not contradict the Riemann`s geometry (Riemann, 1854; Zhizhin, 2014).

By placing the 3D-models of molecules of five - carbon sugar and phosphoric acid residues in a chain, alternating them with each other, a 3D-model of the nucleic acid molecule was obtained. Specifying the lengths of valence bonds, the characteristic sizes of the obtained nucleic acid molecule were calculated, which are in satisfactory agreement with the known experimental data. Various forms of nucleic acids are also determined by the mutual spatial arrangement of molecules of five - carbon sugar and phosphoric acid residues. A nucleic acid molecule consisting of two helices with an antiparallel direction is considered.

It has been shown that, D - ribose or ribose molecules, located in two helices of a nucleic acid, linked by hydrogen bonds with nitrogenous bases form a cross - polytope of dimension 13. It was determined that the 12 coordinate planes of this cross - polytope can accommodate the known 12 possible complementary compounds of nitrogenous bases.

2. Calculation of 3D – five–carbon sugar molecule

Earlier (Zhizhin, 2016), it was shown that a five - carbon sugar molecule is a polytope of type simplex of dimension 12. One of the two enantiomeric forms is presented in Figure 1.
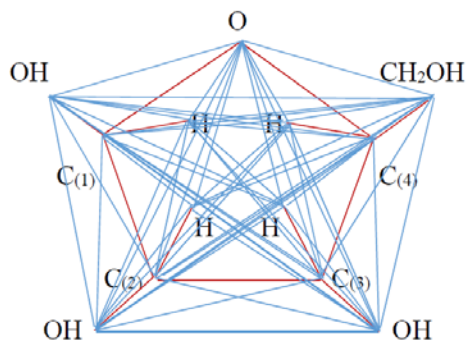
Figure 1. The five – carbon sugar molecule.

The image in Figure 1 is a topological projection of the 12 – simplex polytope on a 2D - plane. If a hydroxyl group OH is attached to the carbon atom C $_{(2)}$ on the outer contour of the image, this corresponds to a five - carbon sugar molecule (ribose) in the RNA molecule. If a hydrogen atom H is attached to the carbon atom C $_{(2)}$ on the outer contour of the image, this corresponds to a five - carbon sugar molecule (D - ribose) in the DNA molecule. To simplify the image in Figure 1, let discard all the blue lines that have only the geometric meaning of the edges of the convex polytope, with the exception of the outer contour; thus, the image in Figure 2 will be obtained.
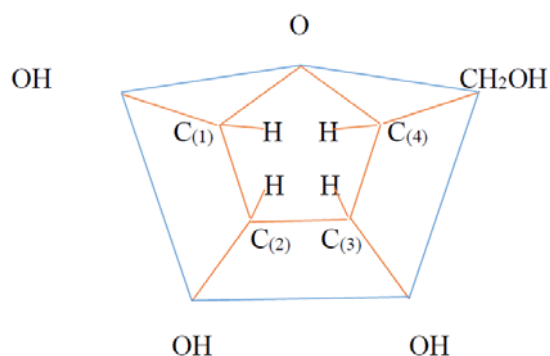

Figure 2. Simplified image of a five - carbon sugar (ribose) molecule.

Since Figure 2 is a topological projection of a spatial figure, then by this projection it is possible to restore qualitatively the corresponding 3D-figure, the projection of which is given in Figure 2. If one takes the carbon – carbon bond length and carbon – oxygen bond, $a = 0.15$ nm, then the length of the edges in the carbon – oxygen pentagonal cycle is equal to a. We assume that the chemical bonds emanating from the four carbon atoms of this cycle are spaced symmetrically relative to the chemical bonds of this cycle and have a certain angle φ with the plane of the cycle. Since the number of valence bonds emanating into the space of four carbon atoms of the oxygen - carbon cycle is eight, it should be assumed, by the symmetry conditions, that four valence bonds extend into a half space above the cycle plane, and four valence bonds proceed into the half space under the cycle plane. Consider a half - space above the plane of the oxygen - carbon cycle (Figure 3).
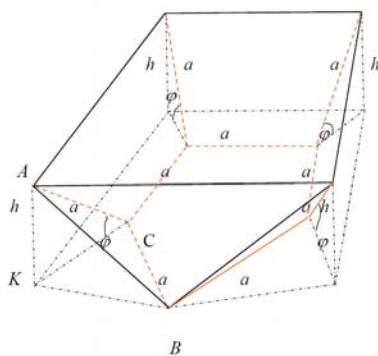
Figure 3. The half - space above the plane of the oxygen - carbon cycle.

Then, the length of the projection of these links on the cycle plane is equal to $a\cos\varphi$, and the height of the figure is equal to $h = a\sin\varphi$. In Figure 3, the orange segments are solid while dashed are the valence bonds; their length is assumed to be a. Fat solid black segments together with orange segments (dotted and solid) define a part of the 3D- shape of the sugar molecule. In this figure, the lower pentagonal face and the upper quadrilateral face are parallel to each other.

In Figure 3, the angle φ is unknown. One defines it from two triangles ACB and AKB, equating the length of the segment AB from each triangle. Note that there is a linear dependence of the angle ACB on the angle φ: $\angle ACB = \alpha\varphi + \beta$. One takes into account that the angle $KCB = 126^o$ due to the correctness of the lower pentagonal base of the polyhedron and the division of the external angle at the vertex C by the segment KC to the half. Since $\angle ACB = 126^o$ for $\varphi = 0$ and $\angle ACB = 90^o$ for $\varphi = 90^0$, so $\angle ACB = 126^0 - \dfrac{2}{5}\varphi.$ Since ACB triangle is isosceles, thus

$$AB = 2a\sin(63^0 - \frac{1}{5}\varphi). \tag{1}$$

From triangle KCB one has $KB = a\sqrt{1 + \cos^2\varphi - 2\cos\varphi\cdot\cos 126^0}$. Since the AKB triangle is rectangular, so $AB^2 = a^2 2(1 - \cos\varphi\cdot\cos 126^0).$ (2)

From (1) and (2) one has

$$1 - \cos\varphi\cdot\cos 126^0 = 2\sin^2(63^0 - \frac{1}{5}\varphi). \tag{3}$$

This is the equation for finding the φ angle. The equation (3) has two roots: $\varphi = 0$ and $\varphi = 90^o$. The first root corresponds to the flat shape of the sugar molecule. This does not correspond to the earlier proof of the multi-dimensionality of this molecule. We want to find a 3D-view of the outer contour of the sugar molecule. This goal corresponds to the second root of equation (3), i.e. $\varphi = 90^o$. The second part of the 3D-figure is under the plane of oxygen – carbon cycle. Obviously, the valence bonds emanating from carbon atoms are also located at an angle $\varphi = 90^o$ to the cycle plane. The parts below the cycle plane and above the cycle plane together form a 3D-model of the sugar molecule (Figure 4).
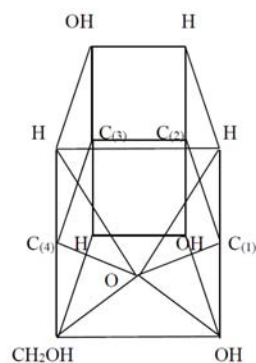
Figure 4. The three – dimensional model of the sugar molecule.

The arrangement of atoms in the sugar molecule, in Figure 4, is determined by their arrangement in the previously obtained Figures 1 - 3, as well as taking into account the alternating sequence of sugar molecules and phosphoric acid residues in nucleic acids.

3. The three – dimensional model of the nucleic acid molecule

A nucleic acid molecule is a chain of residues of phosphoric acid (a tetrahedron with a center) and sugar molecules (a prism with a pyramid). The chain of successively alternating these molecules in a 3D-form is shown in Figure 5. At the junctions of the phosphoric acid residue with the sugar, due to the separation of water molecules, an oxygen atom and the group CH_2 are added (Figure 5). In addition, one of the four nitrogenous bases is attached to the $C_{(1)}$ carbon atom instead of the hydroxyl group at the $C_{(1)}$ carbon atom (Figures 4 and 5).
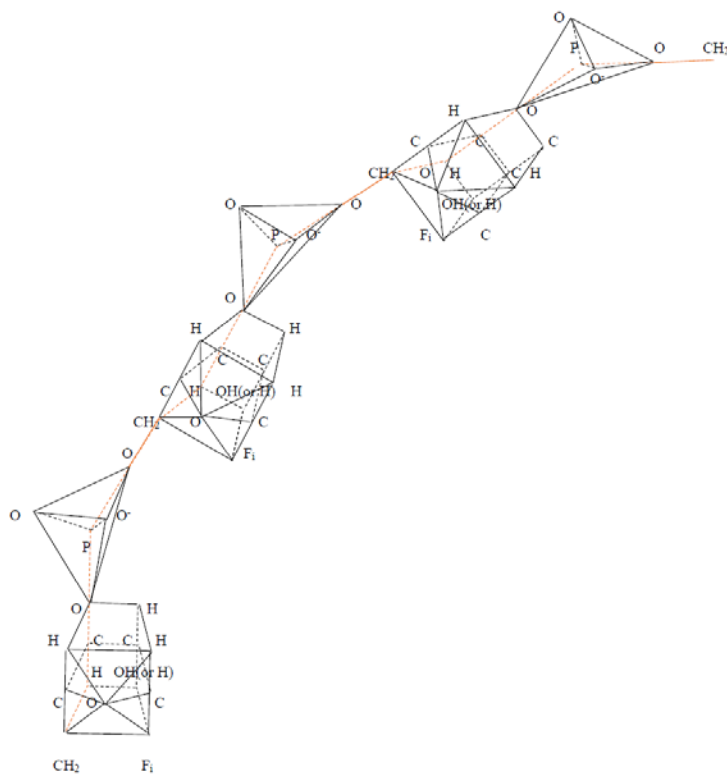

Figure 5. The three–dimensional model of the nucleic acid molecule.

The yellow color in Figure 5 indicates the covalent bonds connecting the phosphoric acid residues and the sugar molecules. It is significant that the communication lines connecting the tetrahedron with the sugar molecule form, by repulsing the electron pairs, uniform straight segments perpendicular to the bases of the prism. In the center of tetrahedron, the chemical bond lines form a kink, since in this center there are straight lines connecting it with the vertices of the tetrahedron. Ultimately, this fracture with simultaneous movement along the vertical coordinate leads to the formation of a helix of a nucleic acid molecule. In the projection on the plane of figure, the covalent bond segments form a broken line close to the ring (polygon). The radius of this ring/polygon will be determined by the angle between the projections on the plane of the chemical bonds of the phosphorus atom with the oxygen atoms at its vertices, belonging to the polygon. The tetrahedron with the center (the residue of phosphoric acid), connecting with the top of the prism base, has a degree of freedom. It can be rotated relative to the connection between the vertex of the prism and the center of the tetrahedron at an arbitrary angle. Therefore, even in the projection, the angle between the chemical bonds emanating from the center of the tetrahedron can be arbitrary. Let this angle be γ. Then the broken line between the centers of the tetrahedrons closes when the product of the number of these rotations n and the angle $\pi - \gamma$ is equal to 2π. Thus, one can find the period of the spiral, given that there is still a movement along a line perpendicular to the projection plane. Thus, to determine the radius of that ring/polygon, we have the equality: $(\pi - \gamma)n = 2\pi$.

Since the number of turns equals the number of segments that makes up a polygon, one obtains approximately the equality

$$\frac{2\pi}{\pi - \gamma} = \frac{2\pi R}{l} \quad,$$

where R is radius of the ring, l is length of the segment between centers of tetrahedrons. From the last equality one can to find the radius of the ring

$$R = \frac{l}{\pi - \gamma}.$$

From Figure 5, it follows that $l = 3a + 2d$. Subject to the accepted values a and d, one obtains

$$R = \frac{0,81}{\pi - \gamma} \text{ nm.}$$

For example, in case $\gamma = 140^o$, $R=1,16$ nm.

This radius value is close to the experimental helix radius of nucleic acids measured by Watson and Crick. At this angle, between the chemical bonds in the projection of the phosphoric acid residue, the number of nucleotides in the period $\frac{2\pi}{\pi - \gamma} = 9$. The number is in satisfactory agreement with the experimental number of nucleotides, 10, given that the helix in the period is somewhat greater than the circumference, at the same radius. This confirms the correctness of the 3D- model of the nucleic acid molecule.

The helix surface is formed due to the fact that, in a tetrahedron with a center, the valence bonds connecting the center with the vertices do not lie in the same plane. Therefore, the valence bonds connecting the two sugar molecules do not lie together in the plane passing through the edge of the prism. The bond leaving the phosphorus atom, about 23 degrees, retreats from the plane in which the bond lies, which is a part of the phosphorus atom. This causes a shift of the chain along a coordinate perpendicular to the ring. The equation of the helix surface in this case can be written as $h = n\Delta h, \Delta h = l\tan(\Delta\alpha), \Delta\alpha$ being the angle between the previous segment l and the subsequent segment l; n is the number of turns, h is the height of the period. Thus, $\Delta h = 0,343 nm, h = 3,43 nm$. This period height value is close to the value found in the Watson and Crick experiments (3,46 nm).

If the valence bond in the tetrahedron connecting its center with the next sugar molecule is rejected in the projection to the left of the valence bond connecting the center of the tetrahedron with the previous sugar molecule, i.e. an angle $\gamma > 180^o$, the nucleic acid is a left - handed helix. If it is $\gamma = 180^o$, then the nucleic acid has a linear appearance.

In ribonucleic acids, a helix return in one molecule is observed (Spirin, 2019). This is possible if the angle γ is variable, i.e. in the chain, the angle γ increases to 180 degrees up to even larger values of this angle. This means that along the chain there is a sequential rotation of the tetrahedron around the valence bond connecting its center with the previous sugar molecule.

4. Polytopes with antiparallel edges

In both single - and double - stranded nucleic acids (RNA, DNA), the constituents of acids (residues of phosphoric acid and sugar molecules) interact with each other. Phosphoric acid residues are connected by divalent metal ions, mainly magnesium ions, due to the interaction of negative charges of phosphoric acid residues with positive charges ions. This interaction is essential for the stability of nucleic acid structures, especially in the ribosomes. Sugar molecules interact with each other due to the hydrogen bonds between the nitrogenous bases attached to the sugar molecules. Being geometric forms, the constituents of nucleic acids interact with each other to form new geometric forms - new polytopes. Nitrogenous bases are known to be flat structures. However, it is not known how nitrogenous bases are oriented in space, whether their orientation depends on the type of nitrogenous base. Currently there is no information on this. There is also no information on how exactly the metal ions are located, connecting the phosphoric acid residues. Recall that, the adopted 3D-model of the components and the nucleic acid molecule itself is only a model for visual perception. As it was shown earlier, the phosphoric acid residue is a polytope of dimension 5, and the sugar molecule has a dimension of 12. When two phosphoric acid residues or two sugar molecules are combined, the dimension of formation in each case increases by one. In this case, as will be shown, the arrangement of flat nitrogenous bases in the space of higher dimension will become clear.

The movement of triangles along a helix leads to the formation of polytopes with antiparallel edges. Consider an arbitrary triangle *ABC* on the plane. Choose some point *O* on the plane outside the triangle. Let this point be the base of the axis of the helix passing through the triangle. Rotate the *ABC* triangle 180 degrees, moving it up to the helix, parallel to the initial plane. In the projection on the plane, both triangles *ABC* and the displaced triangle *A`B`C`* will be located as shown in Figure 6.
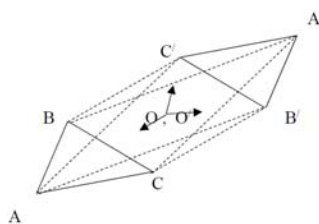

Figure 6. Polytope of dimension 3 with anti – parallel edges.

It is easy to see that the edges of the triangle *ABC* and *A`B`C`* are antiparallel. Now one can connect in space the vertices of the triangle *ABC* with the vertices of the triangle *A`B`C`* so that there are no connections of the vertices with the same letters. In a projection on the plane, the connection are represented by dotted segments. It can be seen that the connecting segments also break up into pairs of anti - parallel segments. Let us now verify that the image in Figure 6, along with the dotted segments,

is a projection of a 3D convex polytope. One uses the Euler – Poincaré equation (Poincaré, 1895) in this respect

$$\sum_{k=0}^{n}(-1)^{k} f_{k}(n) = (-1)^{k} +1, \tag{4}$$

with f_k being the number of elements of dimension k in polytope of dimension n.

The shape in Figure 6 has 6 vertices, 12 edges, 8 triangular faces (rectangles are not faces by construction, since connecting, for example, vertex A with vertices $B`,C`$ it turns out to be exactly the triangle $AB`C`$). Substituting these values of elements of different dimensions into equation (4), one can find: 6 – 12 +8 = 2, i.e. the Euler – Poincaré equation holds in this case for $n = 3$. This proves that the resulting figure is a convex polytope of dimension 3 (if the figure is not convex, the Euler – Poincaré equation would be violated).

The point O in Figure 6, due to the orthogonality of the axis of the helix, in the original plane coincides with the center of the 3D-figure $O`$ located on the axis of the helix. Point $O`$ can be considered as the origin of 3D-space. Coordinate axes in this direction emanate from directions $AA`, BB`, CC`$. Three pairs of these axes define the coordinate planes of the space of this shape.

Interestingly, to transform an arbitrary tetrahedron $ABCD$ into a tetrahedron $A`B`C`D`$ with anti-parallel edges, it is not enough to rotate it along a helix by 180 degrees. To do this, one must turn the helix together with the tetrahedron and move the tetrahedron along the helix in the opposite direction, also rotating it 180 degrees. In the initial state, the tetrahedron on the initial helix and the tetrahedron on the reversed helix, after its rotation by 180 degrees, will have anti -parallel edges. Both tetrahedrons can be shown as in the Figure 7; the point O is the projection of the axis on the plane.
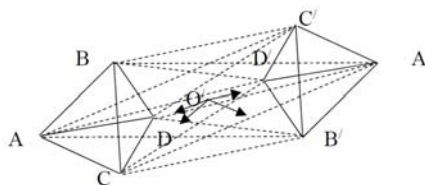

Figure 7. Polytope of dimension 4 with anti - parallel edges.

Now connect the vertices of the tetrahedrons so that the connecting edges (dotted segments) do not have the same letters. The resulting figure (along with dotted edges) has 8 vertices ($f_0 = 8$), 24 edges ($f_1 = 24$), 24 triangular faces ($f_2 = 24$), and 8 tetrahedrons ($f_3 = 8$). Substituting these values into equation (4), one can find: 8 - 24 + 24 - 8 = 0.

Thus, the Euler – Poincaré equation is satisfied in this case for $n = 4$ and the polytope in Figure 7 has dimension 4. It is easy to see (Zizhin, 2018) that this is a 4 - cross - polytope.

The point O in Figure 7 due to the orthogonality of the axis of the helix of the original plane coincides with the center of the forth - dimensional figure $O`$ located on the axis of the helix. Point $O`$ can be considered as the origin of forth - dimensional space. Coordinate axes in this direction emanate from directions $AA`, BB`, CC`, DD`$. Six pairs of these axes define the coordinate planes of the space of this shape.

Let us now consider the figure formed by two tetrahedrons with a center, which models the residues of phosphoric acid. By performing similar constructions, one can see that two tetrahedrons with a center in an anti - parallel position form a cross - polytope of dimension 5. Indeed, this polytope has 10 vertices and the opposite vertices have no edge connections. The remaining vertices are connected to each other by edges. This is a 5 - cross - polytope (Zizhin, 2018). Among the ten coordinate planes in the vicinity of the center of this polytope, only 4 coordinate planes have the opportunity to

locate bivalent magnesium ions within themselves. These are planes based on coordinate axes passing through two vertices of a tetrahedron with a center containing an O^- ion. The second pair of vertex coordinate axes regards the pair of vertices coinciding with one of the four remaining vertices of a tetrahedron with a center in which there are three oxygen atoms and a phosphorus atom.

Let us consider in detail the formation of a polytope of dimension 13 of two sugar molecules with anti - parallel edges. As in the case of the tetrahedron, to form a polytope with antiparallel edges from two sugar molecules, one must have one sugar molecule on one helix to turn this helix together with the sugar molecule and move the sugar molecule along this reversed helix in the opposite direction to the original helix direction. When the sugar molecule rotates 180 degrees while moving, then the original sugar molecule and the sugar molecule on the reversed helix are two polytopes with anti - parallel edges. Both of these sugar molecules, in a simplified form, are shown in Figure 8 by black solid lines.
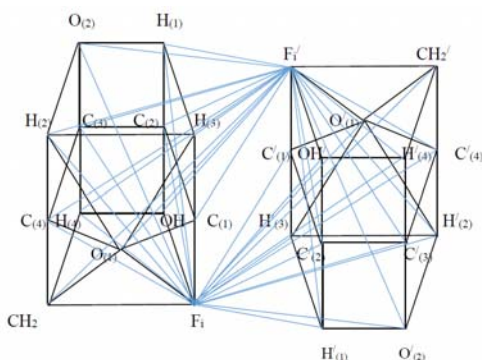

Figure 8. The polytope of dimension 13 with anti – parallel edges.

In full, the sugar molecules have the dimension 12; in the corresponding polytope each vertex must have an edge connection with all the other vertices; knowledge of this is needed. For the formation of a polytope of dimension 13, it is necessary to connect each vertex of one polytope with the vertices of another polytope so that there are no vertex connections with the same letters. All connecting edges break into pairs of antiparallel edges. At the same time, a set of 2D-plane coordinates emanate from the center of the formed polytope, as from the origin of coordinates. Their number is equal to the number of combinations of 13 taken 2, i.e. 48 coordinate planes. In order to clarify the possible geometrical circumstances of the connection of helices in double - helix nucleic acid molecules with nitrogenous bases, we are primarily interested in the coordinate planes containing these nitrogenous bases $F_i, F_i^/$.

There are exactly 12 such plane coordinates in the obtained polytope of dimension 13. They are depicted in Figure 8 by blue solid lines and are indicated below by the vertices of the consisting polytopes

$$\frac{F_i^/ H_{(1)}}{H_{(1)}^/ F_i}, \frac{F_i^/ O_{(2)}}{O_{(2)}^/ F_i}, \frac{F_i^/ H_{(2)}}{H_{(2)}^/ F_i}, \frac{F_i^/ C_{(3)}}{C_{(3)}^/ F_i}, \frac{F_i^/ C_{(2)}}{C_{(2)}^/ F_i}, \frac{F_i^/ H_{(3)}}{H_{(3)}^/ F_i},$$

$$\frac{F_i^/ C_{(4)}}{C_{(4)}^/ F_i}, \frac{F_i^/ H_{(4)}}{H_{(4)}^/ F_i}, \frac{F_i^/ OH}{(OH)^/ F_i}, \frac{F_i^/ C_{(1)}}{C_{(1)}^/ F_i}, \frac{F_i^/ O_{(1)}}{O_{(1)}^/ F_i}, \frac{F_i^/ CH_2}{(CH_2)^/ F_i}.$$

Other edges of the polytope of dimension 13 are not shown in Figure 8, for the clarity of the figure. In the center of each parallelogram, indicated by its four vertices, is the origin of coordinates and the corresponding pair of coordinate axes (they are not shown). To identify the different hydrogen and oxygen atoms as vertices of polytope, they are indicated by numbers in brackets at the lower indices.

It is surprising that the number of coordinate planes containing vertices is exactly equal to the number of possible compounds of nitrogenous bases, namely 12 (Spirin, 2019)

$$A:U, U:A, G:C, C:G, G:U, G:A, U:U, U:C, A \cdot A, A \cdot C.$$

Since each coordinate plane designated by the vertices of the parallelograms has a specific atomic environment, it can be assumed that each of the 12 possible compounds of nitrogenous bases is located on one particular coordinate plane out of 12 possible. This solves the question of the possible orientation of the bonds of nitrogenous flat bases in nucleic acids using idea about the high dimensionality of the constituent nucleic acids. It is also surprising that in order to create 13 – cross - polytopes, providing the connection with nitrogenous bases $F_i, F_i^/$, nature especially created double - stranded nucleic acids with oppositely directed spirals. This is realized in DNA and RNA when creating regions with inverted helices.

5. Conclusions

Based on the image of a sugar molecule of dimension 12, a simplified 3D - model of a sugar molecule was constructed as an outer boundary in the 3D - space. This model, simplified for visual perception, is used to construct a 3D-model of nucleic acids (DNA and RNA), in which the sugar molecule is of exceptional importance. The calculations of the geometric characteristics of nucleic acids according to the accepted model are in a satisfactory agreement with the values of these characteristics known from experiments (helix diameter, period length). The chain of successively alternating sugar molecules and phosphoric acid residues, as shown, has an internal degree of freedom - the rotation of a tetrahedron with a center representing a phosphoric acid residue around a valence bond connecting the phosphorus atom of the phosphoric acid residue with a sugar molecule. Depending on the angle of rotation of the phosphoric acid residue around this bond, (it is provided that this angle remains in the chain), right - and left - handed nucleic acid helices, as well as linear nucleic acids, may occur. The existence of plots in RNA molecules with inversion of the helix in the opposite direction can be explained by the possibility of continuously changing the angle of rotation of the phosphoric acid residue around the valence bond connecting it with the sugar molecule, within the same chain.

In a variety of nucleic acid molecules, the issue of chain interaction is important. In ribosomes, RNA interacts with each other due to bivalent metal ions (mainly magnesium ions). Positively charged magnesium ions attract negative charges of phosphoric acid residues, ensuring the stability of the ribosomes. In double - stranded nucleic acids, the helices are connected to each other by means of nitrogenous bases complementarily interacting with each other by a hydrogen bond. However, the magnesium ions and nitrogen bases in nucleic acids could not be specifically located. It has been established that magnesium ions and flat nitrogenous bases can be located inside special polytopes of higher dimension. Here knowledge is needed on the higher dimension of phosphoric acid residues and sugar molecules. Such polytopes are polytopes with anti - parallel edges, i.e. cross - polytopes of higher dimension. Binding agents are located on the free coordinate planes of these polytopes in the vicinity of the center of the polytope.

In this case, the 2D- coordinate plane on the boundary of the polytope should contain the objects to be joined. In the case of magnesium ions, there are four specific coordinate planes inside the 5 – cross - polytope, in which an ion can accommodate, combining negative charges. In the case of nitrogenous bases, the existence of 12 coordinate planes inside a cross - polytope of dimension 13, in which flat nitrogenous bases can be located, connecting the helix of nucleic acids, was discovered. Exactly as much as there are options for combining nitrogenous bases. It was shown that each coordinate plane of these 12 planes has a specific environment of atoms. It should be assumed that only one of the 12 possible compounds of nitrogenous bases is placed in each of these planes. It is surprising that the

existence of higher - dimensional polytopes with anti - parallel edges is possible only in the case of the opposite direction of interacting helices, and this is exactly what the nature provides in the double-helix DNA and in the RNA segments with self - inversion of the helix in the opposite direction.

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