Fundamenta Informaticae XX (2005) 1–12 1
IOS Press

On the logic and geometry of bilinear forms

Vincenzo Manca
Università di Verona
Dipartimento di Informatica
Ca' Vignal 2, Strada Le Grazie, 15 - 37134 Verona - Italy
e-mail: vincenzo.manca@univr.it

Abstract. The double stranded structure of DNA molecules is investigated in an abstract setting. Only the general structure of bilinear strings is taken into account regardless of specific physical and biochemical aspects of DNA molecules. In this context, the principles which DNA processes are based on are formulated in an abstract form. Surprisingly enough, some intrinsic features of DNA molecules turn out to be implied by these general principles.

Keywords: DNA structure, Bilinearity, Complementarity, Antiparallelism, DNA Helix, DNA Computing.

1. Introduction

DNA molecules are informational bio-polymers floating in fluid environments and having a double stranded structure that is the basis of fundamental bio-molecular processes [3].

An abstract mathematical analysis of the DNA structure can provide a deep understanding of its internal logic. Bilinearity seems to be a golden rule implying an enormous amount of geometrical and computational richness. A mathematical analysis of bio-polymers was already investigated by many authors, according to different perspectives [8, 9]. In [9] Marcus reports Pawlak's triangle representation of protein language and indicates some directions of investigation in which the discrete viewpoint of Formal Language Theory plays a central role in revealing key aspects of biological informational processes. In the pioneering paper [4] DNA molecules were considered as strings, and DNA recombination was formulated in terms of operations over strings.

In this paper we continue the investigation line of [5, 2] where DNA bilinear structure was analyzed in the algorithmic perspective of DNA duplication, essentially related to the Polymerase extension mechanism. In other papers, more oriented to DNA Computing and related to experimental topics [6, 7, 1] a

formal analysis of DNA Polymerase reactions provided the basis for developing a new DNA extraction algorithm. In this paper, the intrinsic algebraic structure of bilinearity will be considered in conjunction with some very natural geometrical principles that are inherent to double linear discrete configurations. Also, the typical helix conformation of DNA will be revealed as a mathematical necessity postulated by simple requirements that can be formulated in terms of *monomeric triangles*. The possibility of figuring out mathematical DNA properties, by using general principles and abstract forms, seems to disclose new perspectives in the understanding of this marvelous biological reality.

2. Monomers, Strands, and Double Stranded Strings

If we abstract from any specific aspect concerning DNA molecules and we focus on the structure needed for their informational functionality, we get the mathematical notion of *double stranded string* which is based on the following four basic principles.

We assume an unbounded number of *monomers*, we may index them using natural numbers, that have a *head* and a *tail*. These monomers float in a fluid environment and can be *concatenated* in *strands* that are sequences which obey to **The Uniformity of Concatenation Verse Principle** because the tail of each element is linked with the head of the next one. The first element of any strand has the head with no link, and the last one has the tail with no link. The verse head→tail of a monomer m is indicated by an arrow: $m\!\rightarrow$. The same monomer in the opposite verse is indicated by $\leftarrow\!m$. Strands can be considered as elements of the free monoid generated by monomers. According to the uniformity of concatenation verse, we put an arrow in a strand only once (at the end in the case of $\rightarrow$, at the beginning in the case of $\leftarrow$).

Monomers have types which are denoted by the symbols of a quaternary alphabet $\{A, T, C, G\}$. If a monomer m has type X we write $m : X$. The free monoid over alphabet $\{A, T, C, G\}$ generates the types of the strands. Typing commutes with respect to the concatenation, in the sense that:

$$\alpha\!\rightarrow : \varphi \text{ and } \beta\!\rightarrow : \psi \quad \text{implies} \quad \alpha\beta\!\rightarrow : \varphi\psi$$

$$\leftarrow\!\alpha : \varphi \text{ and } \leftarrow\!\beta : \psi \quad \text{implies} \quad \leftarrow\!\alpha\beta : \varphi\psi$$

Two monomers can *pair* only when their types obey to the **Complementary Pairing Principle** expressed by Chargaf's rule: A pairs with T and *vice versa*, C pairs with G and *vice versa*. The complementary of a type X is indicated by $\bar{X}$. Moreover, the **Mirror Pairing Principle** requires an orientation in the pairing direction with a verse going from one head to the head of the paired monomer, in such a way that any monomer can be paired at most with one other monomer, and two monomers that are concatenated can pair only with other two monomers that are concatenated. This implies that monomers of a single strand have the same orientation in the pairing direction.

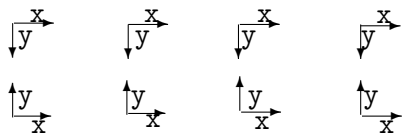
Complementation commutes with respect to concatenation. Two strands $\alpha\!\rightarrow, \beta\!\rightarrow$ are *complementary* if $\alpha\!\rightarrow : \varphi$ and $\beta\!\rightarrow : \bar{\varphi}$. They are *anticomplementary* if $\alpha\!\rightarrow : \varphi$ and $\beta\!\rightarrow : rev(\bar{\varphi})$, where rev is the usual reverse operation on strings ($rev(\lambda) = \lambda, rev(\alpha\beta) = rev(\beta)rev(\alpha)$, λ being the empty string). We write $\alpha||\beta$ when $\alpha\!\rightarrow, \beta\!\rightarrow$ are anticomplementary strands. Two strands that are complementary can *pair* by producing a *double stranded string* in a parallel bilinear arrangement, whereas two strands that are anticomplementary can pair in the antiparallel bilinear arrangement.

A **Free Bilinear Location Principle** holds: under the three other principles, any monomer may occur on either strand of a bilinear arrangement.

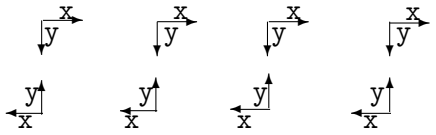
Bilinear strings can be *denatured* resulting in the two single strands that were paired in the bilinear structure. This means that *forces* that couples two single strands in a bilinear string are *weak* with respect to the forces that produce strand concatenation.

Weak forces postulated in the pairing are related with the complementary pairing principle. In fact, if monomers that pair would have the same type, when monomers are molecules, chemical bonds between them should be *covalent*, that is, very difficult to break in denaturation. In general terms, the difference of types and the 1 to 1 correspondence between paired strands can be obtained by requiring that for any $X \in \{A, T, C, G\}$ there exists one and only one different type $Y \in \{A, T, C, G\}$ such that $\bar{X} = Y$.

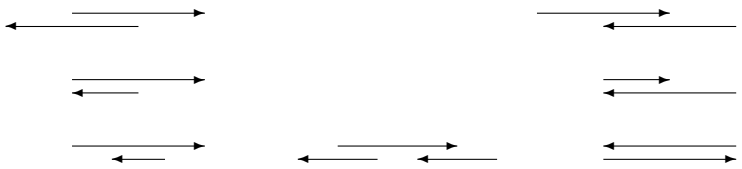
If x is the concatenation direction and y is the pairing direction, then we can represent bilinear arrangements of a double stranded strings with the following geometric structure. For example (types are not specified, but Chargaf's rule is assumed for elements that are opposite w.r.t. y):



In order to satisfy the uniformity of the concatenation verse and the mirror pairing principle, there is another possibility of *antiparallel* arrangement, depicted in the following picture.



We will show that, under suitable hypotheses, only antiparallel arrangements are possible. In more abstract terms, they can be represented in the following way, where it is also shown that, in general, the pairing may involve complementarity only between proper parts of the paired strands.



Bilinearity and complementarity are strictly related to the bilinear duplication mechanism [5, 2], but why antiparallelism? Now we want to consider more carefully this aspect.

In a bilinear structure monomers have:

1. A concatenation direction, say x, along each strand. In this direction let us choose the head-tail verse corresponding to nucleotide 5'-3' verse.

2. A pairing direction, say y, along which a monomer is paired with its corresponding one on the other strand. In this direction let us choose, for each monomer, the verse going from its head to the head of the monomer which is paired to it.

3. A third direction z that is normal to the xy plane, that we can identify with the direction where a reader is placed. In fact, our polymers convey information, therefore they need to be read.

In the following we shortly say that an object is *asymmetric with respect to a direction* if there is no plane orthogonal to that direction with respect to which the object is symmetric.

According to the uniformity of concatenation verse, and to mirror pairing, monomers are asymmetric with respect to both x and y directions. The following proposition shows that they are asymmetric also with respect to z direction.

Proposition 2.1. Monomers must be asymmetric with respect to z direction.

Proof. If a monomer were symmetric with respect to the z direction, then it would not change its shape after a rotation of π around the y axis. But after this rotation it lays in the opposite verse with respect to the x direction, therefore it should be symmetric also with respect to x, and this is against the asymmetry required by the concatenation verse. An analogous argument holds also if we apply a rotation around the x axis, which would contradict the asymmetry with respect to the y direction. □

The asymmetry with respect to the z direction suggests us that it is natural to postulate a preferential reading verse. Therefore, we can put an orientation in the z direction going from the plane xy to the side where, preferentially, a reader is put when it (for example Polymerase enzyme) is reading the monomer.

The **Reading Verse Uniformity Principle** establishes that a reader can read all the monomers of a strand staying always on the same side with respect to xy plane, that is, all the monomers of a strand must have the same z verse.

We say **chirality** of a monomer the cartesian frame associated to its x, y, z directions with the following verses: head→tail for x verse, head→paired-head for y verse, and the verse with respect to which x moves clockwise to y for z direction.

The word “chiral” comes from a Greek word for hand. An object is chiral if it is asymmetric with respect to the three space directions. In this case a chirality can be assigned to it, by establishing a rule for associating a cartesian frame F to it. The rule given above defines chiralities of monomers. There are two possible chiralities: *left-handed* and *right-handed*. Moreover, it is easy to prove the following lemma. Two chiral objects, with chiralities F1 and F2 respectively, are *homo-chiral* if there is a rigid movement of one of them such that after it F1 and F2 coincide (in directions and verses). Otherwise they are *hetero-chiral*.

Lemma 2.1. Two chiral objects, of chiralities F1 and F2 respectively, are *hetero-chiral* if, after a rigid movement, F1 coincides with F2 apart the verse of only one axis. If F1 and F2 differ in the verses of two directions, then the two objects are *homo-chiral*.

According to the given definitions, we obtain the following proposition.

Proposition 2.2. Reading Verse Uniformity implies that all the monomers of a single strand must have the same chirality.

Proof. For the uniformity of concatenation verse, these monomers have the same x verse, moreover, for the principle of mirror pairing they have also the same y verse, therefore if they were hetero-chiral, then

they should differ on the z verse, but this contradicts the uniformity of reading verse. □

However, a stronger result holds:

Proposition 2.3. Reading Verse Uniformity implies that all the monomers in a double strand must have the same chirality.

Proof. If monomers with different chiralities exist, when they occur in the same strand, then they must differ on the z verse, therefore they will have different reading verses, and this contradicts the previous proposition. Then monomers with different chiralities should necessarily occur in different strands, contradicting the free bilinear location principle. □

Proposition 2.4. In a double stranded string, the reading verses of the two strands coincide if and only if the bilinear arrangement of the two strands is antiparallel.

Proof. If) In the case of antiparallel arrangement, the frames of any two monomers in different strands differ in two verses: the pairing verse and the concatenation verse. But, for the previous proposition the monomers of the two strands are homo-chiral, therefore, being the two verses opposite, according to the lemma, the z verses must coincide. In conclusion, they have the same reading verse.

Only if) If the arrangement is parallel, then monomers of two strands differ only in the y verse, but for proposition 2.2 we know that monomers are homo-chiral, therefore, according to the previous lemma, they must differ in the verse of another direction, and this direction, under the assumption of parallelism, has to be the z direction, therefore they have different reading verses. □

The last proposition shows a big advantage of antiparallel arrangement with respect to the parallel one. In the next section we will prove, by using only geometrical arguments, that for floating double stranded strings the antiparallel arrangement is the only possible one.

3. Monomeric Triangles

In this section we develop, in a more systematic way, the intuition outlined in the previous section. Strands are elements of the free monoid generated by a set of monomers, and types are elements of the free monoid generated by a set of base types (therefore concatenation is defined on strands and types). Bilinear structures obey to four main principles: i) Uniform Concatenation Verse, ii) Mirror Pairing, iii) Complementary Pairing, and iv) Free Bilinear Location.

Three points are essential in determining the monomer functionality: i) the head point H, which is the first point of the monomer along the concatenation verse, ii) the tail point T, which is the head of the next monomer along the concatenation verse, and iii) the point H', which is the head of the paired monomer. These three points specify the triangle HTH' that we call **monomeric triangle**. Given two consecutive monomers $mm' \rightarrow$ such that m is paired with $\bar{m}$, then the head of the second monomer m' coincides with the tail of m. In terms of nucleotides, point H of m corresponds to the Phosphorus group in $5'$ of m, T corresponds to the Phosphorus group in $3'$.

If HTH' is the monomeric triangle of a monomer m and $HH'T'$ is the monomeric triangle of a monomer $\bar{m}$ which is paired with m, then we refer to points $THH'T'$ as the **monomeric butterfly** of these two paired monomers, having triangles HTH' and $HH'T$ as *wings*. The HH' line is the

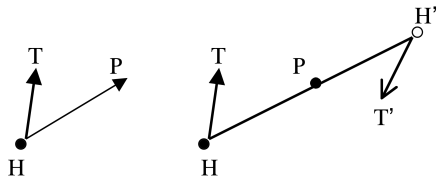


Figure 1. A Monomeric triangle and a Butterfly (segments TP and TP' are not indicated).

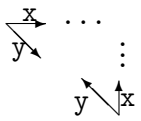
pairing axis of the butterfly, HT and $H'T'$ are the concatenation axes of the butterfly. Of course, there are four types of these triangles and two types of these butterflies, corresponding to different types of bases. In the biological reality, the information that a triangle carries (the types A, T, C, G) depends on two parameters: i) the position (left or right) where pairing bonds are located in the segment HH' with respect to the middle point P of segment HH', and ii) the strength of the pairing bonds. In the following, for the sake of simplification, we assume that all monomeric triangles are equal.

In conclusion, monomeric triangles completely specify the role of monomers in the bilinear arrangements, that is, from an abstract point of view, a monomer is a triangle having a type in the base alphabet.

We assume that monomeric triangles are acute (i.e., all three angles are acute). This corresponds to reality and implies a more economic spatial allocation.

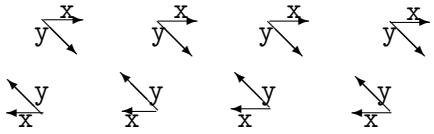
Proposition 3.1. If the angle $T\overset{\triangle}{H}H'$ of monomeric triangles is acute then bilinear parallel arrangement is not possible.

Proof. It is easy to verify that, in this case, if two monomeric triangles are paired along their pairing axis in such a way that tails are put on the same side with respect to this axis (see figure below, where pairing segment is drawn with a gap). Then, if they are coplanar the two concatenation verses follow two crossing straight lines.



If they lay on different planes, they follow two straight lines where the distance between monomer heads increases along the concatenation verse of the two strands, but this situation is against bilinearity. □

An antiparallel bilinear arrangement with acute monomeric triangles can be obtained in the following way:



Nevertheless, in the previous bilinear structure monomers are in the same plane, but this is almost impossible in a fluid environment, especially in the case of very long polymeric structures. In this case, a rotation angle of the butterfly wings along the pairing axis is possible if, contemporarily, the head-tail

axis of any monomeric triangle rotates with respect to the head-tail axis of triangles to which is linked. In fact, the angle of rotation around the pairing axis is so compensated by a *concatenation angle* in order to keep uniform the distance between the heads of paired monomers.

Figure 2 shows this possibility, where a helix structure appears that will be analyzed in the next section.

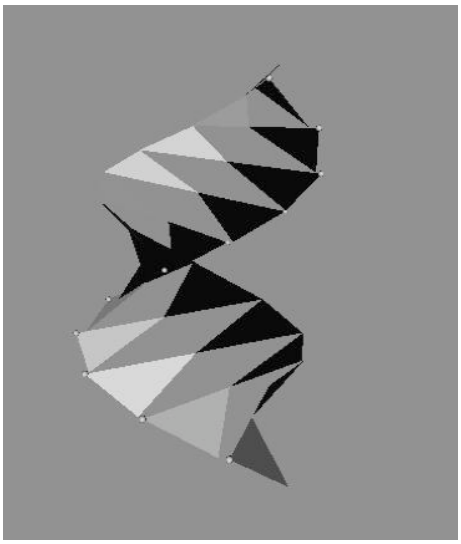


Figure 2. Monomeric acute triangles arranged in a bilinear non-planar structure.

4. Abstract Bilinear Helix

Let us denote with δ the angle $T\overset{\triangle}{H}P$ and call it *monomeric angle*. This angle is related to the *rotation angle* ρ of monomers around the surface of a *bilinear cylinder* of radius r (see Figures 3, 5). If we call *rotation number* of the bilinear cylinder the number n of monomers in a complete rotation, then $\rho = 2\pi/n$. This means that if $n = 10.5$, as in typical B form of DNA helix, then $\rho = 34.28$ degrees. Let us denote with f the length of head-tail distance, we say *concatenation distance* of monomers, and with b the pairing distance between two paired monomers.

The radius r of the bilinear cylinder and the rotation angle ρ (or equivalently, the rotation number n) are two *bilinear helix* parameters. Other two bilinear helix parameters are: i) the *torsion* angle τ given by the angle formed by the head-tail axis with the horizontal planes (those which are orthogonal to the cylinder axis); and ii) the *phase* angle, that is, the rotation angle ϕ of the cylinder radius between two monomers that are paired. The angle τ determines the vertical *torsion factor* of monomers, that is, the number $\theta = \sin\tau$ such that θf is the distance of the monomer tail T from the horizontal plane where its head H is placed on (see figure 3).

Figure 3 shows a butterfly included into the cylinder where bilinear helix develops. The pairing segment is between the two heads indicated by black and white bullets, the two arrow ends are the tails corresponding to the two heads. Rotation angle ρ is horizontally covered by the cylinder radius between any head and its tail, phase angle ϕ is horizontally covered by the cylinder radius between two paired heads, torsion angle τ is formed by the head-tail segment and a horizontal plane. This picture also shows

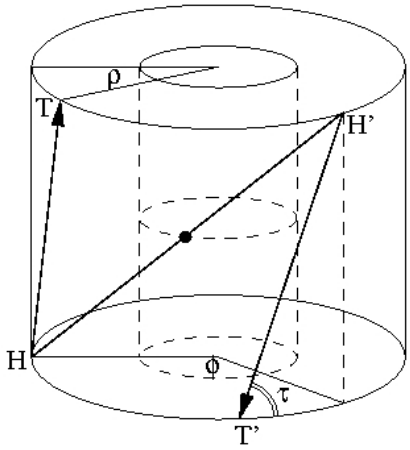


Figure 3. The butterfly into the bilinear cylinder: Rotation, Phase, and Torsion angles.

that when the pairing segment does not intersect the cylinder axis, then the pairing segment is tangent to an internal cylinder having a radius which depends on the value of the phase angle.

Figure 4 is a look at a bilinear structure with three monomers for each line.

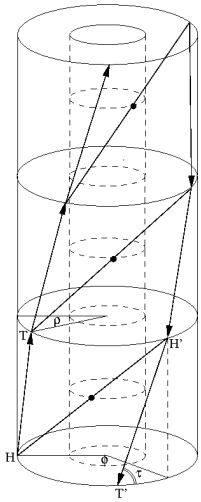


Figure 4. Three butterflies in the cylinder.

The following figure 5 was obtained with a graphical tool developed in OpenGL under Linux[1]

Pairing happens between points on different cylinder levels, that is, the helix cylinder can be divided in slices between horizontal circles. The two heads of the monomers which are paired are one on the top

[1]This tool was developed by Luca Trombin in a project for my course “Unconventional Computation Models”, at the University of Verona.

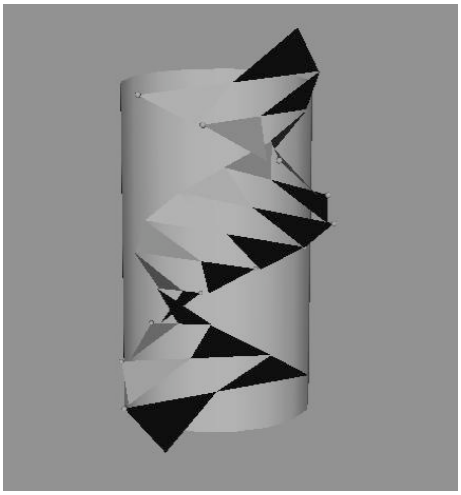


Figure 5. Bilinear helix and the related cylinder.

circle and the other one on the down circle respectively of the same slice. The distance θf between these circles depends, as we will see later on, on cylinder radius r, on rotation angle ρ and on the torsion angle τ.

The following figure 6 shows the two bilinear cylinder strands projected on a strip between two parallel lines at a distance $2r$ equal to the diameter of the of helix cylinder. The difference between *major grove* and *minor grove* observed in DNA helix can be explained in terms of bilinear cylinder geometry as a consequence of the torsion angle and of the phase angle. It can be shown that the phase angle is proportional to the ratio between minor and major grove defined as the greatest and the smallest vertical distances between the two strands when they intersect the same vertical line on the cylinder surface. For the sake of simplification, in the picture the phase angle is π.

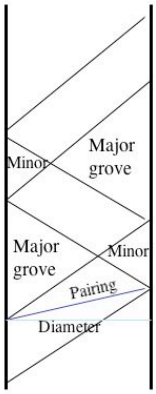


Figure 6. Bilinear helix in projection.

Now we show that bilinear helix parameters r, ρ, τ, ϕ completely identify the monomeric triangle.

Proposition 4.1. The bilinear helix parameters given by the cylinder radius r, the rotation angle ρ, the torsion angle τ, and the rotation phase ϕ completely identify the monomeric triangle.

Proof. Let a be the length of the cord relative to the monomer rotation angle ρ. We easily see that

$$a = 2r\sin(\rho/2)$$

but, according to the definition of torsion factor $\theta = \sin\tau$, the following equation also holds:

$$a = \sqrt{f^2 - (\theta f)^2}$$

therefore

$$f = \frac{2r\sin(\rho/2)}{\sqrt{1-\sin^2\tau}} = \frac{2r\sin(\rho/2)}{\cos\tau}$$

This means that the length f of HT is determined by r, ρ, τ. Now let us consider the pairing distance b and the length p of the projection of b on the horizontal plane (orthogonal to the cylinder axis). Of course, we have:

$$b = \sqrt{p^2 + (\theta f)^2}$$

and $p = 2r\sin(\phi/2)$. Therefore b depends on the four bilinear helix parameters r, ρ, τ, ϕ. But the length of HP is $b/2$ therefore also this measure depends on these parameters.

In order to evaluate the angle δ between HT and HH', we evaluate the distance TH' as $g = 2\sin(\frac{\phi-\rho}{2})$ and apply Erone's formula for the surface of triangle HTH' (in a triangle of dimensions a, b, c, where $2q = a+b+c$, the surface S is given by $S = \sqrt{q(q-a)(q-b)(q-c)}$). From the surface of HTH' we derive the height with respect to HH' and so the sinus of δ. Therefore, by simple algebraic manipulations we get:

$$\delta = \arcsin\frac{\sqrt{(f+g+b)(g+b-f)(f+b-g)(g+f-b)}}{2bf}$$

□

In conclusion, the monomeric triangle depends completely on r, ρ, τ, ϕ and bilinear helix is an element of subspace of 4 dimensions satisfying the following equations in the dimensions space of vectors $(r, f, b, g, \rho, \tau, \phi, \delta)$:

$$f = \frac{2r\sin(\rho/2)}{\cos\tau} \quad (1)$$

$$b = \sqrt{4r^2\sin^2(\phi/2) + (f\sin\tau)^2} \quad (2)$$

$$g = 2\sin(\frac{\phi-\rho}{2}) \quad (3)$$

$$\delta = \arcsin\frac{\sqrt{(f+g+b)(g+b-f)(f+b-g)(g+f-b)}}{2bf} \quad (4)$$

If we consider the values, relative to the B form of DNA helix: $\rho = 4\pi/21 = 34.28^o$, $r = 1\ nm$, $\tau = \pi/6 = 30^o$, and an approximare value of $\phi = 2\pi/3 = 120^o$, which was deduced from data given in [3] for B DNA ($(\phi - \rho)/2 = 5\pi/21 = 42.86^o$), we get a monomeric triangle where HT = 0.68 nm, HH' = 1.76 nm, $H'T$= 1.36, and angles $\delta = \overset{\triangle}{H} = 44.39^o$, $\overset{\triangle}{H'} = 37.99^o$, and $\overset{\triangle}{T} = 97.61^o$.

In the bilinear helix we call *butterfly angle* the angle β between butterfly wings. This angle. depends on the radius r and on angles of rotation, phase and torsion. In fact, by a rotation of $\pi/2 - \tau$ one butterfly wing becomes parallel to the cylinder axis, and by the same rotation also the paired wing becomes parallel to the same axis. Therefore its value results to be $\beta = (\pi - 2\tau)$.

An important aspect of DNA helix is that the pairing segment does not cross the axis of the helix cylinder. In fact, it is a cord shorter than the diameter. This means that when we see the helix in horizontal projection we can see a hole tangent to all pairing segments. In other words, an internal cylinder exists of radius $r' < r$ (p is the projection of the pairing segment on the horizontal plane):

$$r' = \sqrt{r^2 - (p/2)^2}$$

such that pairing segments are always tangent to the surface of this r' cylinder. This phenomenon is conform to our model where pairing is driven by a phase angle. The following picture was obtained by our graphical simulation. For ϕ equal to 120 degrees we obtain $r' = 0.50$. It is remarkable that a difference of 0.24 nm between the diameter and the pairing distance produces an internal cylinder with a radius that is about one half of the external radius. We are tempted to say that this is room available for the *reader* of the bilinear helix.

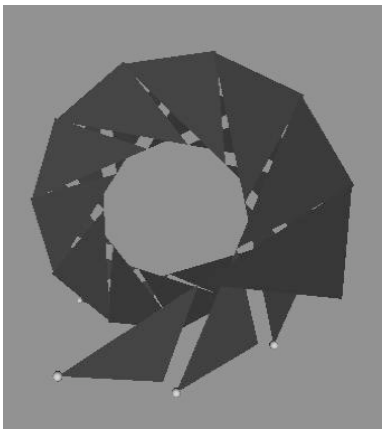


Figure 7. Helix horizontal projection.

5. Conclusions

The approach introduced in this paper has revealed important facts of the bilinear helix that are direct mathematical consequence of general principles. The notion of monomeric triangle, and its requirement

of being an acute triangle, has implied rules of geometrical organization of this helix that showed the way its structural parameters are related. As an important consequence, we deduced that the helix dimensions depend on the cylinder radius r of the helix, while all its structural parameters depend on three angles: rotation, phase, and torsion.

We think that many aspects of bio-molecular processes can be analyzed in terms of purely algorithmic and combinatorial arguments and may provide new perspectives in the understanding of basilar phenomena. Our graphical simulation proved that the radius and structural parameters of B DNA are determined by the general structure of bilinear helix. In fact, these values, and the other values defined within the monomeric triangle model, were confirmed by computer simulations. It would be interesting to improve the visualization aspects by means of more efficient computational tools, and to extend our analysis to the other forms of DNA, the A and Z forms.

In [1] polymerase reactions were considered and some simple trees turned out to be useful in the design of DNA extraction algorithms. In [6] Head's splicing was represented in terms of restriction and ligation enzymes. In both cases a special kind of bilinear concatenation was essential, that was realized in vitro by extending the classical PCR protocol, but many crucial combinatorial problems must be solved for an efficient implementation of these ideas. Therefore, a research line, where bio-technological experiments, mathematical theories and computer simulation are integrated, seems to be a very promising way to proceed in the future.

References

[1] G. Franco, C. Giagulli, C. Laudanna, V. Manca, *DNA Extraction by Cross Pairing PCR*, in [10], to appear.

[2] G. Franco, V. Manca, *An algorithmic analysis of DNA structure*, Soft Computing, to appear, 2004.

[3] R. H. Garrett., C. M. Grisham, *Biochemistry*, Saunders College Publishing, 1997.

[4] T. Head, *Formal language theory and DNA: An analysis of the generative capacity of specific recombinant behaviors*, Bulletin of Mathematical Biology *49*, pp 737-759, 1987.

[5] V. Manca, *On the logic of DNA bilinearity*, Preliminary Proceedings, Masami Hagiya, Azuma Ohuchi (Eds.): DNA Computing, 8th International Meeting on DNA Based Computers, Hokkaido, Japan, p 330, 2002.

[6] V. Manca, *A proof of regularity for finite splicing*, in: N. Jonoska, G. Paun, Rozenberg (eds.), *Aspects of molecular computing*, Springer LNCS 2950, pp. 309-317, 2004.

[7] V. Manca, C. Zandron, *A Clause string DNA Algorithm for SAT*, in N. Jonoska, N.C. Seeman (eds.), *DNA Computing*, Springer, LNCS 2340, 172-181, 2003.

[8] S. Marcus, *Linguistic Structures and Generative Devices in Molecular Genetics*, in: Cahier de Linguistique Théorique et Appliquée, Vol. 11, n. 2, pp. 77-104, 1974.

[9] S. Marcus, *Language at the Crossroad of Computation and Biology*, in: Computing with Bio-molecules. Theory and Experiments, Păun G. (ed.), Springer-Verlag, Singapore, pp. 1-35, 1998.

[10] G. Mauri, G. Rozenberg, C. Zandron, (eds.), *DNA Based Computers: DNA10*, Proceedings of 10th International Meeting on DNA Based Computers, Milan, June 2004, Springer, L.N.C.S., to appear.