# Möbius strip and Klein Bottle Genomic Topologies, Self-reference, Harmonics and Evolution

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**Abstract:** We present the Möbius strips and Klein Bottle non-orientable surfaces, and the non-dual logic of the latter to construct a bioinformatic genomic matrix of arbitrary length, and fractal-like harmonics. We discuss the relation with noise immunity of genetic information, the relation with transposons and palindromes, and their bearing to the evolution of the genome. We discuss the connections to cortical anatomophysiology, the palindromic patterns of time series of seemingly random experiments, pattern recognition, music perception, the biology of development, the non-dual structure of light-waves and the origin of material structures and its non-dual logophysics. We discuss the relations with the Double Helix of Watson and Crick.We present the numerical evidence for these harmonics topologies as provided by BUILD34, from the Genome Project. We discuss the relations with topological and quantum entanglement, and cellular automata. We discuss the generation of complexity through self-organization as induced by these topologies.

**Keywords:** bioinformatics; palindromes; transposons; harmonics; quantum holography; vortices; non-classical logic; complexity; Hadamard matrices; pattern recognition.

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## 1. Introduction. Genomic Matrices, Topology, Non-orientable surfaces and Noise.

Introducing a special issue on the mathematics of genomics, Sergey Petoukhov offers a reflection on the subject, quoting the work of I. Stewart "The biological meaning of genetic informatics is reflected in the brief statement: "life is a partnership between genes and mathematics" [107].But, what kind of mathematics has partner relations with the genetic code and what kind of mathematics is behind genetic phenomenology? This question is one of the main challenges in the exact natural sciences today" [1]. The author proceeds to comment on the relations between the problem of noise-immunity for the transmission of genetic information which comprise as well the coordination of all the subsystems which make up an organism as an integrated being operating through cyclical processes, as well as the problem of self-reproduction of both the genetic system and organisms: these are problems for mathematics to deal with. In relation with the problem of noise-immune transmission of information, these problems have been solved technologically. They resort to the implementation of the theory of Rademacher and Hadamard matrices, which allow for such a feat as the transmission and reconstruction of digital photographs of planets and the Solar System itself, taken by several devices.

Yet, while Hadamard matrices play a role in the theory and practice of coding information immune to noise, in the case of two by two Hadamard matrix , they are nothing but the matrix representation of a two-dimensional surface: the Klein Bottle [14]. This surface, globally considered, has one single side; locally considered it seems to have two sides. This surface is non-orientable,which means that a normal vector, i.e. a perpendicular vector to the surface, is unique; this stands in distinction with

orientable surfaces, which have two different sides, and thus two different normal vectors exist, one for each side. The Klein Bottle surface has no global Inside nor Outside but as local states which are connected and intertransfomed, rather than separated. This connection and intertransformation of local Outside and local Inside is produced by the self-penetration of this surface. Thus, this surface rather than being contained in ambient three dimensional space, it is defined and produced by its self-containment due to the self-penetration. Alike genomes, the Klein Bottle is self-referential [10-14]. As for the mathematics advocated by Petoukhov, they reveal algebraic codings of genomes using structures which are also common to quantum mechanics and to several areas of physics which may appear in first consideration to be unrelated to genomics [8,9] The principle derived from this mathematics which is also basic to physics and chemistry is that of symmetries, which is also basic to biological morphologies. It is impossible to conceive of biochemistry without considering issues of enantiomerism, as early discovered by Pasteur, and enantiomerism is all about symmetry, and its disruption: Chirality (handedness) plays a crucial role to biochemistry and life, and already appears in the double helix model of DNA, which, in principle, may have any of the two chiralities. And as we shall see, enantiomerism is essentially related to the non-orientable Möbius strip surface, which we can think of as a surface contained on a line, which also has no Outside nor Inside; actually, two collated enantiomeric Möbius strips generate a Klein Bottle. As it turns out to be the case, the algebraic structures of genomes revealed by Petoukhov, have a more basic root in the algebraic coding of the Klein Bottle surface as a non-dual logic, which admits a binary representation, which is the cornerstone of informatics and particularly of genomes [11]. This coding leads to reveal a fractal-like topology of genomes, as HyperKlein Bottles, family of Klein Bottles structured as an heterarchy.

Symmetries in genomes appear in many forms, as the chirality of genomes; or still, the pervasive existence of palindromic sequences, as ordered structures interspersed in what is conceived to be an extremely complex genomic structure, whose fundamental changes are considered to be random. But randomness is a word for ignorance: Ontologically, randomness appears not to exist. This follows from sixty years of continuous experiments of great diversity, based in usually conceived random phenomena, that has shown the existence of a universal cosmological factor, influencing the fine structure of supposedly random fluctuations [3, 58]. Indeed, their histograms developed as time series appear to have the form of palindromes, appearing as time cycles. Genomic palindromes are crucial to evolution [193]. Despite their complexity, these data reveal a remarkable topological symmetry, actually a shape, which can be conceived as Möbius strips, as we shall see. In fact, this *shape of data* will be the focus of our attention in bioinformatics and else. It points out to the existence of metapatterns –which can be used to make predictions [206], and in particular, in bioinformatics, to a metagenomic pattern.

Petoukhov puts the case as follows: " Biological organisms belong to a category of very complex natural systems, which correspond to a huge number of biological species with inherited properties. But surprisingly, molecular genetics has discovered that all organisms are identical to each other by their basic molecular-genetic structures. Due to this revolutionary discovery, a great unification of all biological organisms has happened in the science. The information-genetic line of investigations has become one of the most prospective lines not only in biology, but also in science as a whole. The basic system of genetic coding has become strikingly simple. Its simplicity and orderliness presented challenges to specialists from many scientific fields. Bioinformatics considers each biological organism as an ensemble of information systems which are interrelated to each other. The genetic coding system is the basic one. All other biological systems must be correlated to this system to be transmitted to the next generations of organisms."

Yet, there is one fundamental area of mathematics which embodies uniquely in its simplicity these complex structures. This area is topology; etymologically, the study of loci. It is the mathematical study of shapes, yet essentially conceived qualitatively, as equivalent under continuous deformations, rather than analytically nor quantitatively, the latter being at large the predominating conception and operation of mathematics. Topology appears to be especially adequate to explain biological systems.

Already the eminent anatomist and naturalist John Bell Pettigrew(1834–1908) [5,6] and the founder of the mathematical studies in biology, D'Arcy W.Thompson(1860–1948) [4], unaware of topology as a mathematical discipline, intuited its fundamental role in biological systems, as viewed from the experience of glass-blowing surfaces, which the latter conceived of as allometric transformations of bodyplans of organisms as a basis for the appearance of species in terms of previous ones, usually attributed to evolution. Wilhem His, the anatomist and physiologist considered to be the father of human embryology for introducing the three germ layers, practiced a series of topological experiments with rubber and wax tubes aiming to understand morphogenesis. Thus, His was able through mechanical deformations to reproduce the shape of the gut, brain and other organs [234].

In this article we shall present a topological model of genomes and its bioinformatics [11], and still discuss the relations with evolutionary bioinformatics and the evolution of genomes and further to relate them to a novel topological conception of complexity [170]. Yet, shape and locus is associated to logic, and still to a dynamics which altogether conform a logophysics [13,14].The latter has been applied to embryological development and tissue differentiation [10,12]; topological models of embryological developments have also been elaborated in a series of works [15,16,17], and still to a unified conception of remarkable simplicity for the unification of science [13,94,142] .

The topology of the Klein Bottle and the Möbius strip are related to a non-dual logophysics, which in a quite elementary sense, means that it is not possible to divide categorically the world produced by a boundary, in terms of Inside and Outside, since there is a continuity between them, which is basic to physics and to cognition [128,142,150,151,155,156]. In breaking or disconsidering this continuity, we obtain as a particular reduced case the usual dual logic of Aristotle as formalized by Boole which is the basis for informatics and in particular its bioinformatics application to genomes [14]. These topologies which integrate Outside and Inside are associated to self-reference, as a principle of self-organization, and cognition [10,11,12,13,14,94,128]. Specifically we shall consider, as we already introduced them, the non-orientable Möbius strip and Klein Bottle surface. Despite the non-dual self-referential nature of the Klein Bottle, it is naturally amenable to produce a binary codification. The latter, in turn, will produce through a very simple algorithm, the basis for numerics in terms of hidden structures of genomes, which can be elicited by the study of the databases provided by the Encode Program. Remarkably, the frequency of these numerics will appear in the very vein that Pythagoras originally proposed, in terms of harmonics and thus amenable to a musical transcription. In short, bioinformatics as the study of the Genetic Code will be found to stem from a logophysics associated to topologies of self-reference, rather than being inherently about digital data bases. As we said before, data possess shape; already Fisher Information Theory, as derived from Bayesian statistics, shows this to be the case though topology was not addressed in this setting [199]. The digital contents are embodied by the non-orientable topologies of genomes, which have an inherent wholeness as their signature. The underlying conception is that rather than studying genes as singular events, we must consider the genome as a whole in which groups of codons are crucial to the formation of genomes as algorithmic structures derived from the topology. These natural groups of genomes span a harmonics which furthermore is related to the topology of the genome. And yet, these algorithmic structures appear to be amenable to generation as if independent of the topological structures of genomes, say as a finite automata ([37], Chapter 19).

Topology was understatedly introduced with the double helix model (DH) of DNA by Watson and Crick, as an orientable topology, which means that DNA, in being left or right handed, its helixes have a well defined normal vector –i.e. a vector perpendicular to the surface- defining an Outside and Inside, which is crucial to the structure of DNA, as we shall discuss below. These two normal vectors are different states proper to the two-sided character of the DH orientable geometries, rather than the one-sided character of non-orientable surfaces. For the latter kind of surfaces, due to the 180 ° twist of the Möbius strip or the Klein Bottle, there is no globally defined Interior nor Exterior; a normal vector which locally points to what appears to be Inside, can be transported to a normal vector pointing Outside, as supported at the homologous point at the "other" side, but now pointing Inside; see Figs. 1

to 4. Subsequent discussions on the validity of this model and its mathematical-physics aspects, as well as alternative geometries for the DH, have been related to topology [88,114], and remarkably to the statistics of codon frequencies, in relation with the palindromic structures which are recognized in the palindromic structures of DNA. We recall that in topological terms, palindromes can also be thought as Möbius strips, whereby introducing a 180º torsion on the sequence, an identification takes place. This can be nicely illustrated by considering a musical example, Johann Sebastian Bach's Toccata and Fugue in D Minor, the Crab Canon; [101]. Yet, as we shall see, the palindromic structures which are so ubiquitous to genomes, and topologically can be conceived as Möbius strips, are related to an archaic genome. Basically, we shall demonstrate that the remarkable existence of a mirror-codon in single strand BUILD 34 genome reveals the existence of higher order structures that are related to non-orientable topologies of the genome, and further related to the existence of harmonics.

Closed topologies are known to be the case of the mitochondrial DNA (mtDNA), a special kind of DNA that does not reside in the nucleus of the cell, but in an organelle named Mitochondrion. The Mitochondria are structures that reside in cells that convert the food into energy for the use of the cell. The Mitochondria have the special ability to replicate themselves independently of the gene information in the DNA, unlike all the other cells in the organism. Also, unlike normal DNA, mtDNA is in most species solely inherited from the mother. The mitochondrial DNA is a circular structure of approximately 16,500 base pairs, in humans [24]. As for bacterial nucleosomes, as well as those of eukaryotic viruses, such as SV40, they are known to be closed Möbius loops [222]. The organization of chromatin into closed loops is believed to be crucial to DNA compactation and gene expression; each such loop may act as a independent unit of gene activity [223]. Since biological evolution is presently conceived as having arisen from bacteria and viruses [193,224], this identifies a genomic metashape for it, in this non-orientable surface. Indeed, the consideration of the palindromic structure of an evolutionary novelty in prokaryotes, given by a system of adaptive immunity common to most bacteria and archea [193], has served for its promotion as a basis for a Lamarckian punctuated evolutionary theory, in the framework of comparative genomics [224].

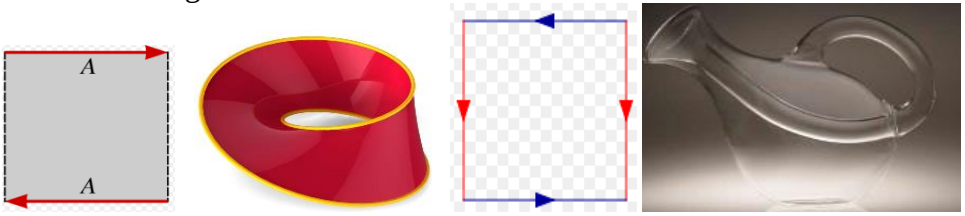


Let us state what we believe to be the ultimate basis for genomes: They are structured and processed by a non-dual logophysics which is keenly associated to the torsion geometries that are basic and pervasive to physics and nature, as primeval vortices [13]. We have revealed their ubiquitous and basic role as a geometry of self-reference, and its instantiations as a unifying principle in anatomy and physiology,perception, physics, geophysics, chemistry, biomechanics and cognition [10,11,12,13,14, 150-156].The role of vortices to biology and the unity of nature was already stressed by Bell Pettigrew [4,5], while most material systems of nature are viscous liquids and thus vortical torsion geometry systems; [156]. This pervasive geometry was subsequently neglected, but for Edgar Morin's theory of complexity [200] and also by the theory of chaos and blowups of non-linear systems due to Yi Lin and Soucheng Ou Yang [201,202]. The latter ultimately rests on the non-orientable structure of the compactified complex number system which signifies a novel cycle of such systems, as a generic renewal principle [13]. (See note no. 1 below). The Möbius strip and the Klein Bottle are two elementary examples of vortical structures, yet in which self-reference is embodied. As for the non-duality which is organized in terms of non-orientable topologies for which there is no global Outside nor Inside, it fails to abide to the principle of the excluded middle: namely that a proposition may be true and not be true simultaneously. Or still, they do not abide to the principle of non-contradiction [14]. It is known that organic chemistry may be conceived in terms of topology which does not abide to the usual dualism of Outside and Inside [13,42] and that biological water, as the non-inert liquid crystal context for chemical reactions and most living systems, also appears to operate in terms of this nondual logic [10,12].The most prominent example to biology is that of liquid crystals, that having dislocations, they self-organize as elastic material, and fold into Möbius strips configurations [27,50] or still, can be caged into ordered water domains or conversely, be a cage for ordered water [108]. Especially, this is the case of carbon molecules, which may form tensegrity structures which as we said, may incorporate water of rather be contained in it [108].Thus, in the relations between the carbon

molecules crucial to life, with water, a principle of literally exchanging Inside and Outside appears to be at work. Also, molecules may appear as having multiple conformations, or a "split personality" in a colloquial dualistic description: on the one hand orientable conformations may turn to be non-orientable, and the converse can also be the case [13,42, 166]. But already the chromosomes, of which genomes are made of, simply fail to behave as respecting this principle of dualism. Indeed, chromosomes are both highly plastic being able to translocate whole parts of its bodies to other parts or to other chromosomes without affecting its survival. And all in all, together with the multifarious changes, the overall result is the extreme rigidity of chromosomes taken as wholes. This coexistence of seemingly antagonic features was noted by the eminent cytogenetist Lima de Faria, for which he coined the term as the "folly of chromosomes". Chromosomes are largely available to change, and still to preservation. But rather this paradox being the signature of the "irrationality" of chromosomes, this possibility of change coexists with that of extreme conservation is the character of chromosomes [28]. They are capable of and operate through change coexisting with overall preservation using constraints. At times this is carried out irrespectibly of chromosomes being coextensive to the environment superposed with the possibility of contextualization with respect to it, producing changes which will ensure its overall survival. The bottomline is that in living organisms, chromosomes are embedded in water, which rather than being a mere solvent, is crucial to the whole biochemistry of the cell, and particularly the nucleus, where chromosomes are placed. Water in living organisms is highly organized as a liquid crystal which may have defects whose topology is that of the nonorientable Möbius strip topology [108], as local sections of the non-orientable real projective space topology [13] of liquid crystals [109].

This article will be devoted to the non-orientable topologies of DNA and its bioinformatics, and its relation to the evolution of genomes. Yet, they are related to vortical geometries which are not related to a notion of a metric which is pervasive to theoretical physics, yet already Pettigrew identified as the geometry of motion and nature, and particularly of biology [4,5]. Particularly, they are related to the the 5-fold pentagonal symmetry of torsion geometry which is basic as much as to spacetime, to biological and chemical structures, to the anatomy and physiology of the human body and to cognition [10,11,12.13,14,94,128,148]. This vortical geometry is related to the Golden Ratio, Φ, the latter discovered by Jean Claude Perez in genomics and proteomics, after 30 years of research. Φ together with the numbers 1 and 2 conform the harmonics of the bioinformatics of the human and other genomes [37,38,39]. It gives support to the proposal due to Rapoport [11] that non-orientable topologies are at the very basis of genomes as wholes, and its bioinformatics. As we shall see, this appears to be related to a deep coherence of genomes in which whole and parts are unseparable to its constitution and equilibrium and stability properties. This introduces from the very outset of the generation of genomes their dynamical character, through topological non-orientable foldings and discontinuities, identified as the basic genomic operations, linked both to conservation and novelty, as we shall discuss below. To do this, we retake the work in [11] to construct genomes through a very simple self-referential albeit topological algorithm, alike to a cellular automata [91].

Our departure point will be a digital numerical representation of the Klein Bottle Logic, and the identification of its four states with the four letters of DNA (alternatively, RNA),for which we need to introduce first the Möbius strip and the Klein Bottle. Later on, we shall see that the latter can be thought as a nondual logic




[*A*] [B] [C] [D]

**Figure 1.** [A] : To turn a rectangle into a Möbius strip (presented at the centre) –in this case a left handed one though right-handed Möbius strips are also the case, join the edges labelled *A* so that the directions of the arrows match. We note that due to the 180 $^{0}$ twist of the red line in [A], the Möbius strip can be conceived as a dimensionalization producing process: namely, a two-dimensional surface which is contained in a one-dimensional single closed curve (now painted in yellow in [B]). The Möbius strip as a surface is contained in three dimensional Euclidean space. [C]: To construct the Klein Bottle in [D], glue the red arrows of the square together (left and right sides), resulting in a cylinder. To glue the ends of the cylinder together so that the arrows on the circles match, you must pass one end through the side of the cylinder. Note that this creates a circle of self-intersection in which the surface self-penetrates; this is an immersion of the Klein bottle in three dimensions. But in distinction with the Möbius strip, the dimensionalization is such that two opposite lines (depicted in red and blue in [C]) gives rise to a surface which due to the self-penetration, is still embedded in 3d-space but rather than contained in it without self-intersections as for the Möbius strip, it is self-contained, while still being able to act as a container, albeit an inperfect one: it may leak.

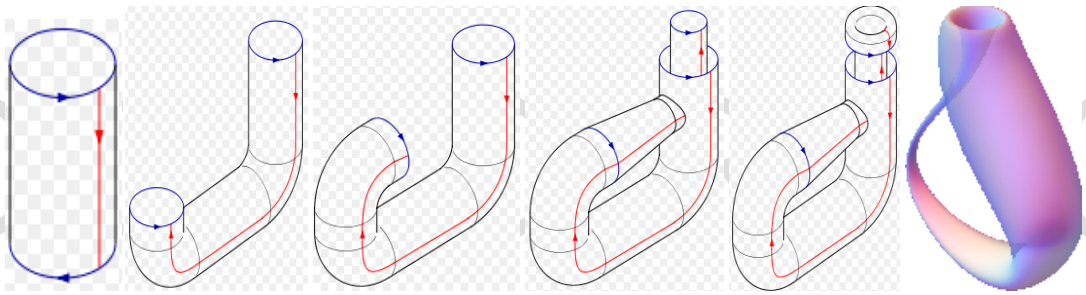


**Figure 2** Sequence of topological transformations leading to produce the Klein Bottle - with slight transparency; rendered with Mathematica 8 using the parameterisation provided by Robert Israel. Creative Commons


[A] [B] [C]

**Figure 3 .**The Klein Bottle and a HyperKlein Bottle. In [A]–courtesy of Theon . we see two oppositely twisted Möbius strips produced by cutting the Klein Bottle along the longitudinal section; conversely, zipping them we obtain the KB. Thus, in distinction with the Möbius strips which can be either left or right handed, the Klein Bottle is neither, yet

possess inherent to it both chiralities. [B]– Image of a HyperKlein Bottle, at the Science Museum, London, created by Alan Bennett; more examples can be viewed in www.sciencemuseum.org.uk/images/I065/10328078.aspx, www.sciencemuseum.org.uk/images/I065/10328078.aspx, www.sciencemuseum.org.uk/images/I046/10314766.aspx.
[C]- the topological identifications which produce the non-orientable real projective space. It is a compact non-orientable two-dimensional manifold, that is, a one-sided surface. Liquid crystals, due to their uniaxial symmetry have this topology as associated with their director vector field. [135].In distinction with the Klein Bottle, the fundamental figure which shows the topological identifications, has the two sides, both oriented oppositely, rather than one, as in Fig. 1. [C] versus Fig. 2. [C]. The Möbius strip can be conceived as a real projective space which one of the pairs of opposite sides identification is frozen. Yet, common to all three, they are all non-orientable two dimensional surfaces. Local section of the real projective space, which is the usual case of bounded structures, say liquid crystals in a cell, are Möbius strips. However, both the Klein Bottle and the real projective space are not contained, but self-contained, realizable by self-penetration, both conditions not being the case of the Möbius strip. The latter has a more restricted self-referential nature, as an embedded surface in ambient three dimensional Euclidean space.

## 2. The Harmonics of the Möbius strip and the Klein Bottle and the Eversion of Organisms



In this article we shall deal with palindromic structures in genomes, namely, lexical structures that admit the same interpretation independently of the order in which they are encoded or decoded. For example: ‘ana’; ‘so many dynamos’ –in omitting the blanks, of course. As already discussed, palindromes are topologically equivalent to Möbius strips. This inverted repeat of a lexical structure that appears to be as identical to the original transcript, either be a music script, parts of a genome or whatever, might be understood in terms of a musical metaphor, that of harmonics. Let us explain this. Consider the following figures, following the discussion in [13]:

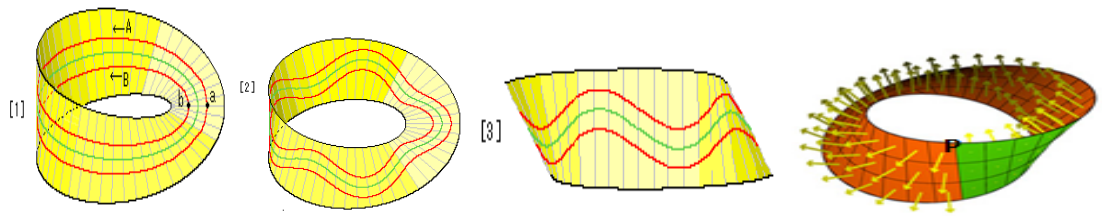
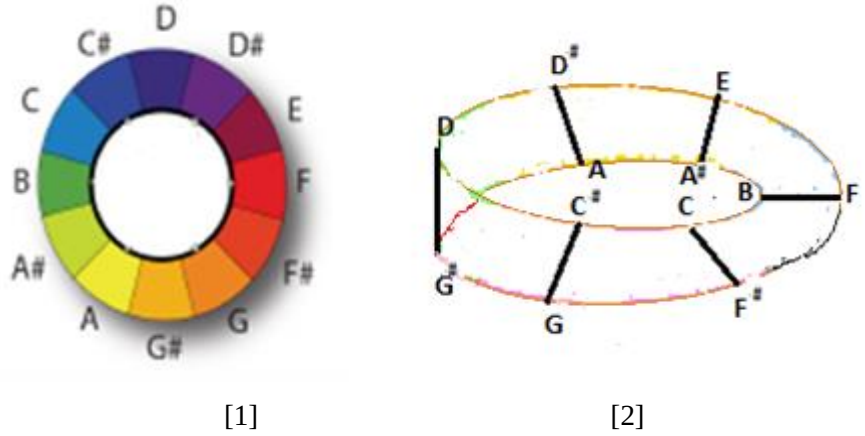



**Figure 4.** (From [13]) The Möbius strip, the 2:1 harmonics and the protoform of Newton’s Third Law. [1]: The green line is a center line. Suppose the red line extends counterclockwise from point a. And it turns back and arrives at point b on the opposite side following a 360° turn –yet it does so *without* crossing the green line; so to return to point a again another complete 360° turn is required. *This is the topological origin of the 2:1 harmonic* (*–and of the topological protoform of Newton’s Third Law*, as we shall see below): We need *two* complete turns to return to the original departure point. The red line

never went across the center green line. Nevertheless the red line runs at both sides of the center line. The red line looks like parallel lines when we see them partially. But it is not true. Route A and route B are actually a single route. The green line looks a median or a central reservation on a road but it does not divide Möbius strip into two. There is no opposite lane on Möbius strip. It is also the origin of a protoform of Newton's Third Law, albeit it does not require, in distinction with Newton's formulation, a dualistic assumption. Indeed, consider a normal vector to Möbius strip say surging from point P; if we move the vector along any curve in a 360° turn as before to stand on P but on the "other" side, we would find it pointing in the opposite direction, and equal in its length, without the need of an assumption as in the Third Law. Another 360° turn will return the vector to the same point and to coincide with its original configuration. Rather than having an action and a reaction, in the Möbius strip and in the Klein Bottle, the opposite and equal modulus of normal vectors is a resultant of the 2:1 harmonic, not an hypothesis for the foundations of physics at large. So it appears that this harmonic is more fundamental to physics than Newton's Third Law, which invokes an instantaneous symmetric causality.

To visualize how the Möbius strip may arise in terms of discrete elements and their identifications, namely musical tones –later will be codons, consider as an example the issue of the perception of the pitch of musical tones lying on an octave, actually the perception of a tritone (half an octave):




[1] [2]

**Figure 5.** (From [13]) The Möbius strip and Klein Bottle structure of music perception of a tritone; [30,148]. Left: topological representation of the chromatic aural space of an octave given by the disk-type real projective plane, represented as disk without a centre, in which opposite areas in relation with the centre, are identified. The colours represent the synesthesic nature of perception in which the pitches are each associated with a colour according to the frequency. Right: we depict without the colours the octave on the single edge of a Möbius strip with the opposite points joined by lines representing the tritone (half octave) perceptual identification of the lhs figure of a circular octave. This represents the fundamental 2:1 resonance: A complete rotation on the lhs circular pitch space of an octave perceptually translates into two complete rotations on the Möbius strip, say D-D#-E-F-F#-G-G# followed by G#-A-A#-B-C-C#-D, completing the single edge of the Moebius strip The perceptual space turns to be the Klein Bottle surface, on identifying the antipodal

points –depicted by lines on joining the antipodal pitches on the edge of the Möbius strip- as perceptual identities. The Klein Bottle thus arises as the identification of the equally oriented sides of Figure 5 [2], since already the identification of opposite orientations of the other two sides produce the Möbius strip. These lines represent the perceptual identification of the tritone (half-octave). Therefore, perceptual space -according to the Tritone Paradox - is a Klein Bottle surface [13]. Music perception assents to the 2:1 resonance of a lived world.

*2. 1 Octaves, 2:1 harmonics and genomics arrangements of Mobius strip and Klein Bottle.*

We still remark for future developments on addressing the harmonics of genomes, that the 2:1 harmonics of the Möbius strip, or still of the Klein Bottle as two such strips fused together, arises from giving *two* complete revolutions to return to a point, an octave above, as is already the case of the tritone paradox. Yet, in this development to one upper octave, what is crucial is that we have in its motion to the octave above, an *equal number of steps which are conceived either as in the "opposite" side –which is actually only a single side- or as lying on both local sides of the surface*. In examining genomes, we shall identify these elements that constitute the first octave as the 62 codons, paired as codon and mirror-codons, which shall be defined, and correspond to the palindrome given by the perception of the octave, as explained above. If wished, the 32 codons will correspond to the first half of the octave, the 32 mirror codons, to the second half of the octave, which in the experience of the tritone, are identified; see Fig. 5 [B]. This leads to conceive the Möbius strip and the Klein Bottle as having a unison 1:1 that makes up the octave 2:1, alike to the case of the perception of the tritone.



*2.2 The relation with enantiomerism*

Let us further consider the 2:1 harmonics with respect to the issue of chirality of molecules

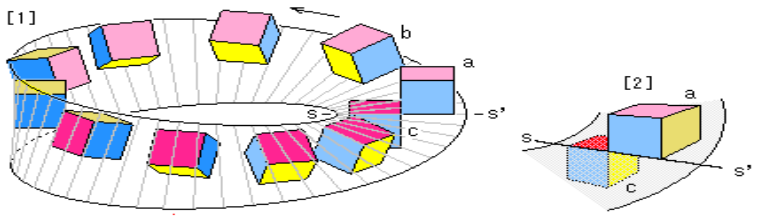



**Figure 6.** Representations of differentiated structures on a Möbius strip (reproduced from [13])

Consider Fig. 6: [1]: We slide a cube on the Möbius strip. It is coloured in light and shade of red, blue and yellow. If one side is light, its opposite side is shade. Cube **a** is at the start line **ss'**. We move it while keeping the shade red face is always on Möbius strip. Cube **b** on thw way is showing the three of light colors. [2]: Cube **c** that has traveled a circuit and now at the start line **ss'** again. Compared with cube **a**, it is upside down, right side left, and shifted to **s** under Möbius strip. In chemistry the issue appears, as we already said related to enantiomerism, the existence of chemical isomers, which have a symmetry which is non-specular but implies a change of chirality.


**Figure 7** 2D representation of enantiomers in organic chemistry, after Emil Fischer. See also Fig. 9 below (from [13]).

The notation in Fig.7 is the Emil Fischer' representation that chemists use for describing three-dimensional structures on 2D: a solid line in in the plane of the paper; a dashed line points in back of that plane; a wedge to the front. The molecule at left is not identical to the one at right; if we superpose **a** and **d**, **b** and **c** won't fit; thus, they are called chiral molecules, since the hand descriptor of a thumb, pinkie, palm and back, play the same role as **a**, **b, c** and **d**., the chemical groups that differentiate enantiomers. The rotation of a three dimensional structure on the Möbius strip describes precisely enantiomers; thus, it is this non-orientability which allows to embody the fact that chirality is a dimension-dependent phenomena [180], and what on a planar surface cannot be reflected to pass from one chirality to the other, it only takes a 180° twist in a Möbius strip as embedded in three-dimensional space, to be able to intertransform both chiralities. Remarkably, Möbius himself, thinking on molecules as three-dimensional geometrical conformations, rather than topological two-dimensional structures –to be discussed below, remarked that a fourth-dimension would suffice to transform one chirality to the other one; [180]. This is crucial to the biochemical activity of molecules, and in particular, of proteins [37]; we recall that Pasteur discovered the chirality of molecules, which lead him to propose the complementarity of form and function in biology, which is known today as the Pasteur-Curie Principle, in recognition of Pierre Curie's work on the subject. Yet, what this examples teach us is that the issue of chirality, in general, can be associated with the non-orientability of the Möbius strip, or still of the Klein Bottle where both chiralities are fused. There has been developed in the last years, a new paradigm of chemistry, and in particular of organic chemistry, in which non-orientable topologies are the very basis of the subject [42].



### 3. Some remarkable biological examples of eversion and the non-orientable topologies of embryos, the human body, stars and light waves.

Cognition is framed in terms of image-schemas which play a crucial role in structuring our language and our conceptions; in this organization of cognition, metaphors play a crucial constructive role [92,93]. One of the most pervasive image-schemas is CONTAIN, which organizes cognition spatially in terms of a boundary or a distinction acting as such; it can be either material or imaginal, dividing the world into an Outside and an Inside. Its surmountal by a non-dual logic, actually the Klein Bottle Logic, is crucial to creation in terms of self-reference [94]. Whenever this image-schema is further associated to the boundary as a logophysical dual divide, then a two-state (true and false) logic appears: This is the classical dualism, in which usually true is associated with Inside, false with Outside. It was first proposed by Aristotle, and algebraically by George Boole and it is very much the basis for informatics and digital computers, and in particular to bioinformatics [8,9]. The importance of this to biology cannot be overstated: Embryology is framed in terms of the foldings of the ectoderm and endoderm (as Exterior and Interior tissues) of zygotes. Yet, this rather than upholding a two-state logic, due to the existence of the mesoderm appearing with gastrulation and altogether forming the three germ layers, rather points to a non-dual logophysics as operating in biological development and

differentiation [10,12]. Also the biology of the cell is conceived in terms of the membrane, acting as a dual operator-barrier, disconsidering thus the fact that the cytoskeleton is continued through the membrane by the extracellular matrix, which is crucial to the organism's integration. The logophysics that arises in considering that the membrane is actually a non-orientable surface, has been considered [12]. CONTAIN is ubiquitous and in most cases it might be associated to a *non-dual* logic of metamorphoses which creates a multiple Inside and Outside which are process- wise *connected*. Indeed, eukaryogenesis -after Margulis, is conceived as a process of *endo*symbiosis of a proteobacterium with an ancestral archaeon, with the *endo*membrane system and particularly the nucleus evolving as defense against intron invasion [224]. This can be assimilated to a cybernetic process creating a HyperKlein Bottle (fig.3B), the eukaryote cell. CONTAIN is crucial to the theory of evolution based on *partially* nested developmental systems [231], which do not ascribe to dual logic. Topologically, they are HyperKlein Bottles with multiple Inside and Outside distinctions. These may include cultural distinctions as evolutionary elements [231,232,233]. In particular, the reduction to a dualistic logophysics is the root of the nature-nurture divide [231], among the many dualisms such as the mind-body divide, biological system-environment, etc. As a notice of a cognitive turning Inside-Out, it is proposed as a methodological recourse to examine in addition to which are the genes in a certain genome, the environment in which the genome bearing organism is placed in [231]. Furthermore, this partial nesting is suggested to be linked with the surmountal of the Central Dogma of biology [231].

Image-schema CONTAIN is no less crucial to genomics. Indeed, whether the Double Helix model (DH) or alternatives such as the Side-by-Side Model (SBS) are the case of genomes, also crucially depend on the existence of well defined Inside and Outside. For the proponents of the latter model, the Double Helix does not have a well defined side [106], while the SBS model claims the existence of a double strand with well defined sides. The latter structure is not a double helix, but consists of a pair of polynucleotide strands lying side by side and held together by Watson-Crick base pairing [66]. For the DH, the Interior is given by the pairs of basis holding the Outside, where the two phosphate chains are located. [82] The DH came in the wake of the observation of the X-cross shape of the x-ray photograph of B-DNA (the famous photograph 51), taken by Rosalind Franklin [99] and of the Pauling-Corey model, which somewhat turns Inside-Out the disposition of the DH, placing the sugar-phosphate basis Inside and the basis pairs Outside;[100]. It was the X-cross shape which was interpreted as a double helix. Yet, the X-cross shape is pervasive to anatomy and physiology [13,142], as the signature of the Klein Bottle one-sided non-orientable surface of the sensorium, as we shall discuss further. And it is no less ubiquitous to nature, say in geophysics [13], to the point of being the metapattern that arises from the pattern recognition of arbitrary landscapes, on carrying the statistical analysis of the pixels of their digital photographs [83,92]. In fact, the universality of this metapattern is elicited from studying the spherical harmonics of the pattern that arises from a sinuosoidal wave impinging on an arbitrary boundary: the first two terms of this harmonics identifies the X-cross topology of the Klein Bottle,or still, of the Möbius strip [103]. It is also elicited as the topology of three-dimensional light waves with a non-uniform phase, as we shall discuss below.

Yet, these non-orientable surfaces which do not have a global Inside nor Outside but only local, and in terms of which we have obtained a coding for the genome, are not exclusive to genomics nor chemistry. Particularly interesting is the fact that they appear in developmental evolution. Indeed, the algae Volvox which is considered to be the case study of morphogenesis, namely that of epithelial bending, remarkably undergoes a change of orientability as a gastrulation-like morphogenetic process [175]. Indeed,Volvox everts its spherical immature embryo, i.e. turning Inside-Out its original spherical configuration with its nascent gonidia on the external surface and the flagella of its somatic cells facing Inside the organism. In order to achieve its final adult form, each embryonic *Volvox* must effectively turn itself Inside-Out, a process known by biologists as "inversion", and by mathematicians, as the eversion of a sphere. Eversion occurs by a change of the monolayer cells that conform Volvox, curling *outwardly*. This movement develops through an intermediate state whereby

the orientable spherical embryo becomes a likewise orientable sphere, yet through a *non-orientable* intermediary state, which by a progressive transformation returns to be a spherical embryo. It has been discovered that a kinesin is essential for this process, and that a transposon may arrest the rotational movement of cells that produce the eversion [32]. Remarkably, this suggests that transposons, which we shall later associate with the non-orientable topologies of genomes, may be related to the eversion of Volvox in undergoing development, by also changing the orientability of its surface. In distinction with monolayered Volvox, coelenterate Hydra also everts, though exchanging ectoderm and endoderm; both Hydra and Volvox do so by migrating cells. Yet, Hydra's cellular motions are such that the eversion is reversible, it will turn Outside the "rightside"-out again as the cells migrate across the mesogloea, the translucent, non-living, jelly-like substance found between the two epithelial cell layers in the bodies of coelenterates and sponges, to reach the "correct" side. On completing the eversion, Hydra starts to create new polyps and thus secures, in principle, its lack of senescence: Hydra is, in principle, biological immortal [31]. Furthermore, it has remarkable regenerative properties. So, the case of Hydra signifies a turning-Inside-Out unending process, which in each stage produces the novel organization necessary for its self-preservation. We shall later see that the material elements of biological systems as they arise from supernova explosions of demising stars, are another manifestation of an eternal cycle, now revealed as the life cycles of stars, rather than of immortal Hydra.

Yet, what is most remarkable is that the Klein Bottle has a crucial role in physiology. This is related to the existence of maps of the sensorial periphery as projected into two-dimensional sections of the neurocortex. Indeed, the topographic maps of both the visual mode [13,25] and the somatosensory modes appear to embody a Klein Bottle topology. This is the topology of the cartographic projections on the neurocortex that represent the three dimensional body's periphery, say the data impinging on the eyes and the skin [13, 33,34,160,161].Again, data appear to have a shape, actually the Klein Bottle as a metapattern. The original work on the somatosensory mapping, developed on macaque monkeys by Werner and Whitsel, was later extended to cats [35]. These topological mappings appear to be based on an analytical mapping , namely the complex logarithmic mapping, as argued in Schwartz for the visual mode [51, 160] and by Werner for the somatosensory system [33,34]. Yet, this logarithmic mapping, due to its periodicity, has helicoidal structures associated to it as is well known in the theory of complex functions in mathematics [102]. In the case of the somatosensory system, these helicoidal representations appear to be dermatoidal trajectories on the limbs. Along these helicoidal trajectories the somatosensory mapping does not distinguish between the Inside, as muscle and joint receptors, and the Outside, as skin receptors. A most crucial characteristic of these topographic mappings is their usually partial plasticity. Namely if the body is locally severed, the topology of the representation does not change, despite images of the severed regions may be shifted to overlap neighbouring areas on the cortex, as is the case of phantom limbs phenomenology [167].Yet, while this cortical mapping of the periphery requires the cortical hypercolumns, at times these appear to fail to provide the elementary units for the representation of the sensorium. In this cases, by considering instead small-world neuronal networks which evolve early in development, they appear to have a multitwisted Möbius strip architecture[120] as if reflecting the multitwisted shape of Möbius light waves, to be discussed below, It appears that the notion of data having a shape at all scales may be worth examining; more of this below.

Materials of most systems are born from the explosion of demising stars, following the formation of the higher atomic number atoms and their isotopes, at their core. In particular, the atomic constituents of all biological systems arise from these explosions. Literally, we are made of the stuff in the Interior of demising stars that explode. Until recently, it was believed that demising stars undergoing gravitational collapse, explode forming a spherical shock wave front. Cassiopeia A (Cas A) is a supernova remnant in the constellation Cassiopeia and the brightest extrasolar radio source in the sky. The original star, about 15 to 20 times more massive than our sun, died in a cataclysmic "supernova" explosion relatively recently in our own Milky Way galaxy. A new x-ray study of the

remains of Cas A reveals that the higher atomic number elements, rather than being found at the centre of a spherical shock wave produced by the supernova explosion, they have literally turned Inside-Out, being present at the Exterior while the lighter elements appear to be closer to the centre. [36]. Yet, this turning Inside-Out of the demising star as it collapsed and was recreated as a new star through the supernova explosion, is compatible with the Klein Bottle topology of the Mendeleev table of elements.The overall structure of atoms and their stable isotopes, is such that the higher order elements appear to be layed on a local side of a Klein Bottle, as identified with the lower order elements lying on the other local side of this surface. In fact, this topology is related to the Aufbau rule for orbitals, in terms of which the orbitals of the higher atomic numbers turn Inside-Out; due to the high pressure at the core of the demising star [18,19] Thus, the turning Inside-Out of a supernova remnant which initiate a novel cycle of life of a star, appears to be related to the non-orientable topology of the overall structure of atoms and their stable isotopes, and still of their orbitals. Mutatis mutandis, replacing codons for atoms and their isotopes, the same principle appears to be the case of genomes, as we shall discuss in the present work.Yet, this raises the issue of a fractal logophysics, that operates at all scales and at all levels of organization (physical, chemical, biological, cognitive, semiotic, etc.), that is essentially non-dual and non-linear, and which sustains a kind of memory all along the evolution of the structures and processes of the cosmos.

Most remarkable, is that light waves can literally be turned Inside-Out and Outside-In, alike Hydra. The phase of light waves with a circular or elliptic polarization may develop singularities; such a light wave presents an helicoidal shape as it rotates on its polarization plane. These are the so-called optical vortices; very much alike the hypercolumnar vortices as the basis for the Klein Bottle shape of the sensorium, the principle of development of non-orientable singularities appears to be the case for both phenomenae, as is also the case of singularities of liquid crystals [27,50]. (We further note that the mathematical background and its physics appears to be the same for all three cases.) Indeed, through the superposition of light waves, vortical light waves may develop a non-planar three-dimensional dynamics which is no longer a rotation on the polarization plane as its wave front advances.These singularities may further produce Möbius strips for the shape of light waves, with any number of odd twists! [76]. Recently, using liquid crystals, Möbius light waves have been produced. [80] This can in principle be extended to sound waves [77]. The importance of this is that DNA strands, which are physically speaking liquid crystals, have been shown to emit and absorb both light and sound waves [81].Furthermore, this non-orientable nature of light waves shows a most remarkable complementarity of form and function of the visual system, that comprises *both* the architecture of the body and of the physical stimuli. Indeed being the case that the eyes in mathematical terms turn Inside-Out the images of the world on the retina [13], for a start, the light waves have an homologous behaviour which is further carried out to the Klein Bottle turning Inside-Out and Outside-In topology of the cortical retinotopic map. Thus, the complementarity of physiology and structure of the visual system goes down to the light waves themselves, and as already discussed, we may suggest that it comprises the level of the small-world architecture of neural networks. We shall later propose that this is also the case of the genome as a coherent system operating through quantum holography [86,88].



**4. The non-orientable topologies of bioinformatics**

Returning to the logical-numerical representation of the Klein Bottle Logic, consider the figure

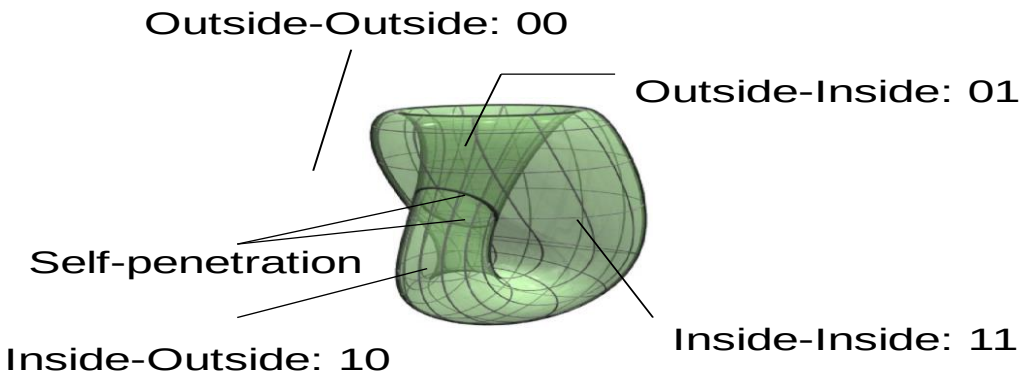



**Figure 8:** The Klein Bottle Logic, and its four states.in which we have identified four states by assigning 0 with Outside, 1 with Inside, so that the states are: Outside-Outside, which we write as 00, the Inside-Inside, 11, and two transitional states arising from self-penetration, Outside-Inside, 01, and Inside-Outside. The Klein Bottle and the Klein Bottle Logic are identified thus by their four loci. Henceforth, we shall identify the surface and its logic as a single structure.

This does not conform a dual logic. Indeed, we think of the above elements, ab, as ordered pairs [a,b], say the elements 00=[0,0]:= **0**, [1,0] = **i**, [0,1] = **j**, 11= [1,1] = **1**, with the definitions [a,b] + [c,d] = [a+c,b+d], [a,b]x[c,d] = [axc,bxd], [a,b]' = [b',a'], with (a')' = a , axa = a, a+a= a for all a= 0 or 1, the latter sum as usual differs from modulo 2, and a' is the operation of a changing side of the boundary of self-penetration, hence: 0'= 1, 1'= 0, as *if* self-penetration would not be the origin of the boundary, i.e. Aristotelian-Boolean logic. Then **i**' = **i**, **j**' = **j**, and **ixj** = **0,** so that **i** & **j** are non-trivial nilpotents. We have mapped the topological states of the Klein Bottle into a 4-state de Morgan algebra which is not trivial since Outside, 0, is different to Inside, 1.



This is a new representation for the Klein Bottle Logic to the one derived by Rapoport [14], from which a non-commutative Matrix Logics –that has quantum, fuzzy and Boolean logics as subcases- is derived. We notice that **i** and **j** are the *imaginary time-waves* [14,102,103] that appeared as imaginary logical values in the Calculus of Distinctions due to Spencer-Brown [97]; we here see explicitly their association with the Klein Bottle self-penetration. These states are associated to the perceptual depth variable of self-penetration, associated to time [14,108].A reduced 3-state logic was posited in the theory of autopoiesis –etymologically, self-creation- of living systems due to Varela [96], in which there is a single reentrance of the form on itself, archetypical Ouroboros. Yet, the distinction between the two states of self-penetration transiting between Outside and Inside, according to which is the departing state, renders the *direction* of self-penetration a necessary distinction by itself accounted by **i** and **j**. Remarkably, Varela proposed for autopoiesis a dualistic logophysics based on the dual (2 state) logic, dismissing this 3-state logic, introducing the notion of operational closure, by which the boundary of a system acts as a dual gate.In doing so, Varela's autopoiesis neglects the two states of self-penetration (or self-reentrance) transiting between Outside and Inside and particularly the direction that relates the latter states. Thus Varela's autopoiesis, is a *reduced* particular case of the more general *ontopoiesis*: a logophysical creation which has for foundation and operates through the Klein Bottle Logic [94, 10-14,142]. Yet, autopoiesis may lead to the self-organization of global neural networks, producing an holographic-like memory related to the Golden Ratio [54].

We relate this 4-state logic to the four letters, A, T (or U), G and C; notably, G is associated to Inside-Inside, C to Outside-Outside, the usual dual Boolean logic states, while the intermediary states

A and T are associated to Outside-Inside and Inside-Outside, respectively. So we follow a topological 4-state logic approach [11], which may be represented as a combinatoric-algebraic approach, originally proposed by Petoukhov and He [8,9] by considering the 2x2 matrix/table

| | 0 | 1 |
|---|---|---|
| 0 | C 00 (0) | A 01 (1) |
| 1 | T 10 (1) | G 11 (2) |

**Figure 9**. Matrix (table) representation of the four letters of DNA or RNA (substitute U for T) in terms of binary digits and the Klein Bottle Logic (taken from [11]).

which we denote as [C,A;T,G], or still, P*(*1). We have written in parentheses the decimal interpretations of the elements of the logic; while the pairs 00,01,10 and 11 will be interpreted in the following –for computational reasons- as binary numbers rather than elements of the de Morgan algebra. We shall introduce another distinctions that will be crucial to the topological theory of the Genetic Code. We know from [14] that the invocation of a distinction, is tantamount to invoke through the self-reentrance of a form produced by this distinction -as a boundary/cleavage, which as an operator is the Klein Bottle, and in fact as we shall be considering three distinctions, we shall be bringing to manifestation a Hyper Klein Bottle. They are produced by three subalphabets of the Genetic Code [109] introduced in an algebraic-combinatorial framework [8,9], in terms of pairs of attributes-antiattributes, described succintly in Fig. 12 below by the following subalphabets:



*Subalphabet No.1*: 0 will code for pyrimidines (one ring in a molecule), 1 will code for non-pyrimidines, i.e. purines (two rings in a molecule), transcribed by C = U/T = 0, A= G =1.

*Subalphabet No. 2*: amino-mutating or non-amino-mutating under action of nitrous acid HNO2 (Ycas) the same division is given by the attributes "keto"or "amino" [34], so that 0 stands for a letter with amino-mutating property (amino), 1 a letter without it (keto), C= A = 0, G = U/T = 1.

*Subalphabet No.3*: 0 a letter with three hydrogen bonds, 1 a letter with two hydrogen bonds; C=G=0, A=U/T = 1; this is the usual subalphabet. This is a codification of Chargaff's rule, either for single or double stranded DNA [59], as we shall further elaborate in the following.

These distinctions introduces further *multivaluedness* in the topological codification of the Klein Bottle Logic, –yet we shall not tag them with a symbol to distinguish which is the subalphabet they stand for- treating them as binary numbers so that we take 0 (Outside), 1 (Inside); their *multivaluedness with respect to the subalphabets* will manifest in the Klein Bottles and Hyper Klein Bottles that will appear in the Genetic Code. In the sequel, the original interpretation of the matrix elements of P(1) by ordered pairs, say C = 00 (Outside-Outside), will correspond to the concatenation of the first digit corresponding to *No.1*, the second digit to *No.2*. Thus already we have introduced *inside* the Klein Bottle additional distinctions, a particular Hyper Klein Bottle as nested Klein Bottles (a simplified non-reentrant version of Fig. 3 [B]), evidencing a *polysemic* and *polysemantic* (several tags and meanings) character of the Genetic Code as an *heterarchy* composed by the Klein Bottles associated to *different* subalphabets indicating the codification of distinct *characters*. This is illustrated in Fig. 12 below. Recalling our previous discussions on the coexistence of orientable and non-orientable topologies for molecules [64], we shall see next that these subalphabets, similarly, produce the same effect for the Genetic Code**.** We consider the 4x4 matrix, P(2) = [C,A;T,G](2), the two-fold tensor (so-called Kronecker) self-product (thus recursion is used for its generation) of [C,A,T,G] , i.e. P(2) =[CP(1), AP(1)*;* TP(1),G P(1)] ([8,9])-which we write as a table:

| | C 00 (0) | A 01 (1) | U 10 (2) | G 11(3) |
|---|---|---|---|---|
| C 00 (0) | CC 0000 (0) | CA 0001 (1) | AC 0010 (2) | AA 0011 (3) |
| A 01 (1) | CT 0100 (4) | CG 0101 (5) | AT 0110 (6) | AG 0111 (7) |
| T 10 (2) | TC 1000 (8) | TA 1001 (9) | GC 1010 (10) | GA 1011 (11) |
| G 11 (3) | TT 1100 (12) | TG 1101 (13) | GT 1110 (14) | GG 1111 (15) |

**Figure 10.** Self-referential recursion on fig.9 to produce the matrix P(2), represented as a table, consisting in the pairs of genetic letters and their binary representation.

We note again the numbering both by decimals in parentheses, while the duplets have their first two digits given by the rows codified by *No.*1 and the final two digits coming from the columns codified by *No2*, as in the original codification.We compute the 3-fold tensor self-product, P(3) = [C,A,T,G](3) = [CP(2), AP*(*2) ; TP(2), GP*(*2) ], i.e. the 8x8 *genomatrix* (table) introduced in [8,9]

| | 000(0) | 001(1) | 010(2) | 011(3) | 100(4) | 101(5) | 110(6) | 111(7) |
|---|---|---|---|---|---|---|---|---|
| 000 (0) | CCC(0) 00000 Pro | CCA(1) 000001 Pro | CAC(2) 000010 His | CAA(3) 000011 Gln | ACC (4) 000100 Thr | ACA(5) 000101 Thr | AAC(6) 000110 Asn | AAA(7) 000111 Lys |
| 011 (1) | CCU(8) 011000 Pro | CCG(9) 011001 Pro | CAT(10) 011010 His | CAG(11) 011011 Gln | ACT(12) 011100 Thr | ACG(13) 011101 Thr | AAT(14) 011110 Asn | AAG(15) 011111 Lys |
| 010 (2) | CTC(16) 010000 Leu | CTA(17) 010001 Leu | CGC(18) 010010 Arg | CGA(19) 010011 Arg | ATC(20) 010100 Ile | ATA(21) 010101 Met | AGC(22) 010110 Ser | AGA(23) 010111 Stop |
| 011 (3) | CTT(24) 011000 Leu | CTG(25) 011001 Leu | CGT(26) 011010 Arg | CGG(27) 011011 Arg | ATT(28) 011100 Ile | ATG(29) 011101 Met | AGT(30) 011110 Ser | AGG(31) 011111 Stop |
| 100 (4) | TCC(32) 100000 Ser | TCA(33) 100001 Ser | TAC(34) 100010 Tyr | TAA(35) 100011 Stop | GCC(36) 100100 Ala | GCA(37) 100101 Ala | GAC(38) 100110 Asp | GAA(39) 100111 Glu |
| 101 (5) | TCT(40) 101000 Ser | TCG(41) 101001 Ser | TAT(42) 101010 Tyr | TAG(43) 101011 Stop | GCT(44) 101100 Ala | GCG(45) 101101 Ala | GAT(46) 101110 Asp | GAG(47) 101111 Glu |
| 110 (6) | TTC(48) 110000 Phe | TTA(49) 110001 Leu | TGC(50) 110010 Cys | TGA(51) 110011 Trp | GTC(52) 110100 Val | GTA(53) 110101 Val | GGC(54) 110110 Gly | GGA(55) 110111 Gly |
| 111 (7) | TTT(56) 111000 Phe | TTG(57) 111001 Leu | TGT(58) 111010 Cys | TGG(59) 111011 Trp | GTT(60) 111100 Val | GTG(61) 111101 Val | GGT(62) 111110 Gly | GGG(63) 111111 Gly |



**Figure 11**. **Three-fold self-referential iteration of table in fig.9** . The 8 times 8 (geno) matrix P(3), as a tabular representation of the 64 codons, with their binary representation and the identification of their aminoacids and stop codons.

In fig. 11 we have represented the 64 codon triplets in which we have also written their decimal (in parenthesis) and binary representations, and written the abbreviations for the enzymes synthetized by them. Each of the 64 triplets has been individualized uniquely by a number consisting of the concatenation of six binary digits, the first three coming from the rows correspond to the *No.1* codification, while the last three binary digits provided by the corresponding column codifies according to *No.2*; for example, triplet CAT is codified by the binary number 001010, where the first three digits 001 corresponds to the *No.1* assignment for CAT whilst the last three digits 010, corresponds to the *No.2* assignment; the decimal notation for the concatenation 001010 is 10.

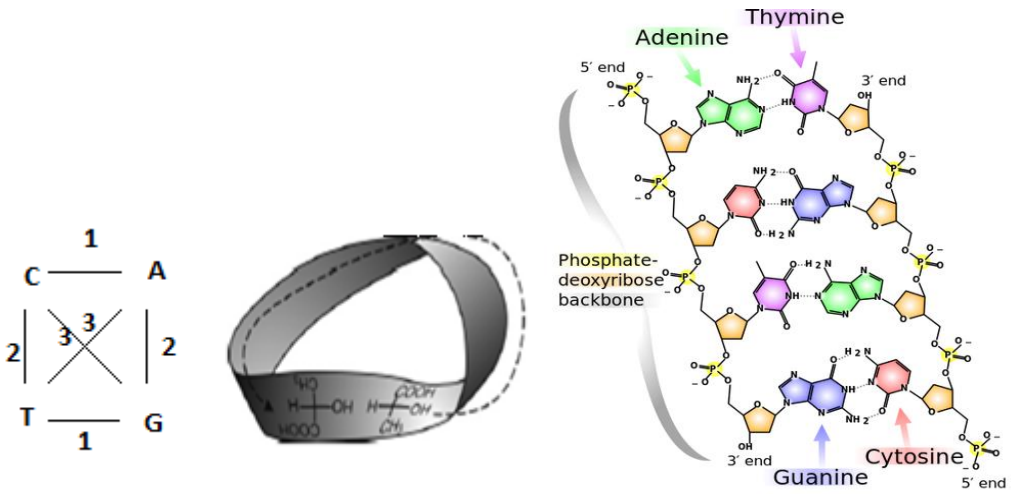
Remarkably, each pair codon-anticodon (and only such pair) has the sum of their decimal numbers equal to 63 (111111, in binary notation), say CAT which is 10 its anticodon GTA has the decimal number 63. We note that *No.3* transcriptions of C with G, and A with T (or U), are completely determined by the other two subalphabets, as shown in Fig. 2 below, and correspond to the mutual transcriptions of Outside-Outside/ Inside-Inside, and of the time waves Outside-Inside/Inside-Outside, and they correspond to the binary-opposition attribute by which the former (latter) correspond to three (two) hydrogen bonds. This *genomatrix* has surprisingly rich symmetry properties studied algebraically [8,9], yet which beg for topological interpretations, which we shall realize next.

Firstly, we have both symmetries along the rows & columns due to *No.1* & *No.2*, respectively, and thus we have, with respect to them, an associated 2-torus; see fig. 12 below. We note that the columns correspond to the classical octets reflecting biochemical properties of elements of the Genetic Code [106]. Secondly, it is bisymmetric (with respect to *No.3*), i.e. symmetric with respect to both diagonals, say TTC which is the matrix element corresponding to 7$^{th}$ line and first column has the anticodon AAG in 7$^{th}$ line and 1$^{st}$ column. Hence, we have a Möbius strip produced by 180$^{o}$ rotation about the central line that divides the genetic code into codon-anticodon sectors, so that superposed on the non-orientable topology, we have all the codon-anticodon pairs, with each codon having its superposed pair that can be thought as positioned on the ¨other¨ side of the Möbius strip; say we have TTC, TTA, TGC & TGA superposed to AAG, AAT, ACG & ACT, respectively.

This is the Möbius strip topology of the genomatrix P(3).While conventionally n-plets are written with the 5' to 3' orientation, as in the fig.13 below, say 5'TTC3' and the anticodon with the opposite orientation 3'AAG5', what this Möbius strip identification of TTC and AAG signifies, is that ultimately to the effect of codon/anticodon coupling, this orientation is redundant, so we have omitted explicitly to write the orientation of the end points. We shall return to this below on introducing the "mirror-codon" as the 5' to 3' anticodon for single strand DNA, which will appear to be the Möbius strip equivalent of an anticodon for single strand DNA as sequenced by the Genome Project.



If we further consider now the (*No.2-wise)* column symmetry, we finally obtain a Klein Bottle. Yet, it is more than a single Klein Bottle, but four of them, produced by the superposed 1$^{st}$/8$^{th}$, 2$^{nd}$/7$^{th}$, 3$^{rd}$/6$^{th}$, 4$^{th}$/5$^{th}$ columns, with the first element of each superposition inverted with respect to the second,yet embedded in a single Klein Bottle given by the 64 triplets: a Hyper Klein Bottle. Finally we can use the row *No.1* subalphabet to produce a folding of the genomatrix along its horizontal middle line, which further using the diagonal bisymmetry we produce a second Hyper Klein Bottle with four others embedded given now by the superposed rows 1$^{st}$/8$^{th}$, 2$^{nd}$/7$^{th}$,3$^{rd}$/6$^{th}$, 4$^{th}$/5$^{th}$, with the same inversion as before.




**Figures 12** (left and centre) & **13** (right), respectively: **Alphabets of the Genetic Code, Möbius strip enantiomerism, and DNA.** Left in fig. 12 introduced as in [8,9] the lines stand for transcription

and the subalphabet by which each operates is the number attached to it; it also provides the symmetries of genomatrixes for coding sequences of arbitray length, and their topologies. Folding for topological identification according to these symmetries, say *No3.* , yields Möbius strip of any of both chiralities, which followed by either *No.2* or *No.1* yields the Klein Bottle; the combination of *No.1* with *No.2* yields a 2-torus. In the right hand side of the Möbius strip, we have drawn the Fischer formula for D-lactic acid which if we continue on the surface to the ¨other¨side we obtain the L-form drawn displaced to the left for allowing its vision; for the genomatrix we have instead the four superpositions of either the pairs of opposed rows (columns) with say each first element opposed to the second drawn on the surface which is a quantum interface.For the Mendeleev table we have instead a superposition of matter/antimatter-atom, in each local side of the Klein Bottle [18,19]. The inversion of each element of a pair of rows or columns mandated by taking *No3.*, plays the role of the antiparallelism in the DH.

We have thus found *two fractal*-like Hyper Klein Bottle structures in the genomatrix P(3), and recursively in P(n) = [CP(n-1), AP(n-1); TP(n-1), GP(n-1)], for arbitrary n natural- according to the choices of *No.1/No.3*, i.e. the choice of attributes pyramidine-pyrimine/hydrogen atoms, and *No.2*/*No.3*, i.e. amino-keto/hydrogen atoms, in the Genetic Code arising from the Klein Bottle Logic, and we also have a 2-torus by using *No1.* & *No.2;* as we can easily visualize from the definition of the tensor product, it produces the fractality which reproduces the original (i.e. n= 1) topological identification introduced in Fig.1.We remark again, this has surfaced from a *simultaneous triple interpretation* which is both perceptual, conceptual and operational–i.e establishing and reading three subalphabets for transcription, which combined in pairs produces the remaining one; this *transcends* the usual approach to the Genetic Code as well as the combinatorial one [8,9]; these topologies apply as well to the codification of the sequences of n letters by 2n digits. Remarkably, it has been claimed that genomes have a polysemic structure, that allows them to play a double role. Some codons can have two meanings, on the one hand specifying amino acids and also a regulatory code specifying transcription factor (TF) recognition sequences These two meanings seem to have evolved in concert with each other. The gene control instructions appear to help stabilize certain beneficial features of proteins and how they are made [127].



The information content in each interior Klein Bottle to the Hyper Klein Bottle is not the same as the one contained by its neighbours. Also, in the transition from P(2) to P(3) or, more generally, from P(n-1) to P(n), in which the latter represents n-plets with 2n binary digits, with the first n digits codifying subalphabet *No.1*, the last n digits codifying subalphabet *No.2*, there is an embedding so that the information of the (n-1)-plets *is* carried into the n-plets, as a kind of memory of self-referential action (self-multiplication). Again, P(n), for arbitrary n, also presents the same symmetries of P(n-1), and ultimately those of P(2), and thus we found the same *coexistence of topologies of the genomatrix*, according to which of the *three* pairs of attributes are considered, for n-plets of arbitrary length. We have thus unveiled in the Genetic Code the same situation of polytopologies (we recall that also DNA is polygeometrical) that appears already in topological stereochemistry [47,48,64] which we claimed to be essential to cell biology and to embryological development, and a fortiori, to evolution [10,12]. If one should construct the catalog of genetic sequences of various lengths and composition, it can be done on the basis of the described natural system of numbering the sequences as multiplets. All n-plets, which begin with one of the four letters C, A, T, G, are disposed in one of the four quadrants of an appropriate genomatrix P(n) because of the specifics of tensor multiplication.

Thus, the codon-anticodon sequence of arbitrary length n, when considering pairs of subalphabets, corresponds to a *discontinuous path* on either two fractal-like Hyper Klein Bottle, or a 2-torus, given by P(n), for arbitrary n. This resembles the jumps of DNA segments or codons, transposons, and as it will turns out to be the case, the resemblance is warranted. This is quite remarkable all by itself, since genomes are usually claimed to be “static”, despite the *post-hoc* introduction of the operations that introduce jumps and discontinuities. In this regard, the present construction identifies these operations

in the very generation of genomes, rather than obligatory -somewhat unrelated-addendums. This construction does *not* require the assumption of the DH; the latter is bound to one *single* subalphabet which is already evident in the *No.3* reading of P(n) which *instead* yields a Möbius strip.A Möbius strip model for *circular* genetic code was proposed by Burdick [26], yet to our knowledge, this model presented by Rapoport [11] has no similar model in the topological studies of DNA [49,89,90].

*4.1 The Shape of Molecules and the Geometrical and Topological Paradigms of Chemistry*

These findings ascribe to the unifying paradigm for chemistry [47,48,64] that claims that the topology of molecules, rather than their geometry relations, characterizes their stereochemical configuration, which we have suggested to be crucial to allosterics, cell biology and embryological differentiation [10,12]. This is also the case as it appears in the formation of clathrates associated to endohedral C60 fullerenes [112]. It is suggested that what occurs is that the charge density literally invaginates or exvaginates allowing the caged molecule to be pushed inside of C60, and the converse [42]. The point is that the *geometrical* model of molecules, and in particular of DNA, is predicated in terms of a curious dualism, which relies on the Heisenberg uncertainty [178]. On the one hand, it combines a classical physics model of nuclei in molecules, as small particles, while on the other hand, the electron distribution is naturally associated to quantum physics. This is the traditional molecular model; implicitly, it is the basis for the Watson & Crick's DH. Yet, this hybrid model of a molecule which fails for its classical particle physics consideration of nuclei in molecules, it does so upon considering molecular vibrations. In this case, the nuclear motions are clearly of quantum physics nature, and prescribed by the quantized vibrational energy levels. If wished, by the existence of harmonics at the level of vibrational energy. We follow the lead of Sokolov's topological approach to molecular shape [42], in highlighting that "molecular shape is the shape of the electron distribution of the molecule" (p.23 [173]). While the hybrid model served as long as no external fields to the molecule are considered, it fails when, say, electromagnetic fields are applied [18,173]. Yet, if external fields are applied to a molecule, they rapid changes of the electron distribution can indeed modify the shape of a molecule, changing both the electron and nuclei distribution. Thus, molecular reactions can be thought as changes of shapes of the intervening molecules, due to their interaction, as each considered as if external to the other, while actually being an interacting unit, which eventually leads to a stable configuration. Thus, in this conception, the geometrical configuration is an abstract model which stays short of considering the actual dynamical shape of molecules, which is a topological structure with possible self-penetrating transformations. In other words, it fails to provide a phenomenological rendering of a process of accommodation that resembles a symbiosis; as such, the geometrical configuration model does not account for chemical shape as a *contextual* interaction. As explicated: "If structure and shape are not intrinsic properties of free molecules and only emerge in response to environmental pressure the interpretation of crystallographic structures becomes less obvious"; p.191, [18]. Indeed, as originally proposed by Sokolov, the changes of shapes of molecules, as *topological* transformations of the charge distribution may occur, and the electron distribution, alike the case of a Klein Bottle, may self-penetrate. It only takes the electromagnetic field of a stretch of DNA acting on another one, for both to undergo within the whole genome, yet altogether as a unity, as we shall discuss below. This novel paradigm for chemistry, which confronts the issue of shape as a topological nature rather than a geometrical abstraction, lies at the basis of structures such as catenanes, rotaxanes,etc., which already appear to be the case of DNA [47,48,180,181]. A remarkable example of this paradigm, is not only the present topological model of DNA (and RNA, by changing U for T), but that of the topological structure of proteins, which considered as a combinatorial object represented in terms of the loci of the backbone atoms and the hydrogen bonds, also identifies them as complex two dimensional surfaces locally given by glueing 2d-tori and Klein Bottles appears to be the gluing of 2-tori and Klein Bottles [111]. This appears to reflect all the topologies –both 2-tori and Klein Bottles- of the Genetic Code as defined by the three subalphabets. More generally, Hadamard matrices appear as chemoinformatic descriptors of molecules as topological networks [209]. As well, a model of

allosterics in terms of this interchanging of Inside and Outside was proposed by Sokolov [179] and by the author as the basis for biological development and differentiation [10,12].

**5. The Chargaff rules and non-orientability.**

These findings are consistent with the so-called Chargaff rules, yet with a 180 degrees twist, which we shall introduce below.After the development of a method for the precise chemical characterization of nucleic acids, Chargaff, in 1950, observed, using current language, that in any double stranded DNA segment , the Adenine, A, and Thymine, T , frequencies are equal, and so are the frequencies of Cytosine, C, and Guanine, G. This observation is known as Chargaff's first parity rule. It is this the rule by which the subalphabet 3 is usually introduced, following Watson and Crick used it to support their DH, while it was also known at that time that the rule had been posited by Chargaff for single stranded DNA.

However, as we have just seen, it naturally reveals a possible single sidedness of the genome. Actually, to obtain the 64 codons as we did by departing from the elementary coding of the Klein Bottle Logic, we do not need to assume any particular number of strands, say single or double stranded geometry of DNA at all. What did turn out that already P(2) for the duplets, P(3) for the triplets and ultimately P(n), for arbitrary n, can be considered as lying on a single sided non-orientable fractal-like topology. Ultimately, whether this is, say, an helix, either single or double stranded, or two intertwined strands as in the Side by Side model [106], is not an issue at stake in the topological nature of the coding here introduced, which any of the two Chargaff laws allow for. It only takes that C and G interchange, and so do T with A, for which a quantitative identity of frequencies, is a prerequisite . We must recall that several model structures were reported from fibre diffraction studies, which could only be described by helical arrangements with more than two chains, giving rise to triple and tetraplex or quadruplex structures [52,98].



Chargaff also perceived that the parity rule at a lower level of accuracy holds in the single-stranded DNA segment: **A** (C) *within a strand* tends to match (numerically) **T** (G) in the *same* strand, with U replacing T for RNA, just as **A** (C) on one strand of a DNA ***duplex*** complements **T** (G) on the other strand of the duplex (Chargaff's first parity rule).This last rule is known as Chargaff's second parity rule (CSPR). Although it is not well understood, it has been confirmed in several organisms [53]. With regards to this second parity rule, we have not *postulated* it as Chargaff, but rather any of the two rules provide for the basis of the identification of the four states of the Klein Bottle Logic and their intertransformations, as given by figs. 8 & 9. Thus they are basic to the 2:1 harmonics of the Klein Bottle Logic generation of the Genetic Code, which will be recursively applied to generate the higher-order fractal-like topologies of the genome, as a Hyper Klein Bottle Logic, or a recursive two-torus.

As CSPR is consistent with the DNA DH (or still with the Side by Side Model to be introduced below), as we shall see, much effort has been devoted to understand the second rule [55]. Originally, CSPR was meant to be valid only to mononucleotide frequencies, i.e. for n=1, but the general case of arbitrary n which our finding has elicited, appears to be the case, as well. Indeed, it occurs that oligonucleotide frequencies follow a generalized Chargaff's second parity rule (GCSPR) where the frequency of an oligonucleotide is approximately equal to its complement reverse oligonucleotide frequency [62]. In other words, as remarked by Forsdyke, it follows from Chargaff's second parity rule, %A = %T, %G = %C for *single* stranded DNA, that the symmetries observed for the two pairs of complementary mononucleotide bases, should also apply to the eight pairs of complementary dinucleotide bases, the thirty-two pairs of complementary trinucleotide bases, etc. In other words, these symmetries should be valid for P(n), with arbitrary value of n; but this is the case by construction of P(n), eitherwise the pairings cease to take place and then there is no genome as we know it! (Unless, we posit that some nucleotides and codons cease to pair, which is the case of the turning sectors of hairpins [170].) Accordingly to the fractal-like structure of P(n), in which the Chargaff rules applies

irrespective of the specific value of n. Discussing the role of loops in the genome, Bell and Forsdyke conclude: "Entire genes, or entire genomes where gene orientation is not considered, are not appropriate controls" [55]. Yet, the pervasive assumption has been that of a linear orientable topology on a double helix, and what was discovered was palindromes of arbitrary length. But palindromes topologically are Möbius strips whenever a 180º rotation is applied to their symmetrical regularity instead of being disposed as a 2-torus, and they were found to encompass ever increasing portions of the genome. But as we already said, in principle, the symmetries of n-plets follow from the case n=1 which was constructed as the recursive iteration of the coding through the Klein Bottle Logic. Yet, what is most remarkable, is that rather than this symmetry being the case, it appears that for several genomes the actual symmetry that holds is the reverse complement symmetry [171]. We recall, given an n-plet or n-genomic word w= $a_1 a_2 ... a_n$, then **R**(w) = $a_n a_{n-1} ... a_1$, is the reverse of w; **C**(w) = **C** $^{a_1}$**C** $^{a_2}$ **…C** $^{a_n}$ is the complement of w, with **C**(T)= A, **C**(A)= T, **C**(C) = G and **C**(G) = C, the basis pairing; and finally **CR**(w) = **C** $^{a_n}$**C** $^{a_{n-1}}$**…C** $^{a_1}$ is the reverse complement of w, which still is equal to **RC**(w). Thus, **fr** (w)= **fr** (**CR**(w)), is the n-plet version of Chargaff's second pairing rule for arbitrary n; here **fr** (x) denotes the frequency of x. Yet, it is argued that this remarkable symmetry, "is not the result of base pairing, but can be explained as the result of countless inversions and inverted transpositions that occurred throughout evolution" [41]. Yet, alike the genomatrix we have just constructed, it appears to be universal, a metagenomic symmetry [172]. Yet, in principle, this universality, can be conceived as unseparable to that of the genomatrices as both having a topological basis, the latter to be described below.

Comparison of the triplet profiles of genomes from a large number of different taxa and species revealed that they were not only strand-symmetrical, but even surprisingly similar to one another [172]. This extension of CSPR to sequences of nucleotides is known in the literature as the Symmetry Principle. As pointed out by Forsdyke, higher order equifrequency does imply lower order, and he conjectured that the original CSPR was actually a particular case of a higher order parity rule [55]. As observed by Ohno: "All DNA base sequences, regardless of their origins or functions (coding versus non-coding) are messages written in palindromic verses" [149]. According to Forsdyke, this consideration of inverted repeats as palindromic, which -in our terms are topologically equivalent to Möbius strips, "…provided a proximate explanation for the symmetry principle." To which Forsdyke further comment: "This indicates that the error detecting role of the genome language (involving various forms of information that can be referred to as secondary) may be of *more* importance than the immediate efficiencies of communicating primary genetic messages (primary information)." (p.72, [170]). So, it is this topological non-orientable structure which ensures the primary role of error detecting in genomes.Yet, we recall that it is precisely the Hadamard matrix representation of the Klein Bottle Logic as an equivalent construction of the genomatrix of sequences of arbitrary length, which operates at the level of physical signal transmission and decoding supporting noise-immunity, as observed by Petoukhov [8,9]. Originally CSPR was conceived as being a resultant of "mutational biases"; yet, quoting Noort et al [173] for which genomes contain palindromic sequences that "may be under selective pressure to preserve their palindromic character and therefore follow [CSPR] (as pure palindromic sequences are effectively base paired)", Forsdyke concludes: " Oligonucleotide equifrequencies do indeed imply a potential of sequences to adopt secondary structures" (p.84, [170]). Thus, we may identify as "selective pressure" the self-referential non-orientable surfaces generating a logophysics by which the production of palindromic sequences, operate as an error-detecting code, and thus reproduce *themselves*. An identical principle is at work in the error-correcting nature of Matrix Logic [110] associated to the Klein Bottle Logic [14]. All this resembles Spinoza's conception of the *conatus*, an innate inclination of a thing to continue to exist and enhance itself [174]. Rather than this selection operating agency being exterior, it is built-in as the usual operations on the Genetic Code itself. The former are the topological transformations proper of

cutting –introducing the singularities proper to the vortical structures of these non-orientable surfaces, reverting and pasting, and as we shall see, it incorporates epigenetic factors. Embryological development uses the same operations [1011,12,15,16,17] Yet, this capability to incorporate environmental factors is proper to the open-closed nature of the Klein Bottle.

A (Hyper)Klein Bottle model of DNA, may explain why only a single 5'-3' polymerase has been found so far, so that the antiparallel 3'-5' invoked by the DH, was early in the history of the Genetic Code claimed to be *unnecessary* for transcription for *closed* DNA [26] a particular case to the one here unveiled. We recall that the two strands that make up the double helix, each have a stereochemical orientation -the so-called 5'-3'- orientation, by which each phosphate group in a strand joins the 5' carbon of one sugar to the 3' carbon of the next. This orientation must be the same for every phosphate group within a strand, which imparts a directionality to the strand as a whole. The two strands of the B-form duplex are oriented so their 5'-3' directions are *antiparallel* in the double helix. Consequently, double helix DNA molecules can be *closed* into a circle only by joining together the ends of each of the two individual strand. *Circularization* by joining the ends of two strands to form the Möbius strip is forbidden because the bonds required would violate the conservation of 5'-3' directionality [114]. We have found that this issue of directionality is redundant rather than being subjected to conservation. All that said, this claimed to-be Nature's prohibition appears *not* to have been realized remarking the topological nature of stereochemistry, rather than the geometrical one [43,44]. Starting with DNA material and through folding and ¨sticky ends¨ (i.e. single strands, consistently with the present findings and Burdick's Möbius strip model for DNA, opposite chirality Möbius strips have been produced and through joining their sides the Klein Bottle can, in principle, be realized.The DNA model advocated by this authors is the DH [46,125]. Indeed, the nano Möbius strip is composed of eleven double helices, assembled in parallel. Each double-helical length has a twist of 180 degrees along its central axis, before it reconnects with itself. The central helix circles around the length of the strip once. The other helices circle twice, while also twisting around the core helix by 180 degrees before reconnecting to close the Möbius loop.



So in principle, a biochip that may embody the Klein Bottle Logic as the logic for quantum computation with self-correcting codes [14,110], is reachable. We note that the crossover effect present at the core of the Klein Bottle and consequently in the Genetic Code, is at the basis of morpho-functional structures in the human organism, such as the crosswise connection of brain hemispheres with the left and the right halves of a human body, of chromosomes, the crosswise gestalt of optic nerves from eyes in the brain [115] and visual hemilateral synchronization [13,128],or still the cortical homunculus [13].

A critical review of the DH has surged in several works. "The discovery of circular DNA, over 30 years ago, introduced an element of uneasiness in what had been, up to that point, the almost picture-perfect story of the elucidation of the molecular biology of heredity. If DNA indeed has the Watson–Crick right-handed helical secondary structure, then in circular DNA, thousands, or perhaps even millions of twists must be removed in each generation, and re-wound in the next generation. Mitochondrias are crucial to cell biology as energy producers, are coded by their own genome, the mitochondrial genome (mitDNA); this genome, inheritor of ancestral bacteria coexist with chromosomic DNA, is the smaller one about 16000 bases in most of the superior organisms. Alike the DNA of most viruses and bacteria, it is "circular" in that if forms a closed loop, its last base is contiguous to the first one" [64,65]. More archaic still is the prokaryote "circular" chromosome, where DNA is packed together with proteins; "circularity" is an understatement for what is more fundamentally non-orientably twisted [222,226]. (See note no.2).

Although enzyme systems adequate for this task have long since been found and characterized, there have nevertheless arisen a number of proposals for alternative DNA structures in which the strands are topologically non-linked, so that they might separate during replication without having to be unwound. These structures have generally been put forth as theoretical only, and have been largely unaccompanied by experimental evidence to support their applicability to native DNA from living

systems. Recently, however, a report has emerged suggesting that it might be possible to separate, intact, the individual single-stranded circular half-chromosomes which constitute the double-stranded circular chromosomes of certain plasmids. This would not be possible unless the chromosomes had one of the alternative, topologically non-linked structures, i.e. any proposed structure for DNA in which the strands are either not twisted at all, or else containing exactly equal numbers of right-handed and left-handed twists, so that the net number of twists is zero**.** So the difference between the Side by Side model (SBS) arises in that rather than positing a topologically linked double strand helical model, it proposes that DNA is not topologically helical, "but rather has a structure …in which the two individual single-stranded circular half-chromosomes twist about each other alternately to the right and left, giving rise ultimately to a structure whose strands are topologically non-linked" [66]. SBS has two well defined sides, while the DH model of DNA, due to its circular uniformity along the length of the duplex has no well defined "side", so that in the SBS model there is a genuine orientability while it claims that it is the DH which introduces a non-orientability. Thus, its author, Rodley as a response to Crick's et al assessment of the DH and SBS [82] dismissing the latter for the former, concluded that: "The SBS structure, as a metastable entity, provides a basis for interpreting *in vivo* and certain *in vitro* results where some uncertainty exists concerning the DH approach. In particular, circular DNA data indicate the presence of some retained SBS." [106]. As mentioned before, bacterial and viral nucleosomes show non-orientability in their closed loops architecture [222].

Yet, as Burdick had noticed, it is not the case of a circular DNA but a Möbius strip instead [26], and till today the 3'5' topoisomerase –the enzymes that do the unwinding of DNA- has not been discovered yet. On the other hand, mathematical considerations on the linking of double strands in terms of writhe and torsion of the DH have raised topological questions for the biological processes that may underlie replication, transcription and recombination, and question the DH itself [88].



## 6. The Hadamard Matrix and the Klein Bottle structure of the Genetic Code

Remarkably, in terms of torsion shear elastodynamics, it is easy to see that the double helix, can be easily obtained from a single rubber band, to which we apply torsion, so that in approaching the two ends of the band, two helical structures appear without breaking the band, and further torsioning still produces four helixes, and so on. These are stable configurations, as observation of the cables that wind out of a telephone apparatus show [116,117].

There is another Hyper Klein Bottle fractal-like structure for the Genetic Code, introduced by Petoukhov and He [8,9] that is produced departing from another matrix representation for the KB, namely consider the Hadamard matrix H(2) = [C,T;A,G] = [1, 1; -1, 1], H(4) and H(8), the 2 and 3-times tensor self-product of H, respectively,

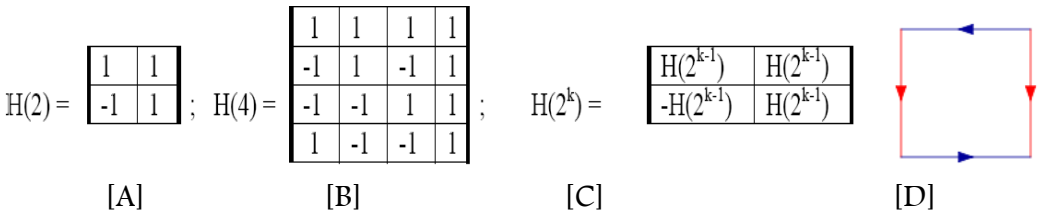



**Figure 14**. The Hadamard matrix representation of the genomatrix. H(2) is the 2x2 (Hadamard) matrix representation of the Klein Bottle representing the anticlockwise (clockwise) direction as 1(-1) as in [D] (the choice of which is arbitrary). [B] and [C] represent the 2-fold and k-fold tensor products, for the genomatrix of duplets and n-plets, respectively.

H(2) is not an arbitrary matrix in the setting of the Matrix Logic form [10,14] of the Klein Bottle Logic, which allows to translate cognitive statements to quantum mechanical statements. In the first place, , H(2) is a 2x2 matrix representation of the Klein Bottle itself! [14]. There are another three such possible representations by Hadamard matrixes, namely, by chosing -1 in any of the four possible entries of a 2x2 matrix having all the other matrix elements given by +1. There are another three such possible representations by Hadamard matrixes, namely, by chosing -1 in any of the four possible entries of a 2x2 matrix having all the other matrix elements given by +1. It is easy to see why a 2x2 Hadamard matrix is a representation of the Klein Bottle. We recall that it is given by the identifications as in the fig. 14[D], or identically in any of its rotations. If we set +1 for, say, the anticlockwise orientation, then one of the values of an oriented segment is necessarily -1.

A Kronecker product of two Hadamard matrices is a Hadamard matrix as well. A permutation of any columns or rows of a Hadamard matrix leads to a new Hadamard matrix.The adjoint of a Hadamard matrix is also a Hadamard matrix, which up to a factor coincides with the inverse: *Hadamard matrices are matricial representations of self-reference, actually as we shall see, associated to the Klein Bottle.* Indeed, normalized Hadamard (2x2)-matrices are matrices of rotation on 45° or 135° depending on an arrangement of signs of its individual elements, which are crucial to introduce the X-cross symmetry. Normalized Hadamard (2x2)-matrices act on the superposition states associated to the two possible representations of the normal vectors to the Klein Bottle, projecting them on the Boolean dual states, from which by recursive application of them we retrieve the elementary dual-states of classical logic: Thus, they are the operators intertransforming classical Boolean logic and quantum logic, or still, more basically are the operators intertransforming classical states and superposition topological entanglement states [14,110]. Thus, they are more basic than quantum entanglement, while they are still crucial to Quantum Computation [118]. In Matrix Logic, Hadamard matrices are at the basis of error-correcting codes. Petoukhov chose them for the algebraic symmetry studies of genomes having in mind several remarkable properties Hadamard matrices. In the first place are used in many fields due to their advantageous properties: in error-correcting codes and the noise-robustness of the transmission of digital photos as far as from Mars. Petoukhov discovered that they play a crucial role to study hidden regularities of the Genetic Code, developing a matrix approach to genomics. They are further related to hypernumbers such as the bi-quaternions, of great importance to physics and as transpires, to genomics as well, fin particular to the symmetries of genomes, and to their noise immunity [8,9].

So, in the present setting, the subalphabet no.3, or still, the Chargaff rule either for one or two strands, is nothing but the standard matrix representation of the Klein bottle surface.

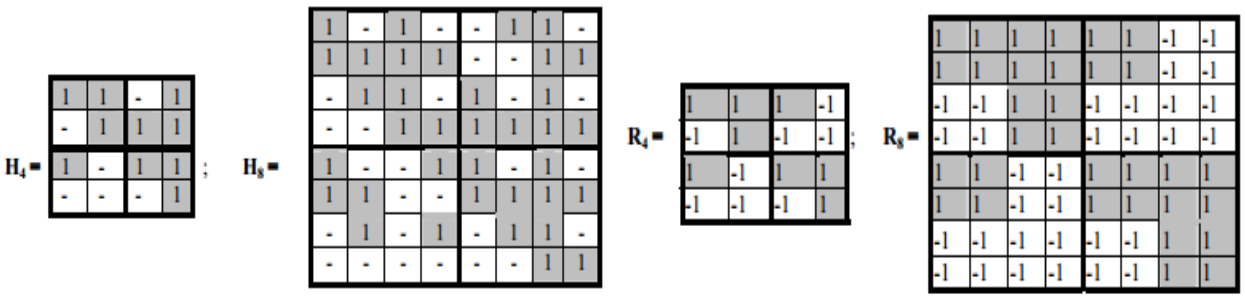


**Figure 15.** Numeric matrices H4, H8, R4 and R8 which are connected with phenomenology of the genetic coding system [8,9]

We now follow Petoukhov in examining the DNA alphabet(adenine A, cytosine C, guanine G and thymine T) and the appropriate Kronecker family of matrices P(n) = [C,T;A,G](n). What kind of black-and-white mosaics (or a disposition of elements "+1" and "-1", respectively, in numeric representations of these symbolic matrices) can be appropriate in this case for the basic matrix [C, T; A, G] and [C, T; A, G](2)? The important phenomenological fact is that the thymine T is a single nitrogenous base in DNA which is replaced in RNA by another nitrogenous base U (uracil) for unknown reason (this is one of the mysteries of the genetic system). In other words, in this system the letter T is the opposition in relation to the letter U, and so the letter T can be symbolized by number "-1" (instead of number "+1" for U). By this objective reason, one can construct numeric representations H(2)and H(4) of mentioned matrices [C,T;A,G] and [C,T;A,G](2) by means of the following algorithm due to Petoukhov of transformation of black-and-white mosaics of matrices [C,T;A,G] and [C,T;A,G](2) together with their Rademacher representations R2 and R4: - in matrices [C, T; A G] and [C, T; A G] (2), each of monoplets and duplets that begin with the letter T, should be taken with opposite color in comparison with appropriate entries in matrices [C,T; A G] and [C,T; A, G](2) from figs. 9 & 10; correspondingly numeric representations of these DNA-alphabetic matrices [C, T; A G] and [C, T; A G](2) reflect the new mosaics of these symbolic matrices. There is an algorithm which transforms P(3) into H(8) and from P(n) to H($2^n$) [8,9] and thus from two different topological codifications arising from the Klein Bottle, we obtain the same genomatrix representations of the Genetic Code. While in the former approach the HyperKlein Bottle was apparent, this is no longer the case for H(8). This minimalistic topological basis for the genetic code appears to be related to its marvelous resistance to environmental hazards. Indeed, the Hadamard matrix approach yields mosaic fractal structures with 36 black (positive) and 28 white (negative) ones, which are associated to Rademacher functions (which only take +1 and -1 values) from the digital theory of signal processing [2]. Painting them as black and white alternatively, we shall get irregular patterns of a chessboard, not evenly painted anymore [8,9]. Hadamard matrices, which play a crucial role in the Matrix Logic realization of the Klein Bottle Logic, as the matrix representation of the Klein Bottle itself [14,110] and its relation with Quantum Logic in quantum computation, are used widely in the theory of coding, being crucial to the robustness of transfer of digital information with regards to environmental noise [2]. Thus the Klein Bottle Logic not only provides the basic codification, but also the robustness under noise of the Genetic Code and a fortiori, that of embryological development [12]. Using the data of BUILD34 provided by Perez [37,38], it was proved that the percentage difference between the blocks in white and the blocks in black is of the order of 0.1% [22]. Thus, as we shall see below, we have an almost quantitative identity of these blocks corresponding to different codons. This is a signature of the non-orientable topology of bioinformatics, as already discussed. We shall later return to this below.

Also the Fibonacci sequence can be introduced in the present framework- We take a corresponding multiplet of the matrix [C A; U G](n) and change its letters C and G to φ, the Golden Ratio; instead of letters A and U in this multiple we place $1/\varphi$ [8,9]. As a result, we obtain a chain with n links, where each link is φ or $1/\varphi$; we recall that they are the eigenvalues of the OR & NAND operators of the Matrix Logic derived from the Klein Bottle Logic, so their appearance in the Genetic Code from this is not accidental. In fact, OR and NAND are represented by the 2x2 matrices [0,1;1,1] and [1,1;1,0], respectively, which coincide with [F(0),F(1);F(1),F(1)] and [F(1),F(1);F(0),F(1)], and the n-th power of OR & NAND are [F(n-1),F(n);F(n),F(n+1)], [F(n+1),F(n); F(n), F(n-1)] respectively, with F(n) representing the n-th element of the Fibonacci sequence. So we are considering [C,A;U,G] = [φ , $1/\varphi$; φ, $1/\varphi$] . For further studies of the numerics of genomes and their "quantum-like" structures see [8,9,23,40]. (See note no. 3).

**7. Genomic Palindromes**

The DH of DNA with the reversed and complementary strands due to Watson and Crick was based on the observation by Chargaff that various sources of double strand DNA appeared to have globally equal amounts of thymine (T) and adenine (A), and likewise, equal amounts of cytosine (C) and guanine (G). This served as a hint for the base pair makeup of DNA and the double helix model. Yet, while this observation of the equal quantities of the doublet pairings came to be associated with the double strand model as the first-parity rule, upon studying single-strand DNA, Chargaff came to propose that the identity of frequencies of T and A, and those of G and C for a single strand; this came to be known as Chargaff's second parity rule (CSPR). To resume, **fr** (T) = **fr** (A), and **fr** (C) = **fr** (G), is valid for *both* single strand or double strand DNA; these are the second and first Chargaff parity rules, respectively. Recent studies have lead to the verification of the second parity rule for single strand DNA as associated with the existence of a mirror reverse-complement symmetry [59]. Takeda and Nakahara developed a frequency analysis of the 64 triplets in the 16 chromosomes and mitochondrial (mt) DNA of the *S. cerevisiae* genome revealing the almost identical number of triplets and their reverse complements, thus establishing the validity of Chargaff's second parity rule and still its validity for the genome of E. coli and H. sapiens [61]. We recall that it is "top" 5'---3' strand that which is kept in the databases of the National Center for Biotechnological Information (NCBI), Washington, D.C., and in another sites across the world.

Especially relevant is the verification of the validity of this in the case of several genomes and its relations with harmonic frequencies of complete genomes, in the work by Jean-Claude Perez, pioneer of self-organized fractal chaos neural networks at the Artificial Intelligence Laboratory of IBM France, which we shall introduce below.The existence of genomic palindromes was revealed by Prabhu [56] in a study of complete genomes and long genome segments from a wide range of taxa, and was rediscovered by Qi and Cuticchia in 2001 in a study of complete genomes [63]. It follows from Chargaff's second-parity rule in single stranded DNA, usually specified as the GC-rule (%GC tends to be uniform and species specific) that, within a species, oligonucleotides of the same GC% will exist at approximately equal quantities in single stranded DNA. Thus, for example, while quantities of 5'CAT3' and 3'GTA5' (pairing complements) will be closely correlated because of both the first and second parity rules Chargaff rules, 5'CAT3' and 5'ATG3' (forward complement or "reverse complement", or "mirror-codon" in Perez's terminology ) will show some correlation only because of the latter rule. 5'ATG3' is the "forward complement" of 5'CAT3', triplet, produced by the following transformations:

1. The original 5'CAT3' is rotated 180º degrees as on the Möbius strip to produce 5'TAC3' and now the Chargaff rules, whether the first or the second, is applied, to produce 5'ATG3', the forward-complement already introduced, in the same strand . We shall call it, following Perez, the mirror-codon of 5'CAT3' . Or, alternatively
2. We take the antiparallel strand 3'GTA5' of 5'CAT3' and we rotate it 180º to the first 5'3' strand to yield the forward-complement, 5'ATG3' or mirror-codon of 5'CAT3', in the same original strand to yield 5'CATnnnnATG3', where nnnn stands for a number of in-between nucleotides.

We can extend this by considering longer sequences. Say, if we take 5'ACTGCAG 3', its mirror-codon 5'CTGCAGT3' in the same strand is produced as follows. We can either take its anticodon 3'TGACGTC' and produce the 180º torsion rotation to obtain 5'CTGCAGT3', or we can produce it as the sequence 5'ACTGCAG 3' → 5'GACGTCA3' → 5'CTGCAGT3', with the first arrow denoting a 180º rotation , and the last arrow denotes the application of no.3 subalphabet C↔G, A↔T, which requires Chargaff's rule, whether conceived for single or double strand [67]. We remark, actually this applies whether the antiparallel strand of DH or a single Möbius strand are the case.We recall that the previous construction of the genomatrices reveal that a jumping is the case for each such identification of codons and anticodons and n-plets, as iterated non-orientable topologies. Now the jumping is transferred to the pairings of codons to mirror-codons.

Let us show the appearance of palindromes as embodiments of a Möbius strip, given by a rotation of a sequence by 180º of two sequences of nucleotides which completed by the Chargaff rule, produces the non-orientable topology, irrespective of the genome being two helixes, two strands –as orientable surfaces-, or a single non-orientable strand. Consider then the sequences representing the antiparallel double-helix (the same observation as above) strands written as

I. 5'TAACGTACGTAC3'
II. 3'ATTGCATGCATG5'

the latter being the complement produced by the no. 3 subalphabet which requires Chargaff's first rule. Here the denotation of 5' and 3' is consistent with figure no. 6. Suppose we know cut this double helix backward complement loosening the couplings which then rotate 180º to produce an "inverted repeat" on a single strand, 5'TAACGTACGTACnnnnnn GTACGTACGTTA3', to differentiate from the "directed repeat", say 5´**TTACG**nnnnnnTTACG3´, or 3´**AATGC**nnnnnnAATGC 5´. Here nnnnnn denote any number of intermmediary nucleotides. Now the Chargaff rule as the no.3 subalphabet, C↔G and A↔T, can be used to produce either

1) the following two helical antiparallel (or still, side by side) strands as in (I) and (II) or still 2) these two inverted repeat sequences which can be thought as lying each on a local side on a Möbius strip in which red (brown) elements are identified as the X-cross identification of the Möbius strip or the Klein Bottle (see Fig. 2, or 3) the mirror representation which now appears in either "side" or as on a double strand, made of the pairing of I & II.

I: 5' TAACGTACGTAC nnnnn GTACGTACGTTA 3',

II: 3'ATTGCATGCATG nnnnn CATGCATGCAAT5'.

We may rewrite this as

I': 5'$\vec{X}$nnnnn$\vec{Y}$3' with $\vec{X}$= TAACGTACGTAC, $\vec{Y}$ = GTACGTACGTTA

II': 3'$\vec{Y}$ nnnnn$\vec{X}$5' with $\vec{X}$ and $\vec{Y}$ the 180º reverse of $\vec{X}$ and $\vec{Y}$, respectively.



Here, we have used two different typos to indicate the topological identification of each kind. Yet, in distinction with the initial introduction of these non-orientable topologies through the Klein Bottle mononucleotides identification of T (U) with A, C with G, from which we identified them as extending to n-plets (or n-words made of n mononucleotides), the present identification is a trivial identity: an n-plet appears repeated through the X-shape cross forming two palindromes, while the two strands are still identified as before, and still each strand locally has an inverted repeat on the other strand. We can illustrate this as in the following figure

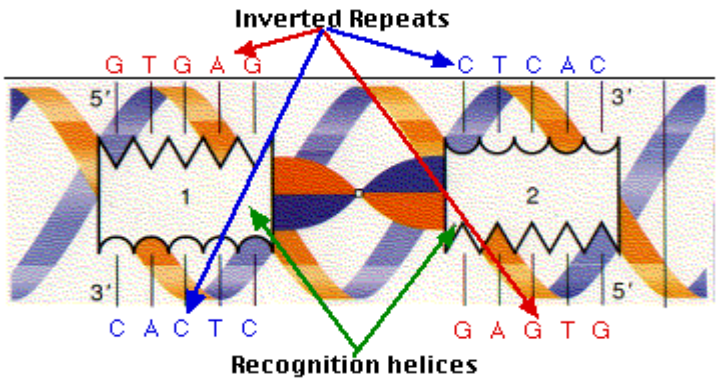



**Figure 16.** Illustration of the inverted repeats with the X-cross topology of the Möbius strip and Klein Bottle, expressed as X-crossed palindromes on deleting the intermediary nucleotides, and still the no.3

subalphabet of the KBL introduced in Figs. 9 & 12. Figure from Kimball's Biology Pages © John W. Kimball, Creative Commons; http://biology-pages.info.

Indeed, the juxtaposition $\vec{X}\ nnnn\overleftarrow{X}$ is TAACGTACGTACnnnnCATGCATGCAAT, and $\vec{Y}\ nnnn\overleftarrow{Y}$ is GTACGTACGTTA nnnnATTGCATGCATG, both are palindromes (up to the omission of the mediating nucleotides nnnn; they can be indistinctly read from right to left of left to rigth. But in the double strand or double sequence of above, the X-cross Möbius strip or Klein bottle topology is elicited: We can identify the elements of the opposite diagonal corners by a 180º rotation and we further superpose the corners diagonally. They are indeed identical. But seen as elements of a double sequence or a double strand, when juxtaposed they produce palindromes.

But now, 5'TAACGTACGTAC3' can be attached to 5'CATGCATGCAAT3' on the "other" side of a Möbius strip which reproduces the 3' to 5' inverse orientation of the former. Likewise 5'GTACGTACGTTA3' has its palindrome 5'ATTGCATGCATG3' also superposed on the "other" side of a Möbius strip or a Klein Bottle which superposes with the 3' to 5' orientation of the former.

Transpositions are related to noncoding areas as well as coding areas [70]. Particularly, the so-called Class II transposons consist of DNA sections that move directly from place to place; see note no.4. Sometimes there is a palindrome-like swap of the transposon during this move. Say, the original sequence described as I & II above, move to another genome region to become the palindromic reversed appearing in the posterior slices of I' & II'. We found the same process here. It joins a codon with its mirror-codon or reverse complement.We can now state that the non-orientable topology of the genome explains the second Chargaff rule. Furthermore, we can either understand the genome in the following two manners, which appear to be equivalent:



1. As a double strand (either DH, or the SBS which as observed by Burdick actually is a Möbius strip [26]) which verifies the first Chargaff rule, coded by the Klein Bottle matrix, P(1),yielding fractal-like structures: either two recursive Hyper Klein Bottles or a recursive 2-torus, so actually the double strand is nothing but the pairing of n-plets on either side of the non-orientable topology which only locally has two sides and globally is just one side. We note that additionally this ensures the validity of the second Chargaff rule and we find that the previous fractal-like structure can be represented by inverted repeat sequences and especially palindromes, which as we saw have the non-orientable Möbius strip topology.
2. Or we can represent it as a single non-orientable strand in which there is a representation of the Genetic Code in terms of the mirror or reverse complement, so that instead of DH or SBS, we have the same and whole information in a single non-orientable strand just by considering either the inverted repeat sequences and palindromes of the codons/mirror codons pairs. In this representation, the genomatrices are associated through the latter pairs. (see note no.5)

Thus we can not but agree with Forsdyke in putting this thus: "The need for complete genomic sequences in bioinformatic analyses may have been somewhat overplayed" [57]. In this take, DNA has, alike other molecules of organic chemistry, a paradoxical twin topological stereochemistry, transiting from non-orientable to orientable and backwards, very much alike the representation of Crab Canon as in [101]. The difference resides that the "score" of each of the two DNA "instruments" is related by the no.3 subalphabet associated to the Klein Bottle Logic, or still the Chargaff rule. Perhaps this should not appear as surprising; it is the very nature of the Klein Bottle Logic precisely to self-referentially exchange its paradoxical superposition states proper to its non-dual nature, to the Boolean states and back, as explained already with regards to the normalized Hadamard 2x2 matrices. As such, the Klein Bottle plays the role of operator and operand, which transforms its own non-orientability to Boolean dual states and back [14,110]. Still, since the model applies as well to RNA (replacing U for T), which usually is single stranded, the single-stranded non-orientable topology seems to be more

natural, particularly, bearing in mind the role of RNA and retrotransposons in the origin of life [184,185,224].

But this possible primality of RNA would necessarily invite for a revision of the first-order cybernetics implicit to the linearity of the Central Dogma (that DNA encodes mRNA, and mRNA, proteins, but not the reverse), to be actualized by a second-order and higher cybernetics whose metaform is the (Hyper) Klein Bottle [14]. Remarkably, this second-order cybernetics has been raised in terms of the Principle of Recursive Genome Function due to Pellionisz [213,214]. Recursion is the name for the iteration of a function on itself, so it is a manifestation of self-reference, and the basis for fractals and physics [13,14,219]. We have generated the topology of genomes from the recursion of the Klein Bottle. Pellionisz: "Recursive genome function is expressed by a process of already-built proteins, iteratively accessing sets of first primary and ensuing auxiliary information packets of DNA to build hierarchies of protein structures" [213].For the relations with transposons patterns in genomes and their importance for changing genomic information by proteins see [221].

Thus, the present approach in terms of the topologies of system biology, requires a more comprehensive self-referential and hetero-referential causation in which also proteomics plays a crucial role, since "It is now clear that information flows multidirectionally between different tiers of biological information, of which genes, transcripts, and proteins constitute only the most obvious 3" [189]; see [190,191,192,224,213] for further discussions, the last one for references on the fractality of genomes. The present approach is similar to the partially nested developmental systems –actually HyperKlein Bottles- approach to evolution, which furthermore also raises a critique of the linearity of the first-order cybernetics of the Central Dogma in relation to evolution and inheritance [231,232].



**8. Order despite mixings: the universality of vortical motions and their non-orientability.**

Perez proposed the thesis of an ancestor "circular" code with a single strand, which evolved into the double strand of the "circular" mitochondrial genome, the former as well as our present genome which would have both arisen by cutting, reshuffling and pasting origami (with 180° twists) and kirigami (cutting or deleting) with twisting operations of the extension of triplet codon/mirror-codons pairs to n-plets [38]; for further discussion on this ancestor as a prokaryote or a virus (whose nucleosomes are Möbius strips [222]) and non-adaptive evolution in the framework of comparative genomic see [224]. So, the bioinformatics of single strand genomes should, in principle, by assessing the quantity of triplet codon/mirror-codons pairs, provide for a way for assessing the feasibility of these alternative understanding of the Genetic Code. As the acid test for these claims, they should render a one to one correspondence between codons and mirror-codons for whole genomes.

It was revealed by Perez, by carrying out the statistical frequency analysis of the frequencies of the single stranded DNA codons of the complete human genome, this duplication of the information by having the codons/mirror-codons pairs, or if wished the non-orientability of the original "circular" genome thus represented, ensured that the original genetic information was never lost. By studying the latest version of the human genome, Perez discovered that there is an almost perfect correlation between the codons and mirror codons of the order of 99.99995 %, as obtained by the single strand human genome BUILD34 [37,38,39] .

In this sense, these complex 180º torsion twistings and reshufflings in the midst of cutting and pastings, very much resembles the notion of David Bohm's implicate and explicate orders in his theory of quantum mechanics, which he explained with the following experiment [20]; see note no.6.

An ink droplet is introduced into a flask containing highly viscous substance (such as glycerine), and the flask is rotated very slowly such that there is negligible diffusion of the substance. In this example, the droplet becomes a thread which, in turn, eventually becomes invisible. However, by rotating the substance in the reverse direction, the droplet can essentially reform. We remark the rotational nature of the mixing motion. When it is invisible, according to Bohm, the order of the ink

droplet as a pattern can be said to be *implicate* within the substance. Similarly, could we reverse the order of the kirigami and origami operations starting from BUILD34 as decoded by the Genome Project, we would get the original order of the ancestor genome, or still the Klein Bottle complementary identifications genomatrices P(n), for any finite positive integer n. Nevertheless, is the non-orientable logophysics which sustains and generated this to start with, always present as the organizing and cognizing agent.

Upon his discovery of this intricate implicit order of the human genome (and of other organisms which he likewise subjected to statistical analysis to find the almost perfect correlations between codons and mirror-codons of single stranded genomes,Perez reflected that its most notable explicate order is the organism itself [38]. However, the implicate order is the non-orientable non-dual logophysics, which also and unseparably so is explicate. Perez put it as if Bohm would have done it in terms of his experiment: "However, statistical analysis of the frequencies of each of the 64 codons retains traces and , even today, the fossil of this distant memory original genome , even allowing to deduce the probable evolution , history, memory, our genome somehow." [38].

Bohm explained these notions of explicate and implicate in the following terms. He employed the hologram as a means of characterising implicate order, noting that each region of a photographic plate in which a hologram is observable contains within it the whole three-dimensional image, which can be viewed from a range of perspectives. That is, each region contains a whole and undivided image. To Bohm's understanding, in the hologram is embodied the germ of a new notion of order. This order is not to be understood solely in terms of a regular arrangement of objects (e.g., in rows) or as a regular arrangement of events (e.g. in a series). Rather, a total order is contained, in some implicit sense, in each region of space and time. Bohm: "Now, the word 'implicit' is based on the verb 'to implicate'. This means 'to fold inward' ... so we may be led to explore the notion that in some sense each region contains a total structure 'enfolded' within it" [71]. Yet, there is a reality check for this metaphor of enfolding which actually is topological, unnoticed by Bohm, but for his notion of "prespace" which does not invoke the issue of non-orientability [20]. This prespace is made of the non-linear interference wave patterns from which in-formation surges by beaming ligthwaves upon them. The shapes of the latter whenever their phases possess an inhomogeneous distribution- which is as well the case of holograms, are non-orientable Möbius strips [76]. Yet, their scale may also be cosmological, as it turns to be the case of the Möbius strip at the centre of the Milky Way [195]. But these waveforms can still be Klein Bottle singularities, which integrate the wave and particle nature of in-formation, the latter being the *zero set* of the waves' nodes, rather than an expression of quantum complementarity [150]; they still generate the nilpotent states of the Intelligence Code expressed in Matrix Logic [155]. Thus, the particle-like level of in-formation, as electron distribution or molecular structure, is unseparable of the pattern of interference which is undulatory. The former being generated from the singularities which possess the latter [150,155], and which themselves sustain the vortical patterns that generate the non-orientable shape of lightwaves [77,78]. They still generate the non-dual logic which has quantum, fuzzy and boolean logic as particular cases [110] and the decomposition of the cognitive states of this non-dual logic as light states [128,155]. Yet, as discovered by Gariaev, DNA appears to support holograms [81].Thus, the current non-dual logophysics for both DNA and RNA, integrates the particle, undulatory, holographic, chemical, genomic, semiotic and cognitive levels of in-formation, all of them as expressions of the principle of self-reference [142] .

Of course, the folding and hyperfolding of the topologies of the genomatrixes, as discussed, embody in principle these implicate and explicate orders. Bohm's approach to quantum physics as the interplay of implicit and explicit orders, points to the so-called quantum potential, which is an "active information field". Much work has been produced to elicit the meaning of this informational field [176], yet no indication to the fundamental role of *vortical* motions was ever provided, despite the "guiding field" is given by the gradient of the *phase* of the wave function which begs for this identification [20,71].Yet, at a more basic level, the quantum potential is deeply related to the torsion geometries that lie at the basis of the most universal kind of motion, vortices, as already the above

experiment is the case [128,150,151,152,153,154,155,156]. Particularly, they are elementary motions of fluids [156] and liquid crystals [27,50]. Already in the 19th century the naturalist Bell Pettigrew had noticed the universality of vortical motions in nature [4,5]. D'Arcy Thompson chose out of this ubiquity only the spirals and further identified the Golden Spiral [6]. Currently, they reappear as crucial to complexity, in the cybernetic epistemology of Morin, yet with no treatment of the non-orientable topology [200]. But till today, linear motion occupies most of the attention of theoretical physics at least at the particle level, while contemplating spin as a merely quantum internal motion on which quantum entanglement shows up. To remark, vortical motions are indeed carriers of active information, as DNA and optical vortices show to be the case; they have as an elementary property that they intertransform Inside and Outside. Indeed, they merge the implicate and the explicate order, in a Klein Bottle logophysics which is crucially related to non-orientable surfaces and their vortical processes. Furthermore, vortical dynamics appears to play a fundamental role in inducing not only the organicity of life through ordered water domains, but as well, the transition from the inorganic to the organic chemical realms: Namely, the transference of chiral information out of a mineralogical crystal to organic molecules that are in immediate contact with its surface [182].

Bohm noted that although an hologram conveys undivided wholeness, it is nevertheless static. In Bohm's notion of order, laws represent invariant relationships between explicate entities and structures, and thus Bohm maintained that in physics, the explicate order generally reveals itself within well-constructed experimental contexts as, for example, in the sensibly observable results of instruments [20]; see note. no.6. However, with respect to implicate order, Bohm asked us to consider the possibility instead "that physical law should refer primarily to an order of undivided wholeness of the content of description similar to that indicated by the hologram rather than to an order of analysis of such content into separate parts …" It was argued by Rapoport [14], that it is the Klein bottle logophysics which sets the ground, both ontologically and epistemologically, for a contextuality by which the holographic nature of the self-penetrating surface projects the wholeness to the partiality of its projections. These projections are operations of the whole. In particular, this notion of order by Bohm finds its expression in the genome, in terms of the non-orientability itself, which ensures that different segments of the genome are identified uniquely with their palindromic or mirror-codings equivalents. Whatever the mutations might have produced in the ancestor genome, these parts continue to be related as if single identities, although separated by spatial reshuffling in different loci of the genomes at all times of their evolution. In quantum physics this is called entanglement. And as we already discussed, the very nature of the Klein Bottle as a matrix representation that generates not only codons but n-plets of arbitrary length, is to embody an entanglement which is borne from an intertransformation of Inside-Inside and Outside-Outside, given by the pairing between T and A, which is mediated by Inside-Outside and Outside-Inside. Thus, for genomes entanglements not only occur as spatial events; they do so even in time. So we can think of *entanglements in time*, as manifested in the equal numbers of codons and mirror-codons as revealed by Perez, or as the non-orientable topologies of genomes. But entanglement does not require quantum physics to occur : We observe that genomes due to the non-orientability produced in the first place as a coding of the Klein Bottle Logic transformed succesively by folding, twistings and pastings to obtain the genome as we presently know it. The Klein Bottle or still the Möbius strip are bodies of entanglement, due precisely to their non-orientability, as shown by a vector perpendicular to them at some point, is actually identified as the same vector which points oppositely to the surface, as placed in the "other" side. This is the topological protoform of Newton's law of action and reaction; see Fig. 4 above. So it is a topo-logical (as the logic of locus) entanglement which is prior to any laws of physics, either classic or quantum. This was the departure point by Isaac Stern in his construction of Matrix Logic that contains quantum logic, fuzzy logic and classical dual logic [110], and provides a matrix form for the Klein Bottle Logic [14] . This is why we can think undistinctly on the Klein Bottle as a surface or as a logic, which is what we have done all along the present work, and on introducing the topological coding of the Chargaff rules. This entanglement in which separate genomic configurations are interlinked in time

and in space, establishes a coherence in time and in space through resonant harmonics –to be presented below- given by the proportions of codons to mirror-codons, which is almost perfectly equal to one, and to the proportion of the 32 most frequent codon-mirror codons pairs to the 32 less frequent pairs, which is 2 to 1; both being the signature of non-orientability as introduced in §2. It has for "explicate" manifestation the appearance of discrete waves as suggested by Perez [37,38,39,218], very much alike the electromagnetic and sound emissions identified by Maslow and Gariaev, upon their discovery of the natural language character grammar of the genome –Zipf' law [85]. This topological entanglement in which, say, one vector unfolds to its opposite to later become itself, is a protoform also of other forms of topological order, as in physics of superconductors. This is a phenomenon of zero electrical resistance and expulsion of magnetic fields occuring in certain materials when cooled below a characteristic critical temperature, which originally was found to been found to be near absolute zero but actually to occur in room temperature . When attaining this critical temperature, infinite spin ½ fields which by the Pauli exclusion law already for a pair of them are forbidden to be in the same state, fuse to become a superconductive spin 1 bosonic field. This is called boson condensation, and is quite common to many materials, as we said, even at ambient temperatures. These materials are called superconductors, since they have exactly zero resistance and infinite conductance. This also means there is no joule heating, or in other words no dissipation of electrical energy. Therefore, if superconductive wire is made into a closed loop, current will keep flowing around the loop forever. Remarkably, a superconductor placed on a Möbius strip magnetic field will levitate [157].

Perez suggested that the codon/mirror-codon pairs, although very distant , still remain as coupled and matched to long distance indicating that they would behave as electron pairs of a superconductive genome, the so called Cooper pairs. Superconductivity is a quantum physics phenomena, whereby this pairing is caused by an attractive force between electrons from the exchange of phonons and magnetic fields are expulsed.It can be produced at room temperatures, and is believed to be crucial to biological systems [123]. In type II superconductors, including all known high-temperature superconductors, magnetic vortices in the electronic superfluid, dissipates some of the energy carried by the current.If the electric current is sufficiently weak the vortices are stationary, and the resistivity vanishes. There is another phenomenon of great importance to life as already noticed by Lima de Faria [177], which is the separation of charges in water, with the ensuing concentration of negative charges forming ordered water domains. It involves the process of formation and dissociation of nanovortices in water [60]. Indeed, in water, at long distances this attraction between electrons due to the displaced ions can overcome the electrons' repulsion due to their negative charge, and cause them to pair up. In fact, this is the *same* principle that sustains superconductivity: In a conventional superconductor, electrons with opposite spin come together to form Cooper pairs that pass through the atomic lattice without scattering. This interaction occurs because the presence of one electron pulls in positive ions from the lattice, and this in turn attracts the next electron; this requires the electrons to be relatively close together.These pairs then interact with each other to form a condensate from which individual electrons cannot be easily scattered. But an attraction and local nucleation of negative charges with the ensuing expulsion of positive charges is, in general conceptual terms, another manifestation of the Feynman-Ize principle. This principle which embodies a departure of classical dualism, and is known as the *like likes like* principle –a non-dual logophysical principle indeed, stands as the basic process of formation of ordered water domains which are crucial to life and DNA [60]. In the case of superconductivity, the electrons in a pair are not necessarily close together; because the interaction is long range, paired electrons may still be many hundreds of nanometers apart. Herbert Fröhlich was the first to suggest that the electrons might act as pairs coupled by lattice vibrations in the material, so that it is a resonance effect rather than a physical proximity [123]. These excitations necessarily contain essential non-linear features. One example of resonance attraction in biology is the behaviour of erythrocytes in blood. Indeed, erythrocytes are negatively charged; still, they actively attract each other and form "rouleau", where they are held together by coherent excitations [126]. The same principle is

claimed to be the case of the brain oscillations, which are invoked to be the basis for the sense of unity of the self [122], and particularly, the multitwist Möbius strip architecture of the small-world cortical neuronal networks which are related to them [120]. Remarkably, EEGs are structured as a geometric series having the Golden Ratio for their ratio [196]. As discussed in [13], the torsion vortical geometries are unseparable of the five-fold symmetry which produces Φ, and ultimately, of the non-orientable topologies here introduced.

Perez suggests the following scenarios : 1) 2-electron bonds of bases G and C for example in an "ancestral" DNA, where CTA - GAT had managed to balance their energies shared electrons . - There were suddenly "separated" forever by the division type " hairpin " palindromes described above ; 2) Although located very long distance , they continue to "communicate" according to the principle of "Cooper pairs ", say as resonant vibrations; 3) The base G of double-stranded DNA that faces the distant base simple C strand will then , too, benefit from this energy balance ; 4) Thus two bases G could "communicate" very long distances. With respect to the ordered water domains, they would play in this scenario a fundamental role as resonating with the DNA background ensuring the quantum coherence of both the water domains and the DNA molecules. Perez concludes thus: "Generalizing such processes we can "imagine" a GLOBAL UNITY, a genome in which billions of bases TCAG would "communicate" "electronically " long distance ... up to establish a BALANCE ENERGETIC, A GLOBAL SCALE OF WHOLE GENOME" [38] (our translation from the original French version, capitals from the author). In view of the universality of vortical motions, we return to genomes, a paradigmatical biological system that is organized as such.

**9. Vortical motions, transposons and non-orientability**



The transposon hypothesis is that introns originates from the transposons [124]. Inverted repeats are commonly found 1. in DNA to which transcription factors bind; 2. the DNA of many transposons is flanked by inverted repeats such as I & II; 3. Inverted repeats at either end of retroviral gene sequences aid in inserting the DNA copy into the DNA of the host; and 4. Duplicated Genes: The human Y chromosome contains 7 sets of genes — each set containing from 2 to 6 nearly-identical genes — oriented back-to-back or head-to-head; that is, they are inverted repeats like the portion shown here: (The dashes represent the thousands of base pairs that separate adjacent palindromes.)

5′….*CACAAT TCCCATGGGTTGTGGGAG*…3′----------5′CTCCCACAACCCATGGGATTTGTG…3′

3′… GTGTTAAGGGTACCCAACACCCTC….5′ ------- 3′*GAGGGTGTTGGGTACCCTAAACAC*… 5′.

We notice again the X-cross identification proper of the Mobius strip or the Klein Bottle, forming the palindromic structures interspersed by other nucleotides, while horizontally, we have the Klein Bottle original identification of complements following Chargaff's second rule, i.e. subalphabet no. 3, yet, repeated as well. Indeed, the in-formation is duplicated in each such gene.

This orientation and redundancy may help ensure that a deleterious mutation in one copy of the set can be repaired using the information in another copy of that set. All that is needed is to form a loop so that the two sequences line up side-by-side. Repairs can then be made (probably by the mechanism of homologous recombination). Here, for example, the single difference in the sequences can be eliminated (red for blue or vice versa). An hypothetical scenario is that double strand DNA resulted from an ancient ancestral single stranded "circular" DNA, which can be reconstructed from the double strand alike a hairpin-like DNA that might have been unfolded. This would produce a single-stranded DNA where T=A and C=G as observed here. A possible explanation offered by Perez is that of an "Ancestral Genome" and transposons. But as turns to be the case, as discovered by Perez, "We are confronted with an obvious perfect symmetry between the codons and their mirror-codons. We see odd/even [codon/mirror-codons to be described below] pairs on the level of the whole human genome… we show that this law remains conserved regardless of individual genome SNP variability"[38]. So, as it turns out to be the case, indeed it is ancestral, but rather in the sense of being

the manifestation of a logophysics operating through the non-orientable structure of the genome and its transformations described above, as a fractal-like surface of self-reference, as already identified as a HyperKlein Bottle surface. It is this logophysics which ensures the reparation of mutations through the redundance of the information produced by the non-orientable topology or its mapping to a single strand by introducing a mirror copy of the superposed pairs on the single global side which locally is two sides. Thus in the single strand we have a copy of the base pairing of the no.3 subalphabet which produces the superposition as if two strands now represented in a single one.

As for the role of all these redundancies, with regards to his theory of autoevolution, cytogenetist Lima de Faría puts it thus: "The chromosome changes its structure permanently, by using its "magical tricks" such as inverting its segments and yet functioning with equal efficiency, or still, by deleting or adding extra copies of its genetic materials. All in all, the chromosome has been restructured and maintained its organization; for the human chromosome, this has occurred for over one million years." Geneticists have tended to consider these rearrangements as random events. Upon the identification of DNA sequences, those responsible for these changes, the transposons were singled out. Lima de Faría: "They are mobile and can migrate to other regions of the same or to other chromosomes. They consist of a region of insertion into DNA which is flanked by duplicate sequences, of which DNA are known. But as the report by the International Genome Sequencing Consortium published in 2001, although they were described as junk, they are the rich "paleontological record", the "extraordinary trove of information about an earlier evolution of the chromosome. The repeats are "considered to have been, and continue to be, active agents that reshape the chromosomes by causing rearrangements, creating new genes, modifying existing ones and modulating the overall DNA base content" (pp. 131-133, [28]). We shall later see how fine this modulation is.

The numerics for extending Prabhu and other researchers' findings for large sequences of nucleotides to the whole human and chimpanzee single strand genomes was identified by Perez, in considering the Chargaff second rule for single stranded DNA. Perez revealed the harmonic fractal structure of the genome (in its BUILD34 version of August 2003 [72]), when considered as a single strand architecture. We can consider the genome as a single sided non-orientable Möbius or (Hyper) Klein Bottle surfaces and logics, as already revealed by using the no.3 subalphabet for codifying the Klein bottle biochemical alphabet. But now we can frame this findings in terms of either palindromic structures or non-orientable topologies since actually the human and chimpanzee genomes hold a quantitative basis for this to occur. The rules for the formation of a copy of the double strand genome which we already posited that it can be construed as a unique structure in which bases are paired by the Chargaff rule, but now as mirrored in a single strand are given as follows. We shall call this latter code as the mirror code, in distinction with the master code of Chargaff which we already introduced as the Klein Bottle identification of Outside-Outside with Inside-Inside, and Outside-Inside with Inside-Outside.

Indeed, in the double strand sequence of above (I and II), the X-cross Möbius strip or Klein bottle topology is elicited: We can identify the elements of the opposite diagonal corners by a 180º rotation and we further superpose the corners diagonally. They are indeed identical. But now, say, 5'TAACGTACGTAC3' can be attached to 5'CATGCATGCAAT3' on the "other" side of a Möbius strip which reproduces the 3' to 5' inverse orientation of the former. Likewise 5'GTACGTACGTTA3' has its palindrome 5'ATTGCATGCATG3' also superposed on the "other" side of a Möbius strip or a Klein Bottle which superposes with the 3'to 5' orientation of the former. Evidence of such a chromosomal palindromic architecture in several genomes is already established [227,228].

## 10. Transposons and Evolution

As for the biological function of non-orientable surfaces, which as we see should better be called bio-logical, the diverse genome-wide repeats are derived from transposable elements. They are currently understood to "jump" about different genomic locations, without transferring their original copies

[119]. We recall that the construction of the genomatrices of any length elicited a jumping along the non-orientable topologies of these matrices, as a kind of metapattern and metadynamics. Transposons are DNA sequences which manifest an ability of moving to new sites in genomes through what in its most elementary sense is a topological transformation of a genome, by cutting and pasting the moved sequence, for the case of double strand DNA (DNA transposons -Class I), and copy and paste TEs (retrotransposons or transposons class I); see note. no. 4. It has been established that TEs catalyze different types of mutations, which have different potential impacts on genome structure, gene expression, and specia-tion.They are genetic elements of a more general kind of DNA sequences transposable genetic elements (TEs) which may also move through an RNA intermediation, the so called retrotransposons, also called transposons via RNA intermediates. They were discovered by geneticist Barbara McClintock, in her experiments with maize plants. While originally they were viewed as genomic parasites, and further dismissed in the ground of being "junk" DNA, nowadays the understanding on TEs has changed. TEs are present both in prokaryotes and eukaryotes, for the latter being know to constitute more than half of DNA. The traces of their operation as well as of transpositions are omnipresent in the genomes of higher order eukaryotes, "from the coarsest features of genomic landscapes and how they change through real and evolutionary time to the finest details of gene structure and regulation" [68]. They are known to contribute to speciation, and in particular to rapid speciation; indeed TE activation appears as response to wide crosses, and still "…the ability to evoke rapid genome restructuring is at the heart of eukaryotic evolvability—the capacity of organisms with larger and larger genomes to maintain evolutionary flexibility" [68]. The rapid form of genomic restructuring and speciation stands in contrast with Darwin's conception of evolution as a gradual process, which in geophysical terms required a continuous overlaying of the geological column (i.e, the seemingly vertical sequence of material deposition of the Earth's crust), rather than the inversion and discontinuities that have been encountered; in fact, the non-orientability of geophysical configurations appears also to be the case [13]. In a recent review on TEs, Fedoroff places them on the perspective of epigenetics, the heritable, reversible regulation of gene activity, from which they originally arose in the work of McClintock. Presently epigenetics is a central issue, since it is realized that phenotypes reflect not only genotypes. They also reflect the epigenetic response as well of development vis-à-vis environmental influence. As such, they correspond to a phenomenology typical of the open-closed integration of the environment and system which is proper to the Klein Bottle. But rather than TEs operating in a chaotic manner, they are "… well-orchestrated genomic stress responses that can rapidly restructure genomes – the quintessence of evolvability" (p.xii,[121] ). While the original claims that framed TEs in terms of epigenetic silencing which evolved to control their proliferation as well as their perceived destructive potential, nowadays another view on TEs has been elicited, which inverts the previous take. Namely, that "ETs and the transposases they encode underlie the evolvability of higher eukaryotes' massive, messy genomes". Or still, "it is precisely the elaboration of epigenetic mechanisms from their prokaryotic origins as suppressors of genetic exchanges that underlies both the genome expansion and the proliferation of TEs characteristic of higher eukaryotes" [68]. So ETs appear to play a crucial role as "controlling elements", conceived originally by McClintock as, " unmoored gene regulatory systems that had become associated with different genes by virtue of their ability to move" [121]. Indeed, transposons are called "jumping genes" because of their ability to "jump" to completely different regions within the chromosome and later "jump" back to their original positions. But their role of controllers as conceived in cybernetics, already assumes implicitly a first-order cybernetics, in which the controller is detached from the controlled, in distinction with second-order cybernetics in which they are integrated as elements of a cycle of control. Second-order cybernetics corresponds to a Klein Bottle logophysics, in which controlled and controller are conformed and operate integrally through a non-linear causation [14]. In fact, there is growing evidence that a second-order cybernetics is the case, in which "epigenetic regulatory systems are themselves modulated to facilitate damage control and restore genome integrity remains for future investigations to unravel [121].Yet, if ETs are known to operate as regularity

cybernetic systems within completely sequenced genomes from bacteria, archaea, eukaryotes and viruses, it is still more crucial to evolution would they act as *metacontrollers*, i.e. controllers of *pools* of genomes in a specific ecosystem. Thus a study based on the notion of the most successful genes in terms of their persistence and DNA dissemination capability has singled out ETs as those that meet this requirement , namely that genes encoding transposases are the most ubiquitous and abundant in nature . The natural interpretation is that their pervasive capacity is the signature of their essential role, while when this abundance is the case but for their pervasiveness, then this is the signature of a functionality which is either specific to an habitat or to an organism. Yet the prevalence was understood not in terms of the number of genes that express the most proteins, but those which succeed in securing self-dissemination. It is their "unmoored" mobile capability which in addition of providing dissemination of ETs within genomes and between genomes (i.e. metagenomes, communities of genomes in a specific ecosystem) also "lead to mutations and rearrangements that can accelerate biological diversification and –consequently- evolution. By securing their own replication and dissemination, transposases guarantee to thrive so long as nucleic acid-based life forms exist" [70]. Thus, they are called "selfish" [230], rather than being associated to the principle of self-reference.Thus, the authors concluded that "transposases are the most abundant genes in both completely sequenced genomes and environmental metagenomes, and are also the most ubiquitous in metagenomes" .

Remarkably, in terms of the genomatrix and its non-orientable topologies, we have a similar meta-genomic order. Independently of the *geometry* of DNA, which is far from being unique [98], the geno-matrix provides a metaform which in principle applies to all genomic information and its digital co-ding. We can perhaps think of it as a metapattern, as it appears in the pattern recognition of digital photographs of landscapes. Despite the seemingly disorder of their geometry and topology, and the lack of common features but for their fractal patterns, all these photographs share a common meta-pattern: the Klein Bottle [83,90]. As we already said, this surface is a metapattern which can be simply generated by extracting the first two terms of the spherical harmonics of a sinusoidal signal (need not be electromagnetic) impinging in an arbitrary boundary [13]. It is universal; the name metapattern is appropriate, though the alternative usage of "metaform" would not be an ontological relapse. The essential difference between the Klein Bottle metapattern elicited as the shape of data, as is the case of digital photos of landscapes, and the metapattern of genomes is as follows. While landscapes are unique but can be thought as arising one from the others by deletions or moving the pixels from one place to the other in a photo, in the case of the latter, we are lead to believe that the metapattern plays an active role, though it may have been broken and transformed in its local details. Whereas in the case of pattern recognition of landscapes, it is to us to attempt to rebuild one photo from others. Indeed, active information appears to be the case of genomes (see note. no. 8), while we cannot dismiss this to be the case of arbitrary data, as a matter of principle.We shall see that it is the first two harmonic terms on the 64 codons of single strand BUILD34 as revealed in the work of Perez, to be introduced below, which will be identified as the signature of the non-orientable topologies of genomes. We turn now to this topic



## 11. The Numerical Evidence of non-orientability of genomes

Let us return to the notion of the Klein Bottle as a metapattern of vision recognition, and its equiva-lent in the genome: the HyperKlein Bottle topology as a kind of a metapattern associated to the geno-matrix of arbitrary sides $2^n$, with n an integer, can be further elicited in the following sense. The rela-tion between the topologically paired elements of this matrix (when n=3) and that given below by the codon/mirror-codon symmetry, is tantamount to replace in the codon/mirror-codon table below, the

codon/anticodon. Say, consider "codon master" and "codon mirror" for any one of 32 pairs of codons matched by mirror symmetry. Say, for example TCG <==> CGA, one plays the exchangeable role of being the mirror (master) codon of the other. and as we shall see, these gives an almost perfect matching of 32 pairings .We now follow Perez in constructing a table of codon and mirror codons relations. But first an observation. In the genome, numerous bases are called undeterminate due to the impossibility of sequencing them. With the progress of the decoding of the genome, with a "final" version BUILD 34 released in August 2003, these bases diminish in number and in length but they always remain. These are called the N bases. On them, we can shift on the *frame of reading*, by this we mean, how we interpret the sequence in terms of triplets. example: consider the sequence AAATGACGCATTC…which allows for three frames of reading:

1. AAA TGA CGA ATT C… (first frame of reading);
2. A AAT GAC GAA TC… (second frame of reading), and
3. AA ATG ACG AAT C… (third frame of reading),

where the empty spaces are used to indicate the triplet grouping.

Taking the single strand BUILD34 sequencing of the genome, Perez considered the 64 codons, grouped in terms of the three different frames of reading. He further classified the 64 codonsorganized in terms of the codon/mirror codon already introduced, as the 180º torsion followed by the Chargaff rule, either thought as the first or the second rule. For example, CGA is transformed to AGC to finally produce TCG. He further grouped the 64 codons in terms of two groups, according to their frequency, and additionally to the three frames of reading. Those 32 having the highest frequency he called them "dominant" and the other less frequent 32 codons, the "dominated". He further extended this to the two strands of the genome and still to the two 5'→3' and 3'→5' readings. He found that the differences according to what frame of reading was used were unsubstantial since all the correlations were of the order of 0.99999 introducing a difference only in the order of $10^{-6}$; p.95 [37]. Thus, Perez concluded that the frame of reading was irrelevant, and that the organization of the single strand triplet frequency could be subsumed into the division of the 64 codons into the dominant (higher frequency) 32 codons, and the dominated lesser frequency 32 codons, for which all three frames of reading produced a ratio of the order of 1.995. In other words, up to the error that the sequencing technique has, the relation between the dominant and the dominated was equal to 2. But instead of departing from them, we shall find them in the no less remarkable unison 1 to 1 relation between the 32 codons with the higher number of T's ("odd" codons) and their mirror-codons with the highest number of A's ("even" codons). Similarly to our discussion on music perception of the tritone in §2.1, we consider them as lying as if identified along a Möbius strip, completing a whole octave; see Fig. 5 [B].This is the fundamental identification of the Möbius strip and Klein Bottle as a topology in the case of the human genome, which as we shall see, it is given for all 64 codons organized as the 32 pairs of codon and mirror-codons, produced by the 180º twist and the Chargaff second rule for single strand. We further introduce a second axis of symmetry in the two 32 pairs in dividing them in terms of dominant and dominated, to produce four quartile groupings, in order to identify the dominant most frequent and dominated less frequent codons.



**Figure 17 (**after Perez's [37,38,39]): **Populations of the 64 codons of single stranded DNA -as in BUILD34- sorted in descending order in the case of the first codons reading frame.** Notice the matching numbers of codon and mirror codons, which is a prerequisite for the topological identification of them as pertaining to non-orientable Mobius strips and (Hyper)Klein Bottles: Each odd sorted codon lying on one local side while on the other local side the even sorted mirror codon is matched to.

| "Odd" sorted codons (#T > #A, #G or #C) | "Even" sorted mirror codons #A > #T, #G or #C |
|---|---|
| 1st TTT 36530115 | 36381293 AAA 2nd |

| | |
|---|---|
| 3rd ATT 23669701 | 23634011 AAT 4th |
| 5th TCT 20990387 | 20948987 AGA 6th |
| 7th TTA 19750578 | 19721149 TAA 8th |
| 9th TAT 19568343 | 19548709 ATA 10th |
| 11th CTG 19195946 | 19176935 CAG 12th |
| 13th TGT 19152113 | 19073189 ACA 14th |
| 15th CTT 18944797 | 18894716 AAG 16th |
| 17th TTC 18708048 | 18678084 GAA 18th |
| 19th GAA 18678084 | 18562015 TGA 20th |
| 21th TTG 18005020 | 17927956 CAA 22th |
| 23 th TGG 17480496 | 17444649 CCA 24th |
| 25 th CAT 17423117 | 17409063 ATG 26th |
| 27th CCT 16835177 | 16810797 AGG 28th |
| 29th CTC 15942742 | 15939419 GAG 30th |
| 31th AGT 15266057 | 15251455 ACT 32th |
| FIRST QUARTILE 1 : 316027664 | SECOND QUARTILE : 315402427 |
| FIRST PLUS SECOND QUARTILES: 631430091. | |

| | |
|---|---|
| 33th GGA 14619310 | 14614789 TCC 34 th |
| 35th GTG 14252868 | 14214421 CAC 36th |

| | |
|---|---|
| 37th GTT 13852086 | 13794251 AAC 38th |
| 39th TGC 13649076 | 13635427 GCA 40th |
| 41th GCT 13252828 | 13242724 AGC 42th |
| 43th GAT 12658530 | 12650299 ATC 44th |
| 47 th TAG 12240281 | 12217331 CTA 48th |
| 49th GCC 11268094 | 11258126 GGC 50th |
| 51th GGT 11026602 | 11007307 ACC 52th |
| 53th GTA 10766854 | 10755607 TAC 54th |
| 55th GTC 8955434 | 8938833 GAC 56th |
| 57 th CCG 2606672 | 2604253 CGG 58 th |
| 59th CGT 2379612 | 2372235 ACG 60th |
| 61st GCG 2247440 | 2244432 CGC 62nd |
| 63rd TCG 2087242 | 2085226 CGA 64th |
| QUARTILE 3: 158309529 | QUARTILE 4: 158064247 |
| THIRD PLUS FOURTH QUARTILES: 316373776 | |



The odd (first and third quartiles) and even (second and fourth quartiles) cumulated codon populations are: 474337193 & 473466674, respectively. Then the odd/even ratio is: 474337193/473466674 = 1.001838607; the approximation to up to the third decimal is also the case of the partials first to second quartiles, and third to fourth quartiles, respectively. This is a trivial consequence of each codon being matched in number by its mirror-codon. This allows indeed to consider that each pair can be thought as lying on a non-orientable Mobius strip or Klein Bottle with a pair being superposed in the "two" sides of what globally is a single side on which the surface is contained. This is the characteristic 2:1 harmonics of these surfaces of self-reference (see Fig. 5. [1] and the text in the caption, or Fig. 8). So that indeed, in concrete numbers the whole classification of the single strand genome in terms of codons and their mirror-codons can be assimilated to a non-orientable surface, both for each individual pair, as well as for the 32 codons and their 32 mirror pairs.

Yet, this surface is not the one that arises from the codon/anticodon identifications in fig.11, but rather by considering the n-plets of the whole single strand human genome, which is tantamount to search in the transposed version of the genomic matrix, pairing codons with mirror-codons.

Furthermore, if we consider the ratio between the most frequent dominant codons/mirror-codons given by quartiles 1 and 2, and the less frequent dominated pairs given by the third and fourth quartiles is almost equal to 2. Indeed, the first and second quartiles, $Q_1 + Q_2$ is almost exactly twice as large as the population of the 32 least frequent quartiles, $Q_3 + Q_4$. The exact ratio is: 631430091/316373776 = 1.995835745.

It is even a real "partition" of the whole human genome as shown in fig.11, the two respective populations of codons forming the two partitions of the genome are correlated to 99.9995%. What this equal partition says is: the non-orientable topology has a real quantitative basis for the pairing, at the level of triplets, to be realizable.

In terms of frequency, each codon/mirror codon can be identified in an octave, very much alike the opposite keys in the tritone perceptual identification; see fig. 5 . In the other hand, taking the 32 dominant in relation with the 32 dominated, the frequency of the former is twice that of the latter, each group corresponding to an octave, so that if the dominant group has, say B for its key, the dominated has also B but in the preceding octave.

But there are other integer numbers produced by this:

**Figure 18. The emergence of "integer numbers codes" connecting 4 quartiles, after Perez [37,38,39]**

$Q_1$ = 316027664; $Q_2$ = 315402427 ; $Q_3$ = 158309529; $Q_4$ = 158064247

Ratios Integer Numbers

The Number 1 $(Q_1 + Q_3)/(Q_2 + Q_4)$ = 1.001838607

The Number 2 $(Q_1 + Q_2)/(Q_3 + Q_4)$ = 1.995835745

The Number 3 $(Q_1 + Q_2 + Q_3 + Q_4)/Q_1$ = 2.99911677

$(Q_1 + Q_2 + Q_3 + Q_4)/Q_2$ = 3.00506206

$(Q_1 + Q_2 + Q_3 + Q_4)/(Q_3 + Q_4)$ = 2.995835745

The Number 4 $(Q_1 + Q_2)/Q_4$ = 3.994768602

The Number 5 $(Q_1 + Q_2 + Q_3)/Q_4$ = 4.996320389

The Number 6 $(Q_1 + Q_2 + Q_3 + Q_4)/Q_4$ = 5.996320389

Other ratios:

½ $(Q_1+Q_3)(Q_3+Q_4)/(Q_2+Q_4)(Q_1+Q_2)$ =0,5019644575009854

3/2 $(Q_1 + Q_2 + Q_3+ Q_4)/(Q_1+Q_2)$ = 1.501043236

¾ $(Q_1 + Q_2 + Q_3+ Q_4)\, Q_4/Q_1(Q_1+Q_2)$= 0,7509600619915957

4/5 $(Q_1 + Q_2 + Q_3)/(Q_1 + Q_2)$ = 0,7995421211968238

5/6 $(Q_1 + Q_2 + Q_3)/(Q_1 + Q_2+ Q_3 + Q_4)$= 0,8332310591951594



Therefore, in the human genome we have found the music harmonics unison 1:1 yet which applies to the Möbius strip and Klein Bottle topologies with the codons of $Q_1$ as identified with those of $Q_2$, and the codons of $Q_3$ with those of $Q_4$, altogether disposed as in Fig. 5. Actually we have one such association between $Q_1$ and $Q_2$; another one formed by $Q_3$ paired with those of $Q_4$, and a third one in which altogether on one side we locate the odd codons and in the "other" side the even ones: Nested

Möbius strips and nested Klein Bottles, the latter indeed being HyperKlein Bottles. In simple harmonic terms: $Q_1 : Q_2 : Q_3 : Q_4$ =2:2:1:1. We also have the Octave (ratio 2:1), Fifth (ratio 2:3),Fourth (ratio 3:4), and Third (ratio 4:5). In addition, there is also the 5:6 ratio, which is the minor third.

As for the 2:1 ratio between the dominant higher frequency and the dominated lower frequency codon/mirror-codons, is quite mysterious in itself. Perhaps it is related to the issue noticed by Burdick, that upon synthesis of viral DNA, some molecules of DNA appear to have doubled their length [187]. This is to be expected for these large circular forms of DNA, upon a topological protoform of denaturation, by which we cut a Mobius strip without breaking the n-plets chains. i.e. along its length, say the green curve in Fig. 4 [1]. This topological "denaturation" produces a double length lemniscate sign-of- infinity ∞-figure, which now is two-sided, each being the enantiomorph of the other one; take a Möbius strip and scissors. So we may place the dominant codons along one of the sides, while we would need to place the available non-dominant codons to match them as if reproduced by a factor of 2, on the other side; yet, now they are indeed separated, as if denatured.This reproduction is *virtual*, or if wished, *imaginal, and still has real results*; see note. no.8 . We can think in this scheme, this 2:1 harmonics as a *lower* form of unity yet derived from the Klein Bottle and the Möbius strip or Klein Bottle topology, as a recurrent loss of coherence [186], which is maximal in the odd/even 1:1 unison relation. These symmetries also extend to the atomic weights of the populations, and several other octaves can be identified from the genomatrix of codons/mirror-codons, and their relative frequencies found to be related to the Golden Mean [37,38,39]. Yet, their relation to the original genomatrix introduced in terms of the Klein Bottle Logic, or its Hadamard matrix representation, are a problem largely open to extensive research [22].

## 12. Conclusions:Non-orientability, metaforms, in-formation as holography, self-reference and mimesis in evolution.



Let us return to the transposons and the reconstruction of damaged areas of genomes, in terms of the non-orientable topology of genomes,or if wished, the palindromic structures; they are the operators of this regeneration. This regeneration follows the principle of wholeness reconstituting its identity when parts of it are altered: wholeness and parts are not separable and it is the structure of the whole that already keeps a copy of the parts by redundancy, that allows the reconstitution to occur.This points out to the need for elucidating a kind of holographic information, which is conserved in time and in space.

### *12.1 Holography, Semeiosis and the Self-referential Physical Basis for In-formation*

Let us start by introducing the meaning of information and its physical representation in its most elementary form. If data - either of genomes or whatever phenomenae may come under scrutinity- are to be the cognitive source for information, we have to recall that information only has a meaning for an interpreter of the source if there is some shape associated to it: information as in-formation. Particularly important at the most elementary level of the constitution of experience, is that of light, which also has a shape, whose topology as well as that of environments of biological systems turns to be crucial to the generation of complexity.

Whenever an observer performing as an interpreter appears not to be involved in making sense of the data, nature appears to exercise a form of semeiosis, a meaning construal of sign systems. It is usually called biosemiotics [144]. Semeiosis is related to self-reference, so the presence of an observer is unnecessary. Self-reference, in particular the surfaces of self-reference here considered, are embodiments of agency, whether a self as an observer is participating or not; see note no.8. Rather than a detached self that provides a meaning in interaction with the sign system, we can conceive of systems, particularly, those that come to be in terms of self-organization, as self-cognizing systems. In other words, there is no clear-cut distinction between Outside and Inside, rather their

intertransformation is the nature of semeiosis. Indeed, the Genetic Code appears to be a *self-signifying* system, yet participating through a cybernetic (i.e. control) non-linear system incorporating the environment, and in particular proteins, as already discussed [213,221]. Thus, it is self-reference, extended to hetero-reference (the HyperKlein Bottle) which appears to be at stake in the Genetic Code; we have ostensibly elaborated this in the present contribution. Remarkably, in semiotics, meaning has been associated to self-reference [140], and its metaform identified as the Klein Bottle [94,141,142]; in particular, biosemiotics has been associated to this metaform [145]. The ultimate structure without which there can not exist any phenomenology at all, is provided by the photon [94]. We shall better say, the experience of the photon, since its ultimate reality is borne from the process of seeing it, rather than being an objective element of reality [94,151]. And as we have already seen, the topology of both the photon –as a singularity of the light wave- and that of the visual system, is non-orientable just like the topology of the Genetic Code.

So, when we think of data, we are indicating to in-formation; see also [200]. On the one hand, it is the construal of meaning associated to self-reference –or more generally to the superposition of self-reference and hetero-reference, the HyperKlein Bottle-, as it appears generating the different levels of experience and organization. On the other hand, it is about the shapes –or more fundamentally still, the topologies from which meaning is created from. Either by ideation or by an actual stimulus, shapes appear to be the ultimate source for the construal of meaning; they are borne by a gestaltic operation.This is already the case of genomes which on the one hand are largely responsible for the generation of the molecules needed by biological systems, and on the other, have a crucial regulatory role, as embodied by the non-coding transposons, and finally, they have the structure of natural languages. This latter structure is built-in the harmonic proportions and the associated topologies. Yet, while organisms and molecules take a three dimensional shape, their in-formation can be encoded or decoded two-dimensionally. Yet, this in-formation has a physical form.



This is the case of holography. It only requires the amplitude and the phase of the illuminating wave from which the three dimensional shape is formed. As already discussed, through the superposition of waves, the phase which originally lies in a plane, may take the shape of a two-dimensional Möbius strip, which appears to be embedded in three-dimensional ambient space. In principle, this is not only restricted to a light wave, an acoustic one may also do. The bottomline of this is that in-formation generically arises from a light beam with *non-uniform polarization*; that is, the state of polarization is different at different points in the beam's cross-section. So, the underlying phenomenae for holographically encoding or decoding data as physical fields ultimately rests on a non-uniform polarization states, which produce complex non-orientable topologies of waves –either light or acoustic, more of this below- which bear the in-formation. In particular, this is the case , in principle, of quantum holography, which operates with circularly polarized wave functions. It was suggested by Gariaev et al, that DNA's signal operations are through quantum holography [81,86,87], which is at the basis of the contemporary technologies of imaging such as magnetic resonance tomography [168].

Yet, while these imaging technologies operate with a singularity free field [129], it is known that in the case of the propagation of light waves in liquid crystals, say DNA, they can be versatilely engineered as to produce light beams with singularities and with particular shapes [130]. These shapes, which we have just introduced in our discusson of holography, can be, in principle. multitwisted Möbius strips [76], as it has recently been shown to be the case for the propagation of optical vortices on a liquid crystal [80]. Thus, in principle, would DNA have a non-orientable topology, light emissions from or to DNA could reproduce this topology, and they would operate in terms of the harmonics of the genome. This may also be the case of the physiology of the visual mode, in which the liquid crystal structure of the eyes and the brain, have as a functional correlate operating with the same principles: non-orientable light waves which reproduce the overall non-orientable anatomy-physiology of vision. To start with, the eye that operates turning Inside-Out the images, and secondly, the X-cross form of the visual system's anatomy [13]. Thirdly, the Klein Bottle topology of the retinotopic and

the somatotopic mappings [33,160,161] that at the cortical level is suggested to have a multitwisted Möbius strip architecture of small world cortical neural networks and operates through rhythms established by resonant harmonics [120] which is claimed to be the basis of the sense of self-hood [122]. Yet, the isomorphy of the logophysics of the carrier of the light wave signal and the visual system itself, as extended to DNA, appears to be the case as well of DNA in relation to the water environment in which it is in interaction, and to the emission and reception of weak electromagnetic signals by DNA samples. Through the absorption and emission of photons, water oscillates from a liquid crystal state which is crucial to life, to the usual unstructured bulk water conceived as a mere inert solvent [60]. The size of DNA that have been shown to emit weak electromagnetic signals is of the order up to several kilo-bases [134].

Returning to genomes, and the capability of DNA of emitting or receiving physical signals we shall further discuss the relations with non-linearity. Early in the 1980s Gariaev and his team showed that DNA emits and absorbs coherent light laser radiation, as well as acoustic waves, which are essentially non-linear waves, solitons [85,86,87]; more recently, through other techniques, this was rediscovered by Luc Montaigner and associates [78,134]. They are ultrastable waves. As any non-linear system, their initial conditions are incorporated in their evolution; as the non-linear systems are driven to chaos, which actually is their generic evolution [202,203], they perform a transformation to a non-orientable state by which they reoriginate in a novel cycle [13]. One such system is that of stars, which on collapsing they appear to perform an Inside-Out transformation by which a new star is born, and the remnants of the supernova explosion constitute all material structures, as already discussed. Another example is genomes as liquid crystals.

Gariaev associated these radiations to the fractal linguistic structure of genomes, particularly embodied in the non-coding regulatory transposons [85,86,87]. In the present work, we have identified this fractal structure with the non-orientable topologies of genomes, and further identified their primary harmonic sectors in the case of the human genome. So, on the one hand we have genetic texts that are organized as harmonics which are further embodied as non-orientable surfaces, all in all, ensuring that the wholeness is represented in the parts through the harmonics. This is the linguistic level of in-formation. In this case, the memory of the initial conditions, say, as an archaic genome, is embodied as the harmonic relations that make the overall structure of the genome with its parts. Despite all the continuous topological operations performed by the genome, the harmonics of this archaic structure is preserved. Epigenetic factors are also incorporated during evolution, and yet the overall harmonics is preserved. Still, there is the physical level of in-formation which can be encoded and decoded as an holograph, whose parts reflect the structure of the whole. We still have light and acoustic waves associated to these harmonics, which –we recall- may have an underlying non-linear wave dynamics –with their non-orientable topologies, as the physical wave counterpart of the textual in-formation. From the holographic decoding, the actual three-dimensional in-formation of the organism and molecular elements needed for its operations may be constructed.



### *12.2. Evolution, Complexity and Palindromes*

The previous discussion is a far cry from to the imperating quantitative notion of information (or entropy) as in communication theory, after Shannon, for which only the amount of bits matter; no interpretation of the data is considered. For this conception, complexity is a measure of the *irreducible* number of bits associated to a message, which disposes of redundance [159]. Here, the notion of algorithmic complexity introduced by Kolmogorov is the measure: Kolmogorov complexity is simply the length of the *shortest* string of symbols in which the given sequence (say, a genome) can be encoded. Yet, this complexity does not provide a measure of biological complexity, as established by comparative genomics [224]. We recall that the ubiquity of transposons appeared to be the evidence for a perpetually dynamic genome. We already proposed that instead of “selective pressure” in the evolutionary sense - regarding the primal role of genomic error-detection in genomes,

it is the non-orientable logophysics that produces palindromes which stands as a more fundamental principle than evolution; it generates, sustains and rules genomes as *dynamical* processes. We already discussed the role of transposons as controllers of *pools* of genomes, and their prevalence in securing self-dissemination.

Notably, genomic evolution is linked to folding, a topological operation, since: "…most of the evolution of protein-coding genes appears to be driven by selection for robustness to misfolding" ; p. 401, [224]. Still, transposons, as crucial regulative operators, are *not* subject to Darwinian selection [224].The point is that they operate as a meta-algorithm (through the Klein Bottle generation of them and a checksum process, to be introduced below) which curtails the growth of algorithmic complexity, which thus is *not* indicative of organismic complexity. As for evolution, comparative genomics has raised the issue whether it exists at all and in what sense [224].

Etymologically, complexity means *folding*, and this is what DNA secondary structures embody. Yet, in the present conception, this topological complexity appears to be the case of *all* DNA (and RNA) across time and space, in its very topological generation, and in its transformations and inheritance. They appear to indicate *Lamarckian* features in which complexity as topological folding and discontinuities play a crucial role, as discussed in this theory. They operate the myriad dynamical genomic operations as much as they produce their conservation from archaic forms, yet with the embodied semeiotic capacity of adaptability afforded by the openness of the closed-open Klein Bottle. We recall that the topology of chromosomes of these archaic genomes shows a Möbius strip topology. As evidence that may support this conception, comparative genomics appears to provide further indication of this non-Darwinian evolution. Indeed, a system of adaptive immunity common to most bacteria and archea, which itself is a novelty in prokaryotes, has been discovered: the so-called Clustered Regularly Interspersed Palindromic Repeats (CRISPR) [193]. This system responds directly to the environmental cue by introducing a genetic change into the organism that is immediately adaptive to the environmental cue. Again, the Klein Bottle Logic embodies such an environmental adaptation, and the basis for error-immune digital codification.



CRISPRs led to suggest a novel paradigm for evolution which purports a non-adaptive theory of punctuated genomic evolution, due to Koonin, in the framework of comparative genetics [224]. In the present theory, complexity itself, through non-orientable transposons transformations, evolves as deleterious random changes are somewhat incorporated into the harmonic fractal structure of genomes. We shall elaborate this elsewhere, to avoid extending the present article further.

*12.3. Non-orientability, the Topological Induction of Complexity and Self-organization in Evolution*

With regards to the isomorphism of the topologies of the physical carrier of in-formation and that of the biological system (light or sound waves and genomes), a "mimesis", if wished, between the electromagnetic weak signal (EMS) and the environment appears to be the case, as previously discussed. Luc Montaigner et al put it thus: " Does the EMS have any specific property related to the coherent dynamical structure …? The question is particularly relevant because the emitted EMS, acting on water molecular dynamics, produces coherent structures such that in PCR [Polymerase Chain Reaction] processes the DNA transduction occurs with the same nucleotide sequence as the one of the parent DNA. The answer to the question is provided by observing that the EMS appears to carry not only the specific information of its frequency spectrum, amplitude and phase modulation, (the syntactic level), but it also describes the dynamics out of which it is generated. In other words, beside the syntactic level of pure information (`a la Shannon), there is a semantic content, which manifests itself in the underlying coherent dynamics of the DNA-water system responsible of the polymerization (highly ordered sequence) of hundreds of nucleotides. We refer to such a semantic content as to the "meaning" of the EMS" [134]. We find again, the issue of mimesis or induction, of a metaform –as a shape of in-formation, acting as the logophysical agency at some level being reproduced at another level of organization.Yet, the isomorphism which exists at the most basic logophysical level, surges

from the non-orientability of the structures involved, DNA, light waves and the ordered water domains, as well as that of molecules in organic chemistry [42]. Thus, the semantics can be , at a logophysical level, ultimately associated to the self-referential nature of the non-orientability that appears to underlie the logophysics of *all* the processes involved. Indeed, it has been known for a long time, and unfortunately forgotten, that liquid crystals develop singularities [27,50], which in principle are precisely the singularities of the phase of light waves which can be shaped as Möbius strips or spontaneously take this form, as in our previous discussion of their role in holography, DNA and information. Just like light waves, liquid crystals develop Möbius strip vortical structures [136,216,217]. But liquid crystals by their very nature of their uniaxial symmetry, are such that the director vectorfield which embodies this symmetry, has the topology of the *non-orientable* real projective space –see Fig. 2; [135]. Yet, as shown in [13], for bounded surfaces, local Möbius strips underlie the real projective space. Since biological systems do not have their boundary at infinity (which is the case of the abstract projective space ) but are bounded in space, the topology of the ordered water domains of biological systems is better characterized by Möbius strips. Remarkably, these domains that correspond to a liquid crystal structure of water, which is cyclically structured and destructured through light waves absorption and emission [60], is conceived to be the very signature of the surgence of life [158]. The remarkable fact is that this topology of liquid crystals can be controlled, and topological changes be induced, say by immersing colloidal particles in the liquid crystal. This arises through the incompatibility of anchoring conditions on the particle surfaces with the alignment imposed by the cell boundaries, or at *large distances* [135,139,215,216,217].Thus, Möbius strips and knotted defects, pervasive to both organic chemistry (catenanes, rotaxanes, etc.) [47,48,181] and DNA, with the former appearing already as optical vortices, can be induced. Furthermore, this is tantamount to what appears to be a general principle for the topological generation of *complexity* as intricate structures in which non-orientable surfaces act as a kind of "glue", simply by inducing them through emplacing colloidal particles on cholesteric nematic liquid crystals, such as DNA. The sole factor appears to be the non-orientable topology of the director field of the crystal, which underlies the formation of these intricate structures in terms of topological dislocations (generically, torsion geometries). It operates through the elastical adaptation of the director field to the extraneous colloidal particles [135,139,215,216,217]. But rather than the non-orientable topology being erased, more intricate robust structures appear to be the case, still carrying as their progeny, the non-orientable structure which make them possible.Thus, complexity –as intricate structures *progenies* of foldedness- appears to be related to non-orientability and its elastic deformation to ensure its preservation under disturbances!



Remarkably, Lima de Faria in his theory of evolution through self-organization, claimed that the complexity of nature, evolved as a phenomenon of mimesis that starts from the physical level of symmetries of elementary particles rising to that of symmetries of crystals, still carrying these symmetries to higher order complexity structures, such as living organism [138]. In the present work, we have associated this mimetics to self-reference and the two dimensional non-orientable surfaces. Particularly to the Klein Bottle, which appear to play a crucial generative role, which is also associated to an hypothetical holographic principle at work in the resonant behaviour of DNA. The foundations for a paradigm for the unification of science has been presented in [13,14]; also the forthcoming [142]. Current studies in theoretical physics claim that the two-dimensionality of spacetime and its relation to an holographic principle, is the basis for a novel paradigm for physical reality [143]. In this work, reiteratively, we have identified dimension 2, as that of Nature [13].

That our visual system may recognize the underlying Klein Bottle metapattern which turns out to be its *own* metapattern as the eye and the visual mode operate through it, is proved by the examination of the pixels of arbitrary landscapes. In distinction with the genome, the individual appears to participate in the construal of the visual metapattern rather than being somewhat controlled by the genomic metapattern it as is the case of genomes, although a symmetrization of this latter relation may follow from [81,84]. Indeed, we recall that the statistical examination of the topology of pixels of digital photos of such landscapes, elicit a metaform for pattern recognition, the Klein Bottle surface [90]. So

there is an non-orientable metapattern for the pattern recognition of physical in-formation, the Klein Bottle, which underlies the creation of in-formation starting from data. That this is the case of any shape, be that biological, geophysical, or whatever, stems from the fact that a sinusoidal wave has for its first two terms of its spherical harmonics the Klein Bottle [13]. Yet, the metagenomic non-orientable topologies which appear to be generated by this surface and its logic are the very logo-physics of the development and surgence of systems rather than the resultant of "evolution". So, rather than the CSPR rule being "the inevitable, asymptotic product of (among other causes) numerous inversions and inverted transpositions that occurred in the course of evolution" [41], they are the expression of this logophysics which actually ensure heredity as a memory which is encoded in the self-referential generation of the genomatrices, and manifests through the palindromic codification. On the one hand, this symmetry ensures conservation, as the reproduction of a structure, through redundance. On the other hand, since it is the expression of a logic which is of integration of the genome with the environment, due to the very character of the Klein Bottle logophysics that integrates the Outside/Outside with Inside/Inside, it ensures that epigenetic factors are incorporated as modifications of genomes which still respect the harmonics, as relative proportions. This may be the case of the CRISPRs, the palindromic structures which produce an immune system as a novelty in prokaryotes. Thus, this non-dual logophysics appears to solve the problem which Forsdyke identified as: " In biological systems where there is competition for genome space, the 'hand of evolution' has to resolve these *intrinsic* conflicts while dealing with other pressures (*extrinsic*) from the environment" (p.70,[170]).This is a kind of logophysical checksum process, which surmounts the dualistic divide between organism and environment.

*12.4 Logophysical Checksum and the Harmonics of Genomes*



Indeed, let us now discuss a possible process by which the linguistic structure of genomes may be at play; its rationale was provided by Perez [37].The proposed method, frequency analysis, stems from Quantitative Linguistics, and is in use in cryptoanalysis. Say, in Spanish, the letter a appears with a frequency of 11.525%, while the letter z appears with a 0.517%. All the other letters appear in bet-ween. This is also the case of genomes, some letters being more often that others. So it is possible to detect data errors in any language just by counting letters. The remarkable distinction between, say, Spanish and a genome, is that for the latter, the appearance of letters is controlled by a mathematical formula, which is embedded in the overall structure of the genome. So, when cells replicate they "count" the total number of letters in the DNA strand of the daughter cell. As for the process by which this counting may operate, we shall further describe it below. If the letter counts don't match certain fairly exact ratios, the cell "knows" that an error has been made. So it "abandons" the operation and "kills" the new cell. Failure of this checksum process may cause birth defects and cancer [207].As for the cognitive agency which produces the checksum, it is possible to state it in terms of the principle of self-reference, which is embodied in the topological generation of the genome matrix itself, in terms of the Klein Bottle logic, as already presented. We suggest that it is the harmonics of the non-orientable topology which sustains the counting checksum, which we suggest that may be ultimately based on resonance; just alike the resonances that gives rise to cortical oscillations through the Möbius strip neuronal small-worlds networks architecture is suggested to provide the sense of a unified self [120].Perez argued that: "Copying errors cannot be the source of evolutionary progress, because if that were true, eventually all the letters would be equally probable… This proves that useful evolutionary mutations are not random. Instead, they are controlled by a precise Evolutionary Matrix to within 0.1%" which is the genomic matrix or its counterpart as the codon/mirror codons 32 pairings, which can also extended to n-plets as already explained. Instead, they are controlled by a precise Evolutionary Matrix to within 0.1%, which is the genomic matrix or its counterpart as the codon/mirror-codons 32 pairings, which can also extended to n-plets as already explained. Still, "When organisms exchange DNA with each other through Horizontal Gene Transfer, the end result

still obeys specific mathematical patterns DNA is able to re-create destroyed data by computing checksums in reverse – like calculating the missing contents of a page ripped out of a novel" [37]. What makes an individual organism of a species a singular entity are the SNPs which "tend, in a global level, to conserve and maintain the symmetry [codon/mirror-codon]" [37]. Furthermore, he claimed there exists a kind of "global strategy" of the variability of SNPs, which tend to reinforce this symmetry, despite apparently erratic mutations; this is most relevant to comparative genomics [224]. As for the physical field that at the most elementary level would carry out the "checksum" as a process of harmonic resonance, the non-linear Möbius strips wave-fields appear to be the natural carrier of the physical in-formation.

Lima de Faria distinguished between "genetic noise" and "genetic music" [74]. Genetic noise refers to the defective mutations of chromosomes arising from the permanent molecular activity and the reshaping of their structure. They are identified as the base deletions, base substitutions, accidental rearrangements and other errors that do not reproduce the initial construction. On the other hand, genetic music arises from the intrinsic mechanisms of surveillance which reestablish order. The already mentioned check-sum would be one such mechanism. Order is reestablished by several processes, such as cut-and-paste repair, mismatch repair, error-prone repair, photo-reactivating enzyme system, proofreading, recombination repair and others. This keeping of "harmony" as stated by Lima de Faria, contributing in the maintenance of the coherence of the chromosome organization is practiced through the ordered rearrangement carried out with the help of transposons. These are flanked by inverted repeat sequences and their movement is directed by transposases and resolvases. A. T. Brown stated: "randomness does not apply to all components of the non-coding DNA. In particular, transposable elements and introns have interesting evolutionary histories" [75]. No man-made language has this kind of precise mathematical structure. DNA is a tightly woven, highly efficient language that follows extremely specific rules. Its alphabet, grammar and overall structure are ordered by a beautiful set of mathematical functions. As for the importance of the secondary structures produced by transposons and palindromes, they play a paradoxical role, or as is called, they possess "a split personality" [132]. All in all, a recent review concludes: " it is only recently that we have begun to appreciate the dynamic role that they and other non-B DNA structures play in the evolution and function of the genomes in which they are found" [132].



There is another way to highlight the overall non-random character of genomes. Already their construction in terms of the recursive application of the Klein Bottle Logic, elicited a fractal-like topological structure associated to the Chargaff rule(s). In terms of this construction, the generation and binary codification of n-plets follows a compositional harmonic self-referential rule in the construction of P(n), for arbitrary integer n. This is a kind of topological form of a cellular automata. Cellular automata were in the modern history of mathematics first formalized by John von Neumann. However, there are examples dating to hundreds of years ago from very diverse cultures, showing that they knew how to create their patterns [8,9]. Cellular automata have a self-referential generation. The most known example, is the Fibonacci series, which is the basis for the so-called Harmonic Mathematics [146], as well as for the complete generation and identification of the prime numbers [210,211]. Stephen Wolfram, upon revealing the amazing complexity that these cellular automata can create by self-referential iteration of a "seed" and a set of simple rules, surmised that a "New Kind of Science" was possible [91]. In distinction with the usual take that complexity is construed from complexity or appear as the outcome of a mysterious "emergence", Wolfram took to show a universe of great complexity generated by cellular automata defined by recursion on very simple rules.We already revealed the appearance of the numbers 1 and 2 on the human genome, as expressions of the elementary harmonics of the codon/mirror-codons couplings, characteristic of the non-orientable surfaces we have dealt with. Yet, there is a third number which is crucial to the architecture of genomes. The Golden Ratio, Φ. This number which D'Arcy Thompson and several of his contemporaries recalled attention to it, is nowadays the focus of much attention among several disciplines. Yet, in all cases, from these only three specific "genomic" numbers, 1, 2 and Φ, and the

genomic length, a cellular automata -proposed in [37], Chapter 19- computes automatically the 64 codon population numbers; see also [38,39]. 1 and 2 being prime numbers they are self-referential, while Φ is the teleo-logic result of the two-depth self-reentrance of a distinction, as an algorithmic recursion tends to produce it [194]. In this derivation, no topological considerations are at stake.

Yet, while cellular automata are usually conceived independently of a topological generation which is the case presented in this article, an underlying topology for the space of states of the automata on which the automata is generated may play an important role. Thus, in the famous Game of Life due to John Conway, whose evolution depends on the initial state, yet run on a closed surface which topologically is a 2-torus, may produce by recurrence the self-organization of patterns in whose generation the topology of the surface on which they unfold is crucial [203,204]. This was the basis for the pioneering work on neural Fibonacci networks due to Perez [54].The Golden Ratio, which has reappeared in several areas of science and particularly to mathematics where it is crucial to the determination of the prime numbers [210,211], plays a crucial role with respect to harmonics. Indeed, would systems, such as the genome, operate through an harmonics resonance phenomenae, and this is particularly the case of non-linear systems, resonances tend to be amplified. As a consequence, the system simply ceases to exist as an integrity. The most obvious image is that of a soprano singing a tune of an aria to a crystal glass, to be suddently rendered as scattered shards. Or we can recall the famous Tacoma Bridge. But why Φ should be such an ubiquitous proportion? The reason appears to be provided by music itself, as a system of proportions, just alike Pythagoras conceived it. Indeed, Φ appears to be the very proportion which *dampens* the superposition of resonances, and makes of architectures "frozen music" [162]; it does so providing coherence in time and in space. (See note no.7).This is the case of standing waves. This Φ-dampening of resonance shows up to be the case of the overall symmetric structure of matter, given by the Mendeleev Table of atoms and their stable isotopes; we recall, it was originally conceived, as an harmonic system. As shown by Boeyens, the Mendeleev Table is generated by a Φ-spiral architecture of the atomic numbers, generating thus a Klein Bottle surface [18,19]. Due to this generation, which in fact can be conceived as produced by a standing wave, the Golden Ratio appears to dampen and structure all the seemingly alterations of the harmonics. A discussion of standing waves and surfaces of self-reference was given by Rosen [186]. Yet, Φ is crucial to cognition and its relations to attention and short-term memory, further related to the energy of neural networks as Bose-Einstein statistical ensembles and the harmonics of brain waves in electroencephalograms [196,220].

So we are reintroducing a topic which we have already mentioned, which is that of the *coherence* of structures, which is very much the case of genomes, and generically speaking of liquid crystals and organisms.As already discussed, alterations of genomes appear to be framed –controlled, if wished-, as the harmonics by which themselves are generated, just alike the overall harmonic organization of matter. In relation to the holographic principle, without coherence it would be impossible to recreate the whole out of the interference patterns produced by the superposition of waves. So the claims that quantum holography could operate to produce and sustain the wholeness of genomes, would be unfounded. Biophysicist and geneticist Mae Wan Ho, has made the case that coherence is the very nature of life [164,165]. The most elementary expression of coherence is self-referential recursion, which as we saw, is at the basis of the Klein Bottle Logic generation of genomes. Living systems often grow in such a way as to produce fractal (i.e. self-similar) patterns. Fractals can be considered as self-referential systems which reproduce their structure in all scales. Capillaries in animals, snow flakes, branches of a tree, etc. are all examples of fractals. A remarkable computational model of growth which reproduces a fractal are the L-systems, after Aristid Lindemayer, who pioneered the approach [147]. Of particular interest is the case of the networks of Purkinje cells in the cerebellum, and their relations to the fractality of genomes [213,214]. Yet, as we have just argued, the existence of harmonics is not the only aspect that this generation creates, or if wished, recreates from a standing wave. The stability of the overall structure is a necessary condition for recursion to achieve the goal of expression: a stable structure in space, which can have a degree of coherence in time and in space. As a

popular song puts it: "*After changes upon changes we* are *more or less the same. "*; in less lyrical terms, we note that "often adaptations are related to the integrity of cellular organization, preventing malfunction and performing damage control"; p.401, [224]. The cellular automata shown by Perez to generate several genomes as a system of harmonics, already suggest that dampening may also the general case. Indeed, while the whole population of codons forming the human genome is thus modelised by three "genomic numbers" which are 1,2 and Φ, the universality of this self-referential recurrent generation of a genome with regards to this three numbers, is shown to be given by other triads of numbers. For Aids (1,Φ, (Φ+10)/9), virus of the avian pest Influenza H5N1 (1,5/3, $\Phi^{1/3}$) agrobacterium (1,1/2,φ), etc. [37,38,39]. Yet, the role of the "genomic" numbers appears to extend from its role as providing overall coherence of genomes. While "junk" –or "selfish"- DNA, as transposons, play a crucial role in the algorithmic complexity, non-adaptive punctuated evolution and maintenance of genomes [224], their fine tuning as harmonics also appears to stem from the atomic masses of the atoms of DNA which produce an "optimal" equilibrium of masses, "of the DNA double helix within whole chromosomes and genomes…" [39]; for a discussion of this and the possibility of an extension to exobiology see [218].Yet, this produces a remarkable relation between form and substance as noted by Perez [39], or still, shape as topology and substance, which may also carry to full genomes and individual chromosomes, and still further to proteomics [39,218].

In synthesis, self-reference appears to be a universal generating principle. Its non-dual logophysics appears to produce and reproduce the different yet integrated levels of self-organization of nature, either logical, physical, biological, chemical, cognitive, semiotic, etc., as its own self-expression. As for the relation of the presently developed theory of genomics and evolution, and quantum physics as a nilpotent universal rewrite system based on recursivity and self-reference, see [217,17], respectively.



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**Conflicts of Interest**

The author declares no conflict of interest.

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Note no. 1. These authors posit an implicit first-order cybernetics, the controller of the system being detached , rather than participating in it. The latter is the case of second-order cybernetics whose metaform is the Klein Bottle [14]. They further chose as the metaform of this cybernetics the yo-yo, as a double funnel with an entrance at one end, and an output on the opposite emerging end, which has no self-reentrance. Thus, *linear* causality is superposed with *non* self-reentrant vortical dynamics. According to Morin, "the nature of nature" is that of self-reentrant vortices, rather than linear causality [200]. In Morin's epistemology, complexity is associated to these structures, but orientability is assumed by default.We shall later see, upon discussing the topology of liquid crystals, genomics and proteomics, that complexity is keenly associated to non-orientability.

Note no.2. The topological model for DH replication and transcription by superhelix creation for "circular" DNA, assumes a $360^0$ twist at a site of cutting of a ribbon, $180^0$ turn for each of two points, then rejoined. Thus, it mimics thus one turn of a DH rather than a $180^0$ turn as a Möbius strip, to preserve the 5'3' orientation, yet it still locally exchanges Inside with Outside in doing so; see fig.2.5c [49].The rejoined ribbon then cut longitudinally, alike to cutting along the mid-red line in fig. 4, models the separation of the two strands.This

produces two ribbons (single strands), linked together as a *non-orientable* catenane, introducing thus the linking number, a topological invariant. Notably, the original loss of orientability is *not* mentioned at all. Instead, for the Möbius strip model, which is a single strand, the cutting itself along this line is what produces an unlinked *orientable* double length ribbon: The lemniscate, or Möbius curve, the figure 8 or ∞, which is ubiquitous to Nature, from celestial mechanics to anatomy-physiology [142] . In the DH, the unlinking is produced by topoisomerases, enzymes which creates a sharp DNA bend in the first bound DNA segment and allow for the transport of the second segment only from Inside the bend to its Outside. It is here that the dynamics of Inside and Outside intertransformation enters the DH model for replication.

Note no.3. As we already discussed, the Fibonacci sequence is a HyperKlein Bottle with a double reentrance of a distinction (simpler than Fig. 3B), a topological meta-algorithm which yields an output from the double reentrance of itself in two levels [194]; it is the "fundamental reality "atom" of information" as already established by Johansen [208]. Rather than the Fibonacci sequence being a subset of the natural numbers, this field and the basic operations of arithmetic can actually be deduced from the meta-algorithm [210,211]. Remarkably, as in the Genetic Code, the structure of the composite natural numbers is generated from an 8x8 matrix which generates *all* composite numbers located at some specific eight positions in strict *rotation* regularities of the chamber; thus it represents indirectly a *complete* exposition of all *prime numbers.* One can ponder whether there is a relation between these *rotational* patterns of composite natural numbers and the Genetic Code.

Note no.4. The DNA transposon is excised from its position via transposase, and reintegrated elsewhere in the genome. These can be identified by the following: i)TIRs, terminal inverted repeats, which allow transposase to recognize the transposon and excise/reintegrate it; ii)TSDs, target site duplications, which are generated during re-integration and are thought to add to the difficulties in recognizing transposons.



Note no.5 Non-linear mechanical stress models for DNA formation, have shown that many of the diverse geometries of DNA can originate as stress deformations of a *single* rope [229] . This suggests that *single* stranded DNA and RNA is at the roots of other more contorted genomic geometries, and particular the double helix

Note no. 6. Bohm's original conception superposed a dualistic logophysics with a metaphysics of wholeness – which later evolved to a theory of order and creativity [225], in which the quantum potential field, controlled the quantum particle, as if exterior to it. Thus the notions of an "active" information and its relation to "passive" information, was intimated [176], later extended to an informational "guiding" field; [225], p.179,180. Creativity appears when the subject is brought into the field to form a closed loop. The former separation into "active" and "passive" information is tantamount to a first-order cybernetics and classical dual logic, in stark contrast with the second and higher order cybernetics associated to the Klein Bottle and the Hyper Klein Bottles, respectively [14]. However, the latter association of creativity to the participation of the subject closing a loop somewhat suggests the latter cybernetics; [200]. Basil Hiley, Bohm's coworker, related the implicate order to an algebra of rotations, ultimately to Spencer-Brown's primal distinction –which we identified as the torsion field [14], and we introduced upon discussing the three subalphabets of genomics. Yet this is done without considering the reentrance of the distinction on itself and developing the theory in terms of the Exterior/Interior divide: in short, no self-reference principle, no Klein Bottle, but the CONTAIN image-schema, further at odds with quantum logic [201]. Yet, the conceptual richness of Bohm's theory, deserves more space that the one we can afford in this article.

Note no.7. Rosslyn Chapel, Scotland, is an exquisite example of "frozen music" as revealed by the Scottish team of Tom and Stuart Mitchell, the latter composer of the *Rosslyn Motet* [188]. Remarkable work on the music of DNA as follows from the genomic matrix due to Perez arranged as the Dragon curve [37,38,39] is Jordi Solà-Soler's [197], following the pioneering work of Perez [198], and recently Petoukhov's work being currently

presented (personal communication). Solà-Soler also concurs on identifying the essential role of Φ as providing coherence to genomes.

Note no.8. Topological operations such as folding and their identifications as to produce the non-orientable surfaces have an imaginal (not imaginary) nature which is that of agency, and is prior to their actual manifestation; see e.g. fig. 2. Already, the principle of self-reference is signed as this agency's self-signification, so that no self is actually attached to the principle, but that of *agency*. This is also the case of algorithms, particulary the Fibonacci meta-algorithm. Thus the Klein Bottle Logic and the Genetic Code, as a topological automata has this same imaginal agency, which in the Klein Bottle is embodied as its self-penetration, which is the very basis for Chargaff's rule. Yet, this introduces the form of *algorithmic causality*, introduced by Johansen (also including causality from a transalgorithmic dimension), which is ontologically prior to *all* other forms of causality, particularly to the more trivial one of *physical* causality operating in material systems [208]. It is as if Nature produces the diverse material systems and their morphologies, such as particles, molecules and molecular "machines", fractals, transposons, palindromes of all natures, etc. as semeiotic operators which *reify* the algorithmic causality, while still they are the actual manifestations of this agency. In linguistic terms, these semeiotic operators appear as injunctions, such as "cut", "paste", "replicate", "recur", or still the instructions to build a mathematical structure (see caption of fig.1). One such semeiotic operation is the computational representation of the principle of self-reference as recursion, which is a protoform of coherence, as already discussed. A most crucial aspect of this imaginal agency, is that structures exist in toto, complete, in zero-time, prior to all manifestations that occur in the perceived time of material organizations [208].