Original Article

Klein Bottle Logophysics, Self-reference, Heterarchies, Genomic Topologies, Harmonics and Evolution.

Part III: The Klein Bottle Logic of Genomics and its Dynamics, Quantum Information, Complexity and Palindromic Repeats in Evolution

Diego L. Rapoport*

Abstract

In this third and last Part of this series, we introduce the Klein Bottle Logic and its digital codification. We present a codification of the four letters of DNA or RNA in terms of the four states of this logic, and further relate it to three subalphabets –introduced by Petoukhov and He- as three primal biochemical distinctions –in the sense of Spencer-Brown- of a HyperKlein Bottle. We present a topological-algebraic algorithm for the generation of genomes, which turn out to have a fractal structure. We identify two possible topologies for them, one related to the 2-torus, the other one related to a HyperKlein Bottle related to these subalphabets/distinctions.We relate the jumps associated to these topological identifications with transposons. We discuss these multiple dynamical configurations with regards to Chemical Topology and the failure of the principle of identity of dual logic with regards to DNA and RNA. We present two dynamical models for the latter and its relations with palindromic sequences and discuss a surmountal of the Central Dogma and its relations with the HyperKlein Bottle logic. We discuss the relations of the previous codifications with the one providing by departing from the Hadamard matrix representation of the Klein Bottle, the robustness with regards to noise of an ensuing system of harmonics and still with algebras of hypernumbers. We discuss the non-dual logophysics for both DNA and RNA, which integrates non-reductively the particle, undulatory, holographic, chemical, genomic, semiotic and cognitive levels of in-formation, all of them as expressions of the principle of self-reference. We present the numerical evidence from BUILD34, the human mitochondrial genome as provided by the Genome Project which elicits the actual existence of the fundamental 1:1 and 2:1 harmonics of the Klein Bottle as theoretically assigned by the previous algorithm of generation of genomes and other ratios . We discuss the relations with topological and quantum entanglement, and holography. We discuss the relations of these non-orientable genomic topologies with the algorithmic complexity theory approach in evolutionary theory in the setting of comparative genomics and the recent findings of palindromic systems that elicit a Lamarckian-like evolution We propose that it is the non-orientable topological dynamical operations of genomes forming palindromic sequences which act as “selective pressure”, so that rather than the usual ascription of linearity to genomes counters the non-linear logophysics which generates and preserves them to noise and the factors producing evolution. We discuss evolution as a metamorphoses related to the principle of heteroreference jointly acting with the principle of self-reference, i.e. a HyperKlein Bottle logic. We argue that Clustered Regularly Interspersed Palindromic Repeats (CRISPRs) may serve as an indication for the feasibility of this theory of evolution, serving as both the memory of genomes as well as providing the adaptability vis-à-vis other alien agents. They are the physical-chemical organization of the non-linear non-dual logophysics which already generated the genomes as well as operates in their dynamical operations.

Key Words: bioinformatics, biocomputation, biophysics, blown-up systems, cognition,complexity, Hadamard matrices, harmonics, heterarchies, image-schemas, morphomechanics neural networks, non-classical logic, non-linearity, ontology, palindromes, pattern recognition, phenomenology, physiology, quantum holography, time-operator, torsion geometries, systems theory, vortices.

Quantum Biosystems **2016; 7 (1) : 107-174**

*Corresponding author: Diego L. Rapoport
Address: (Retiring from) Departamento de Ciencia y Tecnologia, Universidad Nacional de Quilmes, Bernal, Buenos Aires, Argentina.
e-mail: diego.rapoport@gmail.com

5. The non-orientable topologies of bioinformatics and the topological algorithm of generation of the Genetic Code

Returning to the logical-numerical representation of the Klein Bottle logic, consider the figure 1.III.

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, different to the one introduced in Rapoport (2011a), from which the non-commutative Matrix Logic is derived (Stern, 2000).

The latter has quantum, fuzzy and Boolean logics as subcases.

We notice that **i** and **j** are the *imaginary time-waves* (Kauffman, 1978, 1987; Hellerstein, 2010) that appeared as imaginary logical values in the Calculus of Distinctions due to Spencer-Brown (Spencer-Brown, 1969); we here see explicitly their association with the Klein Bottle self-penetration.

These two states and the negation operator produce four basic operators that generate Matrix Logic (Stern, 2000; Rapoport, 2011a). These imaginary time-waves are in-built Cantor's Diagonal Method (Hellerstein, 2010; Zenkin, 2000).

These states are associated to the perceptual depth variable of self-penetration, associated to time (Rapoport, 2011a, 2011b, 2011c).

A reduced 3-state logic was posited in the theory of autopoiesis –etymologically, self-creation- of living systems due to Varela (1979), 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**.

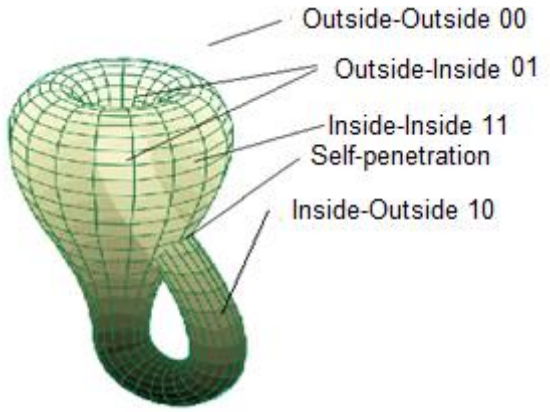

Figure 1.III: The Klein Bottle Logic, and its four states.in which we have identified four states by assigning 0 with Outside, 1 with Inside, so that the states are: Outside-Outside, which we write as 00, the Inside-Inside, 11, and two transitional states arising from self-penetration, Outside-Inside, 01, and Inside-Outside; reproduced from background image by Gnuplot 4.0 (CC BY-SA 3.0; author Tttrung; https://en.wikipedia.org/wiki/Klein_bottle#/media/File:Klein_bottle.svg); modified from (Rapoport, 2011b). 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.

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 (Rapoport, 2011a, 2011b, 2011c, 2011d, 2012, 2014a, 2014b).

Yet, autopoiesis may lead to the self-organization of global neural networks, producing an holographic-like memory related to the Golden Ratio (Perez, 2009, 2013).

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.

Later on, we shall motivate this choice in terms of three subalphabets which codify for different chemical symmetrical aspects, as first produced by Petoukhov (1999) and still with the 2x2 Hadamard matrix representation of the Klein Bottle. So we follow a topological 4-state logic approach (Rapoport, 2011c), which may be represented as a combinatoric-algebraic approach, originally proposed by Petoukhov (1999) and Petoukhov & He (2010; He and Petoukhov, 2011) by considering the 2x2 matrix/table which we denote as [C,A;T,G], or still, P(1).

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

Figure 2.III: 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 (Rapoport 2011c). Notice that the usual codon-anticodon pairing rule of C with G, identifies Outside-Outside and Inside-Inside, while the pairing of A with T (U) transcribes Outside-Inside with Inside-Outside, and the converse. The latter pairing does not remove the non-dual intermediary states while still transcribing Outside-Outside with Inside-Inside, and the converse (0 and 1 are not equal). None of these operations are possible in terms of the dualistic interpretation of CONTAIN.

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 Rapoport (2011b) 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 (Ycas, 1979) introduced in the algebraic-combinatorial framework (Petoukhov and He 2010, He and Petoukhov, 2011, Petoukhov, 2012), in terms of pairs of attributes-antiattributes, described succintly as topological identifications in Fig. 5.III below; these are the subalphabets:

Subalphabet No.1: 0 codes for pyrimidines (one ring in a molecule), 1 codes 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 the same division is given by the attributes "keto"or "amino" , so that 0 stands for a letter with amino-mutating property (amino), 1 a letter without it (keto), C= A = 0, G = 1=U/T.

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.

The latter is a codification of Chargaff's rule, either for single or double stranded DNA, as we shall further elaborate in the following.

These distinctions introduces further *multivaluedness* into 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 *multi-valuedness 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 version of Fig. 3.II.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*.

Recalling our previous discussions on the coexistence of orientable and non-orientable topologies for molecules (Stapien, 2012), 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), GP(1)] -which we write as a table or matrix produced by left-to-right juxtaposition.

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

Figure 3.III. Self-referential Kronecker-product recursion on the Klein Bottle of fig.2.III to produce the matrix P(2), represented as a table, consisting in the pairs of genetic letters and their binary representation, and as a concatenation of topo-logical states. with the binary numbering their columns and rows on the base of the binary sub-alphabets № 1 and № 2, respectively. from Figure 5.III below.

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)]. The result is the 8 times 8 square matrix of fig. 4.III.

In fig. 4.III 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 aminoacids 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 011010, where the first three digits 011 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. (Notice that all triplets of the same column possess the same binary number, which is utilized as the general number of this column correspondingly and the last three digits 011 are likewise constant for the respective row).

CCC (0) **000000** **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**
CCU(8) 001000 Pro	CCG(9) 001001 Pro	CAT(10) 001010 His	CAG(11) 001011 Gln	ACT(12) 001100 Thr	ACG(13) 001101 Thr	AAT(14) 001110 Asn	AAG(15) 001111 Lys
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
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
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
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
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
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 4.III (Modified from Petoukhov and He 2010). **Three-fold self-referential iteration of table in fig.2.III** . 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.The most relevant property of these Kronecker matrices starting already with the Klein Bottle matrix of fig.2.III, is the vertical periodicity of the matrix elements from the viewpoint of the binary sub-alphabet № 1 and the horizontal periodicity of the matrix elements from the viewpoint of the binary sub-alphabet № 2, with an ensuing X-cross symmetry already produced by the Klein Bottle represented as in fig. 2.III; more of this below. The first (alternativey last) three digits correspond to the No.1 (alternatively No.2) subalphabet. Each triplet is produced by a left horizontal rows No1 three numbers concatenated with the Subalphabet No.2 three vertical digits.The genomatrix thus produced provides the digital representation of the 64 hexagrams of the I Ching (Book of Change) (Petoukhov, 1999; Petoukhov & He, 2010).

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 53; or still, TCC which is 32, paired with AGG, which is 31, both adding to 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. 5.III below, and correspond to the mutual transcriptions of Outside-Outside/ Inside-Inside, and of the time waves Outside-

Inside/Inside-Outside, and they corres-pond 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 (Petoukhov and He, 2010; He and Petoukhov, 2011), yet which beg for topological interpretations, which we shall realize next. Remarkably, as observed by Petoukhov (1999) this matrix has a millenary history, which was retrieved by Leibniz in his (re)discovery of binary numbers and the Book of Changes, I-Ching.

Let us examine the symmetries of this genomatrix.

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. 5.III below. We note that the columns correspond to the classical octets reflecting biochemical properties of elements of the Genetic Code (Ycas, 1969).

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 180º 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. 8.III 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.

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.2.III.

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 due to Petoukhov and He; these topologies apply as well to the codification of the sequences of n letters by 2n digits.

Figures 5.III (left) & **6.III** (right), respectively): **Alphabets of the Genetic Code, and DNA.** Left, in fig. **5.III** modified from Petoukhov and He (2010) the lines stand for transcription and the subalphabet by which each operates is indicated in the legends; 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. 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. Right: Chemical structure of DNA, with coloured label identifying the four bases as well as the phosphate and deoxyribose components of the backbone (Madprime; CC BY-SA 3.0 ; File:DNA chemical structure.svg; Wikipedia).

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 (Stergachis, 2013).

In biosemiotics this plurality of co-existing codes as described for DNA, is raised to the status of a principle " which states that any text, any sign, any semiosis assumes the co-existence of several codes, of many codes… meaning is plurality" (Kull, 2007).

This transcends the mere existence of analogical and digital codes, here the former codified in terms of the latter. Upon introducing the three subalphabets and the genomatrix, Petoukhov put it as:

> *"… the genetic text appears as a bunch of parallel texts in three different languages, and genetic sequences have a property of poly-languages. This property was missed earlier from consideration. The sense of the genetic message, probably, is enclosed in an interlacing or simultaneous use of these multilingual texts."* (Petoukhov, 1999).

Indeed, it is known that *"…nucletotide sequences carry genetic information of many kinds, not just instructions for protein synthesis"* (Trifonov, 1989).

Thus there exist several codes, which are degenerate, and such that some nucleotides belong to several messages simultaneously.

Indeed, polysemics appears to be the case of genomic sequences, and they appear as tandemly organized repeats usually in the protein non-coding sequences.

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 (Bonchev and Rouvray, 2010; Flapan, 2010; Herge 2006, Rzepa 2004; Sokolov 1973) which we claimed to be essential to cell biology and to embryological development, and a fortiori, to evolution (Rapoport, 2011c, 2014).

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-adden-dums.

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 (Burdick, 1971).

Yet to our knowledge, this model has no similar one in the topological studies of DNA (Bates and Maxwell, 2005; Flapan, 2010; Swigon, 2009) nor such topological models of bioinformatics appear to exist, to the best knowledge of this author, but for networks models (Mezey, 1993), which in the case of proteins led to identify their Klein Bottle and torus glued topologies (Penner, 2011).

A very important issue is that the HyperKlein Bottle structure of genomes and the process of foldings through jumps which we shall relate to transposons, as an heterarchical dynamical structure, it is essentially interactive with the environment, which appears as a polycontexture, rather than the single contexture which "environ" (viz., enclosed) suggests.

This is in accordance with the view that a genome is not merely a blueprint to the effect of replicating an organism, but is so in relation with the environment: *"An organism's DNA thus is not only a "book" about the organism, but is also a book about the environment it lives in, including the species it co-evolves with"* (Adami, 2000).

Thus, the environment is already codified in the HyperKlein Bottle genomic codification, rather than the latter being a contextual-free structure: in-formation is never contextual-free, but in the case of an undetermined context, in which it is only entropy (Adami, 2002).

In other words, the primal nature of in-formation is such that it mandates a context for its realization as meaning.

But rather than the context being Exteriority, as would be in a dualistic logophysics, it is abstractly and concretely embodied as the dynamics of folding represented by taking ever-higher Kronecker self-products of the original Klein Bottle codification.

This will reappear upon discussing evolution,further below.

Furthermore, the plurality of subalphabets incorporated into this structure indicates that "meaning" may, in principle, be realized in any of them, with novelty being potentially the case enacted through any of them, and still acting together.

5.1 The Shape of Molecules and the Geometrical and Topological Paradigms of Chemistry

These findings ascribe to the unifying paradigm for chemistry (Bonchev and Rouvray, 2010; Flapan, 2010; Herges, 2006; Rzepa 2004; Sokolov, 1973).

This approach led to the 2016 Nobel award in Chemistry to Jean-Pierre Sauvage, Sir J. Fraser Stoddart and Bernard L. Feringa *"for the design and synthesis of molecular machines"*. These developments were initiated in 1983 by Sauvage by linking two ring-shaped molecules together to form a chain, called a catenane, followed by the synthesis of a rotaxane and of more complex molecular motors (Royal Academy of Science, 2016). In the considerations for granting this award it was stated that "…we are at the dawn of a new industrial revolution of the twenty-first century".

The basic principle is that of topological mechanical entanglement rather than the usual chemical bonding which produces space-shifts of the geometrical configurations, which may well be reversible.

So a plurality of shapes of the molecular arrangement for a molecule is the case, a kind of metamorphoses indeed.

More generally this appears to be the case of certain bacteria and viruses, and is known as a pleomorphism, where some bacteria or virions alter their shape or size in response to environmental conditions (McLaughlin, 2002).

These multiplicity of identity is the signature of a non-dual logophysics, see note no. 3, Part I .

This novel paradigm claims that it the *topology* of molecules, rather than their geometrical configurations, what characterizes their stereochemical configuration, which we have suggested to be crucial to allosterics, cell biology and embryological differentiation as already discussed.

This is also the case as it appears in the formation of clathrates associated to endohedral C60fullerenes (Chaplin, 2011; Dodziuk,2011).

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 (Sokolov, 1973).

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 (Mezey, 1993).

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, is based on 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, in highlighting that *"molecular shape is the shape of the electron distribution of the molecule"* (Sokolov, 1973).

While the hybrid model served as long as no external fields to the molecule are considered, it fails when, say, electromagnetic fields are applied (Boeyens, 2005; Mezey, 1993).

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 materialistic 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"* (Boeyens, 2005); in particular, this applies to DNA and RNA.

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 (Bonchev and Rouvray, 2010; Flapan, 2010; Mislow, 1999; Forgan, 2011, Rzepa 2004).

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. Indeed, upon considering proteins as a combinatorial object represented in terms of the loci of the backbone atoms and the hydrogen bonds, it follows their identification 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 (Penner, 2011).

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 basic chemoinformatic descriptors of molecules conceived as topological networks (Todeschini and Consonni, 2000).

As well, a model of allosterics in terms of this interchanging of Inside and Outside was proposed by Sokolov (1973) and by the author as the basis for biological development and differentiation and its relation to the genomic matrix as above (Rapoport, 2011c, 2014).

6. The Chargaff rules and non-orientability

The present findings are consistent with the so-called Chargaff rules, yet with a 180° 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 (Chargaff, 1952). It is this the rule by which the subalphabet 3 is usually introduced, following Watson and Crick (Suzuki and Griffiths, 1976).

They 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 (Rodley, 1995), 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 (Outside-Outside) and G (Inside-Inside) interchange, and so do T (Inside-Outside) with A (Outside-Inside), for which a quantitative identity of frequencies, is a prerequisite if symbolization is to be meaningful and thus effective.

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 (Bansal 1993, Rich 1993).

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 (Mitchell and Bridge, 2006).

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. 2.III & 5.III.

Thus they are basic to the 2:1 harmonics of the Klein Bottle Logic generation of the Genetic Code, which we have 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 (Forsdyke and Bell, 2004).

Originally, the 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 (Karkas, 1968; Prabhu, 1993).

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 tri-nucleotide 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 (Forsdyke 2011).

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, Forsdyke and Bell conclude: *"Entire genes, or entire genomes where gene orientation is not considered, are not appropriate controls"* (Forsdyke and Bell, 2004).

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, which should have elicited a cognitive dissociation, if anything!

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 (Kong, 2009).

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) = $\mathbf{C}\,a_1\,\mathbf{C}\,a_2\,...\mathbf{C}\,a_n$ is the complement of w, with **C**(T)= A, **C**(A)= T, **C**(C) = G and **C**(G) = C, the basis pairing; and finally **C**(**R**(w)) = $\mathbf{C}\,a_n\,\mathbf{C}\,a_{n-1}...\mathbf{C}\,a_1$ is the reverse complement of w, which still is equal to **R**(**C**(w)). Thus, **fr** (w)= **fr** (**C**(**R**(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"* (Albrecht-Buehler, 2006).

Yet, alike the genomatrix we have just constructed, it appears to be universal, a metagenomic symmetry (Albrecht-Buehler, 2007).

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 (Albrecht-Buehler, 2007).

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 (Forsdyke and Bell, 2004).

As observed by Ohno: *"All DNA base sequences, regardless of their origins or functions (coding versus non-coding) are messages written in palindromic verses"* (Ohno, 1991).

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 comments:

> *"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)"* (Forsdyke, 2011).

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 in (Petoukhov and He, 2010; He and Petoukhov, 2011).

Originally CSPR was conceived as being a resultant of "mutational biases"; yet, quoting (van Noort, 2003) 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"* (Forsdyke, 2011).

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 (Stern, 2001) associated to the Klein Bottle Logic (Rapoport, 2011a), and in the Shnoll effect where random processes appear to have palindromic histograms (Shnoll 2012, 2014).

The former case resembles Spinoza's conception of the *conatus*, an innate inclination of a thing to continue to exist and enhance itself¨ (Spinoza, 2005).

Rather than this selection operating agency being exterior, it is built-in as the

usual operations on the Genetic Code itself.

The latter 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 (Jockusch and Dress 2003; Isaeva, 2014, Maresin and Presnov, 1985; Rapoport, 2011c, 2014a, 2014b).

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 (Burdick, 1971) 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 (Benham, 1995).

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 (Yoshikazu and Okazaki, 1975; Yudelvich, 1978).

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 (Han, 2010; Tørring, 2011).

Indeed, the nanoMöbius 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 (Stern 2001; Rapoport, 2011a), 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 –as already discussed in Part I, 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 (Annett, 1985) and visual hemilateral synchronization (Rapoport, 2010b, 2013), or still the cortical homunculus (Rapoport, 2013).

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 (mtDNA); 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" (Biegeleisen 2002; Stettler,1979).

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 (Prunell 1998, Central Dogma for Biology); see note no. 21.

Although enzyme systems adequate for this task have long since been found and characterized, however there have 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 proposed as theoretical only, and have been largely unaccompanied by experimental evidence to support their applicability to native DNA from living systems.

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 (Biegeleisen, 2002).

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"* (Sasisekharan, 1978) 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".

Thus, 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 late response to Crick's assessment of the DH and SBS (Crick, 1979) 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". (Rodley, 1995).

As mentioned before, viral nucleosomes and bacterial genomes show non-orientability in their closed loops architecture (Prunell, 1998).

Yet, as Burdick had noticed, it is not the case of a circular DNA but a Möbius strip instead (Burdick, 1971), 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 (Swigon, 2009).

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 (Goriely and Tabor, 1997; Goriely, 2001, 2008).

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

There is another Hyper Klein Bottle fractal-like structure for the Genetic Code, introduced in (Petoukhov and He, 2010; He and Petoukhov, 2011) that is produced departing from another matrix representation for the Klein Bottle, as introduced in Matrix Logic (Rapoport, 2011 a; Stern, 2001).

Namely consider the Hadamard 2x2 matrix H(1) =[C,A;T,G] = [+1,+ 1;-1,+ 1], and H(2) and H(3), the 2 and 3-times tensor self-product of H, which are given by the 4x4 and 8x8 matrices respectively.

$$H(2) = \begin{bmatrix} H(1) & H(1) \\ -H(1) & H(1) \end{bmatrix}, \quad H(3) = \begin{bmatrix} H(2) & H(2) \\ -H(2) & H(2) \end{bmatrix}$$

The rationale for this choice of the representation for the first genomatrix H(1) , introduced in Petoukhov (1999) is as follows: On the one hand, and in contrast with C,A and G, T is the single base that in the transformation of DNA to RNA, transforms into U.

Furthermore, T (and U) are the single bases which do not have the amino group, NH2, which is functionally important.

To represent this asymmetry, Petoukhov chose to represent them as C= A= G=+1 and T (or U) as -1. Thus the 2x2 genomatrix [C,A;T,G] originally introduced in terms of the digital representation of the positional states of the Klein Bottle –see Fig. 1.III , becomes the Hadamard matrix H(1)= [+1,+1;-1,+1].

Indeed, while the subalphabet no. 3 pairing of C and G, Outside-Outside with Inside-Inside, respectively, both equal to +1, that of A= +1 Outside-Inside pairing with T (or U), Inside-Outside symbolized by -1 is the distinctive 180° twist of the Klein Bottle, altogether being the matrix representation of the topological identifycations that produce the Klein Bottle; see fig. 1C.

Thus, H(1) is the 2x2 (Hadamard) matrix representation of the Klein Bottle representing the anticlockwise direction as 1, the clockwise direction as -1 of two of the opposite sides, as in fig. 2 c (the choice of which is arbitrary).

This matrix represents the metaform for synsymmetry, the dialectics of symmetry and asymmetry, as discussed in §1.1 of Part I.

Instead of a positional states representation, we have now indicated a representation which codifies for the non-orientability and ultimately, the self-penetration of the Klein Bottle, doing away with positional value.

The former representation replaced analogic information by digital information; the latter represents in antipodal manner the non-orientability.

Indeed, while the subalphabet no. 3 pairing of C and G, Outside-Outside with Inside-Inside, respectively, both equal to +1, that of A= +1 Outside-Inside pairing with T (or U), i.e. Inside-Outside, symbollized by -1, is the distinctive 180° degrees twist of the Klein Bottle, altoge-ther being the matrix representation of the topological identifications that produce the Klein Bottle as per Fig. 1.II.C.

This is quite remarkable all by itself, since the already alluded uniqueness of T

(or U) becomes clearly identifiable as the very reverse of direction which upon the topological identification of the two opposite sides having the opposite direction, produces the non-orientability and thus the non-dual logophysics.

Now, it is possible to transform the genomatrix P(3) into a matrix whose elements are either +1 or -1, by applying the former codifications to each triplet, by multiplying the three letters of a a triplet (Petoukhov, 2016). Say GAT (or GAU) is codified as (+1).(+1).(-1)= -1, or CTT (or CUU) by (+1).(-1).(-1) = +1.

Thus, the eight octets of P(3) given by the eight rows can be represented as vectors of eight components given by +1 and -1.

This matrix is H(3), the 3-fold tensor (Kronecker) product of the matrix representation of the Klein Bottle, H(1), based on the topological identifications which produce its non-orientability.

Rows of Hadamard matrices appear in the theory of digital communication, in which they are named as Hadamard (or Walsh) functions.

These Walsh functions are used in the transmission of data from several space missions to planets in the Solar System precisely due to their noise-immunity.

They are represented in terms of the ±1 values taken by the Rademacher functions $r_n = sign(\sin(2^n \pi t))$,n=1,2,....

Indeed, in the case of the 8x8 genomatrix, its 8 rows of ∓ 1 generates an orthonormal system for an 8-dimensional space (Petoukhov, 2016).

Completeness of the system of 8 Walsh functions means that any 8-dimensional vector, say given by a row of the Hadamard representation can be represented as their superposition (i.e., decomposed on their base).

A basic advantage of this representtation in communication systems is that their computer simulation is much simpler than the usual Fourier analysis and still the spectral analysis can be carried out based upon the operation of addition and substraction of elementary mathematics, as observed in Petoukhov (1999), who further developed the relation between genomatrices, patterns as in the theory of automata and the mathematics of digital communication.

However, the basic relation we believe to be highly remarkable is that of Hadamard matrices as algebraic representations of self-reference which is basic to the studies of cognition, and further with quantum mechanics through Matrix Logic and still quantum computation. We turn to this now.

H(1) is a fundamental matrix in the setting of the Matrix Logic form (Stern, 2001; Rapoport, 2011a) of the Klein Bottle Logic, which allows to translate cognitive statements to quantum mechanical statements.

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. To resume: *Hadamard matrices are matrix representations of self-reference associated to the Klein Bottle*.

Indeed, normalized Hadamard (2x2)-matrices are matrices of rotation on 45^0 or 135^0 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, they are the operators intertransforming classical states and superposition topological entanglement states (Rapoport, 2011a; Stern, 2001).

Thus, they are more basic than quantum entanglement, while they are still crucial to Quantum Computation (Nielsen and Chuang, 2011).

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 of Hadamard matrices.

In the first place they 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, in particular to the symmetries of genomes, and to their noise immunity.

Returning to the Klein Bottle –as in Fig. 2.III- from which genomes can be recursively constructed and digitally codified, we note that it embodies the subalphabet no.3, or still, the Chargaff rule either for one or two strands.

Thus, in principle the construction of genomatrices as recursively produced from Fig. 1.III can be carried out using the standard matrix representation of the Klein bottle surface as a Hadamard matrix, from which intricate black-and-white patterns appear.

Genomatrices definitively have extremely rich symmetry properties even under permutations.

Yet they are all referrable to Hadamard matrices (and thus to the Klein Bottle) and to a single algebra, the Yin-Yang algebra already alluded (Petoukhov, 2008).

This is done through the algorithm already discussed based on the codification of the four letters in terms of the non-orientability of the Klein Bottle, with T (or U) embodying the 180º twist. This transforms P(3) into H(3) and P(n) to H(n), the $2^n x 2^n$ Hadamard matrix for arbitrary positive integer n (Petoukhov and He, 2010; He and Petoukhov, 2011).

This minimalistic topological representation for the Genetic Code appears to be related to its perhaps unique resistance to environmental hazards.

Indeed, Hadamard matrices are used widely in the theory of coding, being crucial to the robustness of transfer of digital information with regards to environmental noise (Ahmed and Rao, 1975).

Thus the Klein Bottle Logic not only provides the basic codification for the genomatrices, but also the digital representtation in terms of discrete signals; they further provide for the robustness of the Genetic Code with regards to noise and a fortiori, that of embryological development (Rapoport, 2011c, 2014).

> *"In the case of genetic information, DNA can be considered as a signal transmitter, which should send out genetic messages in such form which provides a reliable and qualitative transfer of genetic information. Ribosomes (or some other participants of genetic systems), which receive nucleotide sequences to create proteins, can be considered as a remote receiver by analogy with the scheme of digital communication"* (Petoukhov, 1999).

Using the previous codification in terms of +1 for C,A and G, -1 for T(U) black and white patterns can be created which can still be represented in terms of Rademacher functions (Petoukhov, 2016).

Using the data of BUILD34 provided by Perez (2009, 2010), it was proved that the percentage difference between the blocks in white and the blocks in black is of the order of 0.1% (Petoukhov, 2012a).

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/φ (Petoukhov and He, 2010).

As a result, we obtain a chain with n links, where each link is φ or 1/φ; 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 (the logical disjunction operator, ∨) and NAND (the negation of the logical conjunction, ∧) 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)] respectively, 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/φ;φ,1/φ].

For further studies of the numerics of genomes and their "quantum-like" structures see Negadi (2011, 2014), Petoukhov and He (2010) and Rakočević (2011); see note no. 22.

The importance of this with regards to genomes operating in terms of harmonics begs to be highlighted.

Petoukhov remarked that the previously introduced Walsh functions as representatives of nucleotide code letters (actually codes for the Klein Bottle, either of non-orientability or positional values) are such that, *"each of the 8 functions of the complete Walsh system is the diagonal of one of the genetic (8x8)-matrices of the diagonal type, i.e., a spectrum of eigenvalues of an oscillation system with 8 degrees of freedom"* (Petoukhov, 2016).

We recall that quantum mechanics surged in terms of eigenvalues and eigenvectors of matrix operators; they reappear in Matrix Logic and in the genomic matrices constructed from the Klein Bottle, equally as a system of resonances.

The Golden Mean which arises from the five-fold torsion geometry plays a crucial role both in organismic development as well as in cognition, as already discussed. Furthermore, the Klein Bottle logophysics plays a double role for genomics.

The Klein Bottle as a primeval resonance and the system of resonances that it generates in genomes, embodies both information actually 'informatics of communication' (Petoukhov, 2016) and the energetics of a coupled non-linear oscillatory system, which several authors have modellized as soliton solutions of non-linear Schrödinger equations (Davydov,1981; Yakushevich, 2004) based on torsion geometries (Rapoport,2007a,b).

The so-called Yin-Yang algebras of hyper-complex numbers associated to the genomatrices and their symmetries (Petoukhov, 1999; Petoukhov and He, 2010) may serve as the algebraic elements for biocomputing based on the (Hyper) Klein Logic(s).

Petoukhov and He further claim that the adequacy of this algebraic approach for biocomputation, is especially relevant in relation with physiological cycles (Petoukhov and He, 2010).

Petoukhov called them as 'algebras for thought', from the consideration of the relation between the genomatrix P(3) and the I-Ching.

Yet, while a digital representation suggests Boolean logic and its tensor products, the non-dual basis of them as presented suggest otherwise: their role as algebras of thought associated to heterarchies as non-dual Hyper Klein Bottles, particularly in view of the non-commutativity of these algebras, and of McCulloch's early findings on the non-transitivity of neural networks (McCulloch, 1945).

As already mentioned in §1, heterarchies are necessary for higher-order learning (Kaehr and von Goldammer, 1988, 1989); this is relevant to the idea of ecological systems operating as a connected neural network with learning capabilities (Power, 2015).

Yet, the bottomline of this is uniquely identified as the non-commutative product of matrices, be that quantum or cognitive operators.

This non-commutativity produces the torsion of cognitive space as embodied in the (+1 , -1) non- orientability of the Klein Bottle as discussed in note no. 11; non-commutativity has been identified as the very core of quantum mechanics and cognition (Khrennikov, 2010), as early suggested by Musès (1977).

8. 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, is the case 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; the former is known as the *second- parity* Chargaff rule.

The studies of Karkas (1968) 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.

Takeda and Nakahara (2013) 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 establish-ing the validity of Chargaff's second parity rule and still its validity for the genome of *E. coli* and *H. sapiens*.

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 (1993) 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 (Qi and Cuticchia, 1993).

It follows from Chargaff's second-parity rule in single stranded DNA, usually specified as the GC-rule (**fr**(GC) tends to be uniform and species specific) that, within a species, oligonucleotides of the same **fr**(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 180° 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 180° 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 180° 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 180° 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 (Shih, 2004).

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 180° 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 fig. 6.III.

Suppose we know cut this double helix backward complement loosening the couplings which then rotate 180° to produce an "inverted repeat" on a single strand, 5'TAACGTACGTACnnGTACGTACGTTA3', to differentiate from the "directed repeat", say 5´**TTACG**nnTTACG3´, or 3´**AATGC**nnAATGC 5´.

Here nn denotes any number of intermediary 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 upper-left and bottom-right elements (red types on I and II, or I' and II'), and upper-right with bottom-left (blue types) are identified as the X-cross identification of the Möbius strip or the Klein Bottle (see Fig. 1.II) the mirror representation which now appears in either "side" or as on a double strand, made of the pairing of I & II.

I:
5'TAACGTACGTACnnnGTACGTACGT3',
II:
3'TTGCATGCATGnnnCATGCATGCAAT5'.
We may rewrite this as
I':
5'$\vec{X}$nn$\vec{Y}$3' with $\vec{X}$= TAACGTACGTAC, $\vec{Y}$ = GTACGTACGT
II': 3'$\overleftarrow{Y}$nn$\overleftarrow{X}$ 5' with $\overleftarrow{X}$ and $\overleftarrow{Y}$ the 180° reverse of $\vec{X}$ and $\vec{Y}$, respectively.

Here, we have used two different typos to indicate the topological identification of each kind, blue (red) with blue (red).

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

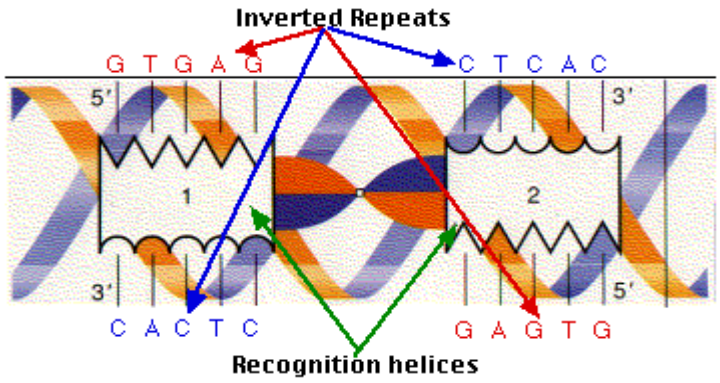

Figure 7.III. Illustration of the inverted repeats with the X-cross topology of the Möbius strip and Klein Bottle, expressed as X-crossed palindromes on deleting the intermediary nucleotides, and still the no.3 subalphabet of the KBL introduced above. Figure from Kimball's Biology Pages © John W. Kimball, CC BY 3.0; http://biology-pages.info.

Indeed, the juxtaposition $\vec{X}\,nnnn\,\tilde{X}$ is TAACGTACGTACnnnnCATGCATGCAAT, and $\vec{Y}\,nnnn\,\tilde{Y}$ 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 180° 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 both noncoding areas and coding areas (Ramy, 2010); see note no. 22.

Particularly, the so-called Class II transposons consist of DNA sections that move directly from place to place.

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.

Therefore, we may note in further accounting for the Klein Bottle X-metapattern, we have provided in our presentation a logophysics for the shape of DNA that accounts for the elements that led to postulate the DH model by *inference*, rather than derived from an *ontology*.

Furthermore, we can either understand the shapes of genome as essentially two *dynamical metapatterns* 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 (Burdick, 1971) 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.23.

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"* (Forsdyke, 2002).

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 (Bach).

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 (Stern, 2001; Rapoport, 2011a).

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 (Jürgen, 2003; Joyce and Orgel, 1993 ; Koonin, 2012; Koonin and Wolf, 2012).

Furthermore, the existence of palindromic secondary structures in single stranded RNA "are responsible for the stability and molecular recognition capabilities of RNA molecules (Garcia-Bellido, 1996).They correspond to emerging symmetries with profound biological implycations. It is precisely these secondary interactions of biological macromolecules (polypeptides and polynucleotides) that have frozen their structural symmetry (Garcia-Bellido, 1996).

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 (Rapoport, 2016).

Remarkably, this second-order cybernetics has been raised in terms of the Principle of Recursive Genome Function due to Pellionisz (2008, 2013).

Recursion is the name for the iteration of a function on itself, so it is a manifesttation of self-reference, and the basis for fractals and physics as a rewrite system (Rowlands, 2007), and crucial to an eigenform called the Self (Rapoport, 2011a).

We have generated the topology of genomes from the recursion of the Klein Bottle.

> *"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"* (Pellionisz, 2008).

For the relations with transposons patterns in genomes and their importance for changing genomic information by proteins see Fedorov (2011).

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" (Frankin and Vondrisk, 2011; Focossi, 2005; Koonin, 2012; Petsko 2000; Pevsner 2013).

The present approach is similar to the *partially nested* (thus actually HyperKlein Bottles) developmental systems discussed in the setting of System Biology 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 (Oyama, 2000, Jablonka and Lamb, 2005).

As discussed by Oyama, although unacknowledged as such, the CONTAIN image-schema with its dualistic divide of Outside (environment) and Inside (genome), while appropriate to the Central Dogma, it still disconsiders the participation of epigenetic processes in evolution (Oyama, 2000, Shapiro, 2011).

9. 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 (Perez, 2009).

For further discussion on this ancestor as a prokaryote or a virus (whose nucleosomes are Möbius strips) see Prunell (1998) and its role in non-adaptive evolution in the framework of comparative genomic see Koonin (2012).

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 (Perez 2009, 2010, 2013).

In this sense, these complex 180° 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 (Bohm and Hiley, 1990).

Yet, it was argued that the Klein Bottle logic integrates the implicate and explicate orders (Rapoport, 2011a).

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 highlight 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, it 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 (Perez, 2009).

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 glycerine 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"* (Perez, 2009).

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.

> *"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"* (Bohm, 1986);

We notice here the invocation of the image-schema CONTAIN; see Part I.

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 (Bohm and Hiley, 1980).

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 (Freund, 2010).

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 (Molinari, 2011).

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 (Rapoport 2009, 2010a); they still generate the nilpotent states of the Intelligence Code expressed in Matrix Logic (Rapoport, 2011d).

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 (Rapoport; 2010a, 2011d) and which themselves sustain the vortical patterns that generate the non-orientable shape of lightwaves (Fadeyeva, 2010; Ruane, 2015).

They still generate the non-dual logic which has quantum, fuzzy and boolean logic as particular cases (Stern, 2001) and the decomposition of the cognitive states of this non-dual logic as light states (Rapoport, 2009, 2010b, 2011d).

Yet, as discovered by Gariaev, DNA appears to produce holograms (Gariaev, 2001).

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 .

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 (Hiley and Pylkkänen, 1997), 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 (Bohm and Hiley, 1980; Bohm, 1986).

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 shows to be the case (Rapoport 2005, 2007a, 2007b, 2009, 2010a, 2010b, 2011d).

Particularly, vortices are the elementary motions of fluids (Rapoport, 2005a), the elementary dynamics of spacetime and quantum physics (Rapoport, 2005a, 2007a, 2007b, 2010a) and liquid crystals (Bouligand, 1978, 1999).

Already in the 19th century the naturalist Bell Pettigrew had noticed the universality of vortical motions in Nature (Bell Pettigrew, 1908).

D'Arcy Thompson picked out of this ubicuity only the spirals and further identified the Golden Spiral (Thompson, 1945).

Currently, they reappear as crucial to complexity, in the cybernetic epistemology of Morin, yet with no treatment of the non-orientable topology (Morin, 1992).

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 (Meinherich, 2008).

Yet, colonies of bacterial ciliates morph as dynamical chiral vortical structures which modify the ambient environment producing a second-order cybernetics, as an holonomous choreography as Bohm would have it (Ben Jacob, 2003).

Communicating through chemotaxis, these colonies appear to have a memory and primitive cognitive functions, making of them a primary example of "complexity" as associated to vortical structures, to be discussed below. Notably, Bell Pettrigrew early insisted in the importance of ciliates and their vortical motions to biotic processes (Bell Pettigrew, 1873, 1908).

Bohm noted that although an hologram conveys undivided wholeness, it is nevertheless static - not alike the swarming vortical colonies of ciliates with their remarkable integrality, formidable resilience and creative adaptability (Ben Jacob, 2003).

In Bohm's notion of order, laws represent invariant relationships between explicate entities and structures (see §1.2, Part I), 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 (Bohm, 1980); see note no.24.

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 in Rapoport (2011a), 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 self-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 to occur as spatial events; they do so even in *time*. This will turn to be crucial to the theory of evolution below.

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 already discussed this in terms of the basis for chemical topology and isomerism.

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.II in Part II.

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 for August Stern in his construction of Matrix Logic that contains quantum logic, fuzzy logic and classical dual logic (Stern, 2001), which further provides a matrix form for the Klein Bottle Logic (Rapoport 2011a).

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 (2009, 2010, 2013, 2015a), 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 (Gariaev, 1996).

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 (Levitation, 2013).

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 (Frohlich and Kremer, 1983).

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 (1995), 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 (Pollack, 2013).

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, elec-trons 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 (Pollack, 2013; Mae Won Ho, 2014); the ensuing separation of charges into segregated domains is a prerequisite for metabolism (Del Guidice, 1988).

In the case of superconductivity, the electrons in a pair are not necessarily close together; because the interaction is long range (1/1000 mm) so that the superconductor behaves as a giant quantum state, 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 (Frohlich and Kremer, 2003).

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 (Rowlands, 1983).

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 (Buszaki, 2011), and particularly, the multitwist Möbius strip architecture of the small-world cortical neuronal networks which are related to them (Wright, 2014).

Remarkably, EEGs are structured as a geometric series having the Golden Ratio for their ratio (Pletzer, 2011).

As discussed in Rapoport (2013), the torsion vortical geometries are unseparable of the five-fold symmetry which produces Φ, and ultimately, of the non-orientable topologies here introduced; torsion is the fifth side of a dislocated infinitesimal parallelogram.

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"* (Perez, 2009) (our translation from the original French version, capitals by the author).

In view of the universality of vortical motions, we return to genomes, a paradigmatical biological system that is organized as such.

10. Vortical motions, transposons and non-orientability

The transposon hypothesis is that introns originates from the transposons (Fedorov, 2003).

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 – as presented prior to Fig. 7.III and next below it;

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'....CACAATTCCCATGGGTTGTGGGAG...3'-----5' CTCCCACAACCCATGGGATTTGTG...3'

3'.....GTGTTAAGGGTACCCAACACCCTC....5' -----3'GAGGGTGTTGGGTACCTAACAC... 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 viceversa, as in I (I') & II (II').

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 which match quantitatively] pairs on the level of the whole human genome… we show that this law remains conserved regardless of individual genome SNP variability"* (Perez, 2009).

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 auto-evolution, 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"* (Lima de Faria, 2008).

Geneticists have tended to consider these rearrangements as random events, although randomness is an extremely elusive concept for mathematicians and physicists (Chaitin, 1999) if existent as a verifiable fact at all (Johansen 1991).

We recall that the Shnoll effect, i.e. the palindromic time series histograms of experiments usually deemed as random, such as spontaneous radioactive decay, places the ontology of randomness into existential question (Shnoll 2104).

As the physiologist and founding father of System Biology Denis Noble already noted upon discussing the central tenet of the Modern Synthesis –randomness of genetic mutations: *"randomness is contextual", meaning the non-independence of said randomness, "randomness with respect to what?"* (Noble, 2013).

And further quoting Shapiro:

> *"It is difficult (if not impossible) to find a genome change operator that is truly random in its action within the DNA of the cell where it works. All careful studies of mutagenesis find statistically significant non-random patterns of change, and genome sequence studies confirm distinct biases in location of different mobile genetic elements "* (Shapiro, 2011).

Following the identification of DNA sequences, namely 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" (Lima de Faria, 2008).

We shall later see how fine this modulation is.

There is another remarkable role of transposons as related to self-reference conceived as a principle of creation and recreation of structures.

It indicates their role as a kind of memory, which allows to reconstitute the whole from a part, as in holography.

Ciliates are unicellular protists, which are estimated to have arisen one billion years ago.

As already highlighted by Bell Pettigrew, their rotational motions are basic examples of rhythmic motions, which are essential to feeding and sensing of the environment by these organisms; he considered them to be the signature of life.

Transposons operate crucially in a computational process which allows for the reconstruction of whole from part, in viewing organisms not just in their life cycle but on their reproductive cycle (Kazazian, 2004).

Indeed, ciliates have a macronucleus whose DNA codes for proteins, and a micronucleus which is non-coding.

It is the latter micronucleus which upon replication of the organism builds a new coding macronucleus.

Thus it appears to be appropriate to state as above, that in ciliates transposons operate computationally to reconstitute the whole from the part.

Furthermore, this is operated through a recursive non-linear cybernetics.

The numerics for extending Prabhu and other researchers' findings of palindromes for large sequences of nucleotides to the whole human and chimpanzee single strand genomes was identified by Perez, by 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 (The Encode Project Consortium, 2003), when considered as a single strand architecture.

We can consider the dynamical genome as having for metaform 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 180° 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 (Betran, 2012; Larionov, 2008).

11. Transposons and Evolution

As for the biological function of non-orientable surfaces, which as we see should better be called bio-logical yet not restricted to biotic systems, 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 (Achaz, 2003).

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. 21.

It has been established that TEs catalyze different types of mutations, which have different potential impacts on genome structure, gene expression, and speciation.

They are genetic elements of a more general kind of DNA sequences transposable genetic elements (TEs) which may also move through an RNA interme-diation, the so called retrotransposons, al-so 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" (Fedoroff, 2012).

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"* (Fedoroff, 2012).

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 (Rapoport, 2013).

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 (Shapiro, 2011).

They also reflect the epigenetic response as well of development vis-à-vis environmental influence.

As such, they correspond to a phenolmenology 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" (Fedoroff, 2013).

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 "TEs 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"* (Fedoroff, 2012).

So TEs 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" (Fedoroff, 2013).

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 implycitly 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 (Rapoport, 2011a); see Part I.

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 (Fedoroff, 2013).

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."* (Ramy, 2010).

Thus, these 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 (Rich, 1993), the genomatrix provides a metaform which in principle applies to all genomic information and its digital coding.

We can perhaps think of it as a metapattern, as it appears in the pattern recognition of digital photographs of landscapes.

Indeed, 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 metapattern: the Klein Bottle (Carlsson 2008, 2009).

As already mentioned, 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 (Rapoport, 2013).

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 genomes, we are led 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. 24), 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.

12. The Numerical Evidence for the Non-orientability of Genomes

Let us return to the notion of the Klein Bottle as a metapattern of vision recognition, and its equivalent in the genome: the HyperKlein Bottle topology as a kind of a metapattern associated to the genomatrix of arbitrary sides 2^n, with n an integer, can be further elicited in the following sense.

The relation between the topologically paired elements of this matrix (when n=3) and that given below by the codon/mirror-codon, or still codon/reverse-complement-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, where the double arrow stands for the transformation of a codon into its mirror codon, 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, due to Perez.

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.

An 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 sequen-cing of the genome, Perez considered the 64 codons, grouped in terms of the three different frames of reading.

He further classified the 64 codons organized in terms of the codon/mirror codon already introduced, as the 180^o 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}; (Perez, 2009).

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 §3 of Part II, we consider them as lying as if identified along a Möbius strip, completing a whole octave, further producing a Klein Bottle; see Fig. 5.II.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 180° 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.

Frequencies (**fr**) of "Even" sorted codons, i.e. **fr**(A) > **fr**(T), **fr**(G) or **fr**(C)	Frequencies (**fr**) of "Odd" sorted reversed complement codons **fr**(T)> **fr**(A), **fr**(G) or **fr**(C)
1st **fr**(CGA) = 2085226	2nd **fr**(**CR**(CGA)) = **fr** (TCG) = 2087242
3rd **fr**(CGC) = 2244432	4th **fr**(**CR**(CGC)) = **fr**(TCG) = 2247440
5th **fr**(ACG) = 2372235	6th **fr**(**CR**(ACG)) = **fr**(CGT) = 2379612
7th **fr** (CGG) = 2604253	8th **fr**(**CR**(CGG)) = **fr**(CCG) = 2606672
9th **fr** (GAC) = 8938833	10th **fr**(**CR**(GAC)) = **fr**(GTC) = 8955434
11th **fr** (TAC) = 10755607	12th **fr** (**CR**(TAC)) = **fr**(GTA) = 10766854
13th **fr** (ACC) = 11007307	14th **fr**(**CR**(ACC)) = **fr**(GGT) = 11026602
15th **fr** (GGC) = 11258126	16th **fr**(**CR**(GGC))= **fr**(GCC) = 11268094
17th **fr** (CTA) = 12217331	18th **fr**(**CR**(CTA)) = **fr**(TAG) = 12240281
19th **fr** (CCC) = 12428986	20th **fr**(**CR**(CCC)) = **fr** (GGG) = 12446600
21st **fr**(ATC) = 12650299	22nd **fr**(**CR**(ATC)) = **fr** (GAT) = 12658530
23rd **fr**(AGC) = 12650299	24th **fr**(**CR**(AGC)) = **fr**(GCT) = 13252828
25th **fr**(GCA) = 13635427	26th **fr** (**CR**(GCA)) = **fr**(TGC) = 13649076
27th **fr**(AAC) = 13794251	28th **fr** (**CR**(AAC)) = **fr**(GTT) = 13852086
29th **fr**(CAC) = 14214421	30th **fr**(**CR**(CAC)) = **fr**(GTG) = 14252868
31st **fr**(TCC) = 14614789	32nd **fr**(**CR**(TCC)) = **fr** (GGA)= 14619310
QUARTILE 1: 158064247	QUARTILE 2: 158309529
FIRST PLUS SECOND QUARTILES: 316373776	

33rd **fr**(ACT) = 15251455	34th **fr**(**CR**(ACT)) = **fr**(AGT) = 15266057
35th **fr**(GAG) = 15939419	36th **fr**(**CR**(GAG)) = **fr**(CTC) = 15942742
37th **fr**(AGG) = 16810797	38th **fr**(**CR**(AGG)) = **fr**(CCT) = 16835177
39th **fr**(ATG) = 17409063	40th **fr**(**CR**(ATG)) = **fr**(CAT) = 17423117
41st **fr**(CCA) = 17444649	42nd **fr**(**CR**(CCA)) = **fr**(TGG) = 17480496
43rd **fr**(CAA) = 17927956	44th **fr**(**CR**(CAA)) = **fr**(TTG) = 18005020
45th **fr**(TGA) = 18562015	46th **fr**(**CR**(TGA)) = **fr**(TCA) = 18565027
47th **fr**(GAA) = 18678084	48th **fr**(**CR**(GAA)) = **fr**(TTC) = 18708048
49th **fr**(AAG) = 18894716	50th **fr**(**CR**(AAG)) = **fr**(CTT) = 18944797
51st **fr**(ACA) = 19073189	52nd **fr**(**CR**(ACA)) = **fr**(TGT) = 19152113

53rd **fr**(CAG) = 19176935	54th **fr**(**CR**(CAG)) = **fr**(CTG) = 19195946
55th **fr**(ATA) = 19548709	56th **fr**(**CR**(ATA)) = **fr**(TAT) = 19568343
57th **fr**(TAA) = 19721149	58th **fr**(**CR**(TAA)) = **fr**(TTA) = 19750578
59th **fr**(AGA) = 20948987	60st **fr**(**CR**(AGA)) = **fr**(TCT) = 20990387
61st **fr**(AAT) = 23634011	62nd **fr**(**CR**(AAT)) =**fr**(ATT) = 23669701
63rd **fr**(AAA) = 36381293	64th **fr**(**CR**(AAA)) =**fr**(TTT) = 36530115
QUARTILE 3: 315402427	QUARTILE 4: 316027664
THIRD PLUS FOURTH QUARTILES: 631430091.	

Figure 8.III (after (Perez 2009,2010)): Populations of the 64 codons of single stranded DNA -as in BUILD34- sorted in ascending order in the case of the first codons reading frame. Notice the matching numbers of codon and reversed-complement ("mirror", in Perez) 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 reverse-complement codon is matched to rather than paired as codons¨/anticodons, as already explained.

Furthermore, if we consider the ratio between the most frequent dominant codons/reversed-complement codons, given by quartiles 3 and 4, and the less frequent dominated pairs, given by the first and second quartiles, it is almost equal to 2. Indeed, the first and second quartiles, P3 + P4 is almost exactly twice as large as the population of the 32 least frequent quartiles P1 + P2. The exact ratio is: 631430091/316373776 = 1.995835745.

It is even a real "partition" of the whole human genome as shown in Fig. 8.III, 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.II.

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.

We denote:
P1= 158064247,
P2= 158309529,
P3= 315402427
P4 = 316027664,
then the following relations appear:

(P1+P3)/(P2 +P4) = 0.99816729≈ 1;
(P3+P4)/(P1 + P2)= 1.995835745 ≈2;
(P1+P2 +P3+P4)/P4 = 2.99911677;
(P1+P2+P3+P4)/P3= 3.00506206;
(P1+P2+P3+P4)/(P1 +P2) = 2.995835745≈3;
(P3+P4)/P1 = 3.994768602≈ 4;
(P2+P3+P4) / P1= 4.996320389 ≈ 5;
(P1+P2+P3+P4)/P1 = 5.996320389≈ 6,
as well as other harmonic ratios are likewise generated.

Thus, Perez showed the emergence of "integer numbers codes" connecting the four quartiles.

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 P4 as identified with those of P3, and the codons of P2 with those of P1 disposed as in Fig. 5.II and Fig. 8.III.

Actually we have one such association between P3 and P4, another one formed by P2 with those of P1, 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: P3:P4:P1:P2 = 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 (Kozinski, 1967).

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.II.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. 26.

We can think in this scheme of 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 (Rosen, 2008), which is maximal in the odd/even 1:1 unison relation.

These symmetries also extend to the atomic weights of the populations.

Furthermore several other octaves have been identified from the genomatrix of codons/mirror-codons, and their relative frequencies found to be related to the Golden Mean (Perez, 2009, 2010, 2013, 2015a).

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 (Petoukhov and He, 2010).

13. 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.

13.1 Holography, Semiosis 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 semiosis, a meaning construal of sign systems.

It is usually called biosemiotics (Barbieri, 2007).

Semiosis 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, as discussed already in note no.26.

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 semiosis. 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 (Pellionisz, 2008, Frankin and Vondrisk, 2011).

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 construal has been associated to self-reference (Merrell, 1997), and its metaform identified as the Klein Bottle (Rosen, 2004); in particular, biosemiotics has been associated to this metaform (Neumann, 2008).

The ultimate structure without which there can not exist any phenomenology at all, is provided by the photon. 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 (Rapoport, 2009).

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 (Morin, 1992).

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.

In other words, what appears to be the case of the active construal of perception as gestalts, this is already the case of genomes.

On the one hand they are largely responsible for the generation of the molecules needed by biological systems.

On the other, they have a crucial regulatory role, as embodied by the non-coding transposons.

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 (two parameters) 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 is coded in terms of harmonics which manifest through different physical fields, in the case of light beams, with *non-uniform polarization*; that is, the state of polarization is different at different points in the beam's cross-section.

Indeed, we have generated genomes departing from the Klein Bottle Logic as a system of harmonics upon taking the Kronecker (or tensor) self-product of this surface/logic, attributing to the four nucleotide code letters either the positional values or still to code for the non-orientability of the Klein Bottle, to later elicit the evidence that indeed several genomes already are embodiments of such systems.

Yet, the fact that the genomatrices so constructed can be rewritten in terms of the Kronecker self-product of Hadamard matrices, which are further related to a complete system of orthonormal Walsh functions, already indicates that *the*

mathematical digital coding system is such an harmonic system.

As Petoukhov puts it: *"...genetic texts are written in the language of resonances"* (Petoukhov,2016).

In particular, the coding for growth development in terms of these harmonics, which already Leonardo showed in the Vitruvius Man to be related to Φ (Ghyka, 1952) generates metrics and eigenvalues of curvatures as descriptors of the effects of foldings; they can also be encoded by these signals related to the genomatrices (Petoukhov, 2016).

For the material carrier of the actual vibrations that synchronize the organisms several authors have pointed out to the ordered water domains (Del Guidice, 2013; Pollack, 2013) which we have already identified its non-orientable topology.

Furthermore, liquid crystal collagen which is abundant in the connective tissue of animals and is crucial for body integration may also develop non-orientable configurations as already discussed.

So, whatever the nature of the physical field, be that vortical Mobius strip sound or light waves, the in-formation is encoded/decoded in terms of the codon/mirror-codons harmonics as in Fig. 8.III, and the in-formation harmonics provided by the ∓1 coding of the genomatrix.

We remark that it is supported by the ordered water domains and in animals by the collagen present in connective tissue which is a transboundary extension of the cell's cytoskeleton, a boundary itself which we have claimed to operate changing from orientability to non-orientability, locally (Rapoport, 2011c).

As a physical embodiment of the holographic in-formation, 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- which bear the in-formation; more of this below.

In particular, this is the case , in principle, of quantum holography, which operates with circularly polarized wave functions. It was suggested by Gariaev, that DNA's signal operations are through quantum holography (Gariaev, 1994, 2001; Berezin, 1996), which is at the basis of the contemporary technologies of imaging such as magnetic resonance tomography (Schempp, 1992).

Yet, while these imaging technologies operate with a singularity free field (Binz , 2003), 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 (Fadeyeva , 2010).

These shapes, which we have just introduced in our discusson of holography, can be, in principle. multitwisted Möbius strips (Freund, 2010; Ruane, 2015) , as it has recently been shown to be the case for the propagation of optical vortices on a liquid crystal (Bauer, 2015).

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 (Rapoport; 2013).

Thirdly, the Klein Bottle topology of the retinotopic and the somatotopic mappings already discussed (Schwartz, 1977a, 1977b; Werner, 1970; Werner and Whitsel, 1968; Swindale, 1996; Tanaka, 1995, 1997) 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 (Wright, 2014) which is claimed to be the basis of the sense of self-hood (Buszaki, 2011).

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 (Pollack, 2013).

The size of DNA that have been shown to emit weak electromagnetic signals is of the order up to several kilo-bases (Montagnier 2015).

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 (Gariaev, 1994, 1996; Berezin, 1996).

More recently, through other techniques, this was rediscovered by Luc Montaigner and collaborators (2011, 2015).

Solitons are ultrastable waves.

As any non-linear system, their initial conditions are incorporated into their evolution for which vortical discontinuities and non-orientable at that are inevitable; see Part I.

As non-linear systems are driven to chaos, which actually is their generic evolution (Lin, 2002; Wu and Lin, 2002), to further perform a transformation to a non-orientable state by which they reoriginate in a novel cycle (Rapoport, 2013) as already discussed in Part I relative to fig. 2.I.

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, as quoted above. 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 incurporated during evolution, and yet the overall harmonics is preserved.

Still, there is the physical level of information 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.

13.2 Evolution, Complexity and Palindromes

The previous discussion in §13 is a far cry from to the imperating quantitative notion of in-formation (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 usual conception, complexity is a measure of the *irreducible* number of bits associated to a message, which disposes of redundance.

Here, the notion of algorithmic complexity developed by Chaitin after Kolmogorov is the measure (Chaitin, 1987, 1989, 1999): the Kolmogorov-Chaitin 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 (Koonin, 2012; Neelekanta , 2003).

Yet, a standing seemingly paradox is that quantity (genome size) seems not to embody quality.

Indeed, the largest known genome is Amoeba dubia with about 670 billion base pairs, over 200 times larger than in humans.

The largest known vertebrate genome is the African Marbled lungfish with about 130 billion base pairs, forty times larger than in humans.

This is known as the C-paradox, namely the discordance between genomic size and organismic complexity (Gregory, 2005).

The proposed solution was related to:

> *"the nature of non-coding DNA, which even in the first decade after its discovery was variously described as being 'junk' (that is, now functionless gene copies)..., or 'pseudogenes', as serving a structural (nucleoskeletal) function.., as consisting entirely of introns, and of representing strictly 'selfish' elements..."* (Gregory, 2005).

Actually gene loss which can be produced by the mobilization of a transposable element or through a sudden mutation or still the accumulation of mutations have shown that gene loss may play an important role in evolution, either adaptive or non.

They suggest a qualitative "more is less" response to environmental stress, rather than a dual logic.

Actually a relaxation of purifying selective pressure which plays the role of organisms' dealing with Otherness may be created by dietary or other environmental agencies leading to certain genes becoming unnecessary.

Furthermore in laboratory conditions it has been demonstrated that only a few hundred bacterial genes are indispensable and in some cases up to 80-90% of protein-coding genes are dispensable (Albalat and Cañestro, 2016).

While the theories of evolution have considered the individual gene as its unit, rather than genomes, comparative genomics has shown that the notion of the Tree of Life is undermined by this dysfunctional atomization; this atomization is very much an expression of the Newtonian paradigm (Rosen, 1985).

Yet, the sequentiation of complete genomic sequences from diverse phylogenetic lineages

> *"reveal notable increases in genome complexity from prokaryotes to multicellular eukaryotes. The changes in-clude gradual increases in gene num-ber, resulting from the retention of dupli-cate genes, and more abrupt increases in the abundance of spliceosomal introns and mobile genetic elements"* (Lynch, 2003).

On the other hand, it is known that inverted repeats and palindromes are responsible for mutagenesis in a wide variety of organisms, bacteria, mammalian cells, etc. (Voineagu, 2008).

Returning to the C-paradox, upon completion of the sequencing of several genomes, in terms of comparative genomics, it turned out to be possible to identify a meaningful difference.

Indeed, whereas

> "*small genomes are engaged in an active campaign to keep their diverse and active transposable-element populations in check, whereas in larger genomes one or a few types might spread relatively unhindered and then persist as identifiable fossils long after they lose their capabilities for self-replication. Conversely, it could be that organism- level selection for a small genome creates strong intragenomic selective pressure for the maintenance and/or diversification of active transposable elements"* (Gregory, 2005).

Thus, upon discussing the usual Darwinian thesis that Natural selection promotes the evolution of organismal complexity, it was noted that far from this, a lack of supporting evidence appears to be the case, and that *"...substantial evidence exists that a*

reduction in the efficiency of selection drives the evolution of genomic complexity" (Lynch, 2007a).

In fact, this is related to the notion of "purifying selection", i.e. whereby an organism or a population of them is unable to reject the alien elements, particularly transposons belonging to the other organism, wherein organismic complexity will appear as a consequence of a weak "purifying selection" (Koonin, 2012).

That is, weak "purifying selection" is the incapability of organisms of rejecting the Other upon its introjection by symbiogenesis,or still, in the present setting, the cancelling out of perturbations to the resonance system of genomes.

That is, the failure to reject alien transposable genomic elements by a species, producing thus an assimilation, appears to operate towards increasing organismic complexity, which rather is the contradictory stance to the Darwinian thesis (Koonin, 2012).

Indeed, already Koonin noted that transposons have no adaptive value for the host organisms, however they are pervasive to most prokaryotic genome (Koonin, 2012).

This came in the wake of the revision of Darwinian evolution (Lynch, 2007b), upholding factors such as mutations as the most fundamental event driving evolution, genetic drift and recombination assorts variation within and among chromosomes, which in distinction with natural selection are non-adaptive events, meaning by this that they do not contribute to the survival conceived in terms of the fitness properties of individuals (Lynch, 2007a, 2007b); see note no. 28.

While Darwinian evolution has kept its hegemony, *"[I]t is now clear that many (and probably most) aspects of genomic biology that superficially appear to have adaptive roots-including the numerous features that contribute to complexity, modularity, robustness, and evolvability-are almost certainly also products of nonadaptive processes"* (Lynch, 2007b).

Furthermore: *"evolution is a population-level feature: individuals are subject to selection, whereas populations evolve"* (Lynch, 2007b).

And still, referring to the conflation of evolution with the notion of complexity:

> *"no observation from the several hundred genomes that have been sequenced can be taken as support for the idea that genomic architectural changes have been promoted in multicellular lineages so as to enhance their ability to evolve. Indeed, other than the appearance of spliceosomal introns, some forms of mobile elements, and organelles in the stem eukaryote (all of which arose prior to the origin of multicellularity), there is no discontinuity in the basic features of genomes across the entire domain of cellular life"* (Lynch, 2007b).

Thus the facile conflation of evolution and complexity has been contested by comparative genomics.

Also the notion of the genomic space-time is glossed upon, which we already identified with the dynamical HyperKlein Bottle genome generated by the Klein Bottle genomic matrix P(1); this genomic space-time determines the *"remarkably uniform general organization of prokaryotic genomes… along with the intensive purifying selection underpinned by the large effective population size of most prokaryotes that, considering the looming and otherwise inevitable mutational meltdown catastrophe, is itself contingent on the extensive gene exchange"* (Koonin, 2012).

Notably, in the phenomenological approach in the neurosciences, it is the enaction of assimilation which is conceived as the basic process which enacts the primacy of action vis-à-vis perception (Freeman, 2000).

In other terms, the topological folding and shuffling operations -described above, on small genomes appear to keep their stability, as a system of resonances, as already evinced to be the case of genomes as derived from the Klein Bottle Logic, whereas for large genomes they appear as high-entropy modifications to later stabilize as inert with respect to self-replication, in their current configuration.

We can venture that these "inert" sections may be responsible for the metamorphosis that takes place in the lifetime of organisms such as the tadpole or Axolotol –or even the putative terrestrial precursor of whales-, upon migrating to a novel environment, prompting hormone-directed metamorphosis (Lima de Faria, 1988, 1995) or still in certain bacteria and viruses as pleomorphisms already discussed; see note no. 29.

Still, for small genomes this system of resonances appears to couple with that of *other* genomes, either producing maintainance of the status-quo or allowing for diversifications.

So here we retrieve a proposal which in logophysical terms is based on an extended identity, or if wished, a distributed identity, rather than the simple identity claimed by dual logic.

We have already argued that the mirror neuron phenomenology is one such example of a Self as distributed together with the Thou.

The notion of complexity arising from happenstance induced modifications which are "frozen" in the sense of being lite-rally incorporated as order, was already intimated by Jacques Monod, with his notion of Nature operating as a tinkerer, as it were.

Upon discussing happenstance vis-à-vis complexity:

> *"Paleontologist Stephen Jay Gould comments on how happenstance provides an opportunity for selection when he argues that the complexity of forms is due to "poor fit, quirky design, and above all else, redundancy [as in palindromes].. Pervasive redundancy makes evolution possible. If animals were ideally honed, with each part doing one thing perfecdy, then evolution would not occur, for nothing could change and life would end quickly as environments altered and organisms did not respond."* (Beltrami, 1999).

In the early stages that led to the Central Dogma, the study of populations of bacteriophages both empirical and through statistical models as those in usage in statistical physics led to conclude that their mutations were random, yet with the rather surprising evidence that they took place in anticipation of the would-be selective agent (Summers, 2006).

We have argued that the notion of randomness as independent of symmetry such as in palindromes and their non-orientability which stems from torsion geometry, (Rapoport, 1991, 1997, 2000, 2005a) appears to be questionable upon examination of general phenomena deemed as random in *several contexts*, as is already the case of the Shnoll effect (Shnoll, 2012; Rabounski and Borissova, 2014).

Remarkably, they can also be interpreted as anticipative due to the palindromic structure of their histograms associated to several astronomical cycles .

The role of environmental randomness such as Brownian motion or still of fluid turbulence -both being dynamical torsion geometries (Rapoport 2002a, 2002b, 2005a), also continuously drives organisms out of equilibrium, as is the case of colonies of ciliates, producing further order which appears as embodying cognition (Ben Jacob, 2003).

Resuming: "Whether it be at the level of cells, organisms, or ecosystems, chance and order comingle to unfold the vast panorama of the living world.

This underscores the utility of randomness in maintaining variability and innovation while preserving coherence and structure" (Beltrami, 1999).

We recall that the ubiquity of transposons appeared to be the evidence for a perpetually dynamic genome.

We already discussed the role of transposons at the level of pools of genomes as metacontrollers, so that this operates at a metalevel.

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 the usual Darwinian evolution appeal to "selective pressure"; 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.

Let us now proceed to the alleged paradox of tagging evolution as complexity, as considered by comparative genomics.

> *"As soon as comparison of the genomes of simple (prokaryotes) and complex (animals and plants) life forms became possible, researchers realized that there was something strange about these genomes, something hardly compatible with the idea of steadily increasing genome complexity in parallel with the growing organismal complexity. Indeed, the genomes of multicellular eukaryotes might be more complex than those of prokaryotes and even unicellular eukaryotes, but these complex genomes also appear awfully disordered and full of mobile elements and other junk; they represent high-entropy states"* (Koonin, 2012)

It is this paradox which led to the notion of a non-adaptive theory of evolution, which very much turned upside-down the established conception.

The solution that was proposed can be naturally related to our previous discussed phenomenology of the distribution of the I with respect to Other, which is the underlying ontology of the HyperKlein Bottle, and which Günther related to heterarchical polycontextures, which as "partial inclusions" are considered in the Systems Biology approach to evolution (Jablonka and Lamb, 2005; Oyama,2000).

Indeed, already Koonin noted that transposons have no adaptive value for the host organisms, however they are pervasive to most prokaryotic genomes.

Yet, the relevant notion from which Koonin departed is that of "purifying selection", already discussed, related to the assimilation or rejection of transposon elements of an alien species, which as we have shown, operate through topological transformations linked to non-orientability.

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"* (Koonin, 2012).

Still, transposons, as crucial regulative operators, are *not* subject to Darwinian selection (Koonin, 2012).

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 (Koonin, 2012); see note no. 30.

In the Systems Theory approach for biology, which purports to give a computational setting for biology in terms of a non-hierarchical first-order cybernetics, and particularly for physiology in the framework of the Physiome Project (Noble, 2010, 2015), it is claimed that transposons are the basis for evolutionary novelty, and still that

> *"we can understand the succession of larger and more intricately organized forms over time to illustrate the tendency of living organisms to retain, amplify, diversify, and reuse their evolutionary inventions"* (Shapiro, 2011).

We recall that the scenario for eukaryogenesis which is deemed to be the most eventful is that of symbiosis between prokaryotes (which, we recall that they are known to have closed non-orientable genomes) and bacteria.

We already discussed that this scenario is related to the distribution of selfhood between the I and the Thou, as an extended unit.

Thus symbiogenesis is precisely one such heterarchical phenomenology, where the bacteria believed to be the invader of the prokaryote, worked to produce a novel self out of their HyperKlein Bottle interaction.

Yet, we must recall that the environment is not the independent agency vis-à-vis an organism that dualism proclaims to be the case, but rather the organism's Umwelt of its own making, as ciliate bacterial colonies show to be the case (Ben Jacob, 2003).

In Systems Biology which stays short of identifying the non-dual basis of its ontology and the role of semiotics , this is expressed as

> "[T]he effective environment for a developing organism, however, is very much a function of its genotype, and to some extent is produced, chosen, and organized by the organism" (Oyama, 2000).

In this take, what is transmitted through genomes are not traits but "developmental means (or resources, or interactants).

These means include genes, the cellular machinery necessary for their functioning, and the larger developmental context, which may include a maternal reproductive system, parental care, or other interaction with conspecifics, as well as relations with other aspects of the animate and inanimate worlds.

This context, which is actually a system of *partially nested* contexts [my emphasis; we already discussed that rather the HyperKlein Bottle is the case], changes with time, partly as a result of the developmental processes themselves" .

This state of integration which contributes to metabolism, also posed a tension since a new identity had to be fused, while rejection as distinguished self-preservation superposed to a stable assimilation vis-a-vis the Other was enacted: indeed a state of cognitive superposition that is ireducible to the dualistic CONTAIN image-separation that divides Inside and Outside, I and Thou, as discussed in Part I.

The solution to this state of superposition may have not led to the self-destruction of the prokaryote host if early the new eukaryotic identity was secured: an eventful metamorphosis for its processual outcome.

But then, for these initial stages of evolution, self-hood is labile, very much in distinction with more complex organisms, such as mammals for which lability is not notoriously considered to be potentially the case (but for Kafka's Gregor Samsa in *Metamorphosis*); we have discussed related issues in note no. 29.

A review closes putting it thus: "Over millions of years of evolution, mobile elements have achieved a balance between detrimental effects on the individual and long-term beneficial effects on a species through genome modification.

Indeed, we may soon learn that the shaping of the genome by mobile elements has played an important role in events leading to speciation" (Kazazian, 2004).

This is most remarkable because the lability at the level of the individual vis-à-vis the intruders is introjected beneficially at the level of the species, as if a *resonance* effect between the members of the species would be instaured as a consequence of the individual changes, as argued above.

In fact, the sizes of populations play a crucial role in determining whether assimilation or rejection of alien elements may be the case of the species (Lynch, 2007a, 2007b).

Still, "whether these repeated sequences are now "junk DNA" is a complex issue. Some may have had an important function long ago, but have lost that role today.

Others may never have had a function, yet the cluttering of our genomes with nonfunctional DNA was a small price to pay for the genome malleability they provided" (Kazazian, 2003).

The introns identified to this effect were the Group-II introns, "[they] would create a powerful driving force for a cascade of evolutionary innovations (Koonin, 2012).

So the Group-II introns which provide the "selection pressure" –a rather metaphorical transphysical agency which determines the true state from the Outside environmental "pressure", and thus coincides with the Eye of God of Objectivism (Lakoff and Johnson, 2003)-, while at the same time they operate within the host to create the new structures. In fact, in mitochondrial genomes, the crucial evolutionary novelty with the appearance of eukaryotes, it is considered that palindromic repeats may have played a crucial role in their generation (Kamikawa, 2016; Wikner, 1986).

From our findings, we can already state whatever mutations may be produced in genomes, there is a system of resonances (or of harmonics) as identified by Perez, produced by the self-multiplication of the Klein Bottle Logic, which embodies wholeness. Mutations as a matter of principle

may reproduce this system or modify it to produce a novel system of resonances, which necessarily must stabilize or in the contrary, no reproducible structure would be the case; see note no. 31.

Whatever the case may be, a stable system of resonances must be emplaced, be that of an organism, or of the Solar System after the perturbation by a novel agency, say an incoming celestial body (Blekhman, 2000; Abraham and Marsden, 1987).

In the case of genomes, seemingly redundancy as palindromic sequences play a crucial role, that of conservation -and seemingly paradoxically if conceived as the dual logic, to open up to the assimilation of changes, precisely by a checksum process which is most efficiently done by the cell, and by the pluricellular organisms as a whole.

This is dynamically operated by the topology of the genome associated to the resonances, and by the transposons as the material elements of in-formation.

Yet, as we have argued, this HyperKlein Bottle topology which generates this system of resonances as well as produces the in-formational background manifesting as light or sound waves according to its resonance system of signals, is about the preservation of the self-identity vis-à-vis its distribution with respect to otherness.

We recall –as discussed in Part I- that already Günther argued of the self as distributed with the Thous, upon introducing the heterarchical pluricontextualities, which is the case of genomes and its relation with proteomes, metabolomes, epigenetical factors at large, and still other organisms.

We recall that biological evolution conceived as the appearance of new species is thought to have occured in this distribution of Self with Other, since eukaryotes appeared as a process of symbiosis of prokaryotes and bacterias.

Etymologically, complexity means *folding*, and this is what DNA secondary structures embody.

Etymologically, evolution is also a topological operation, actually the contrarian one to folding, as in Latin it meant the unfolding of a scroll.

The appreciation of evolution in terms of a topological disclosure, such as the dynamic HyperKlein Bottle logophysics of both genomics and epigenetics suggests a novel interpretation for the famous claim that *"nothing in biology makes sense except in the light of evolution"* (Dobzhansky, 1973), which we may also extend to biological development as discussed in §1.

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.

These structures 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 ge-nomic 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) (Koonin and Wolf, 2012).

In the following, we quote from Wikipedia (2016):

"CRISPR is part of a normally occurring bacterial process. Bacteria may incorporate foreign DNA and even scavenge damaged DNA from their environment…In 2005, three independent research groups showed that some CRISPR spacers are derived from phage DNA and extrachromosomal DNA such as plasmids …In effect, the spacers are fragments of DNA gathered from viruses that have previously tried to attack the cell…".

Thus, CRISPRs are indeed related to the distribution of selfhood between I and Thou that is embodied in assimilating

alien genomic elements by the immune system.

CRISPRs sequences and Cas (CRISPR-associated) proteins are the two elements of an ancient defence prokaryotic adaptive restriction system conserved in bacterial genomes. *CRSPRs represent the memory of the system* (McKenna, 2016; Waldon, 2016), a repository of short, directly repeating nucleotide sequences flanked by short unique unique DNA fragments, acquired from previous infections.

Thus, the association of CRSPRs with a system of archaic resonances that are partially conserved is indeed natural.

As for the second element of the defence system, the Cas proteins are the actual effectors.

They are able to process the CRISPR sequences into small RNAs, and to cleave those infectious DNA molecules that perfectly match those CRISPR-derived RNAs.

Hence, CRISPR systems provide their prokaryotic hosts with small RNA-based defense against mobile genetic elements such as viruses and plasmids (Barrangou, 2007).

More recently, a CRISPR RNA- guided system that targets RNA rather than DNA has been discovered (Abudayyeh, 2015).

Although evolutionary and mechanistically diverse, all such systems comprise CRISPR DNA arrays of identical repeats separated by unique spacers and cas genes.

Returning to our introductory discussion of torsion geometry associated to spatial *dislocations* (Fig.1.I)- either a singularity or heterogeneous material which can be introduced (the Volterra operations)- to be a primal semiotic agency, it is known that CRISPRs are indeed space acquirers producing dislocations.

A recent review in Wikipedia (2016) puts it thus:

> *"When a microbe is invaded by a virus, the first stage of the immune response is to capture viral DNA and insert it into a CRISPR locus in the form of a spacer. Cas1 and Cas2 are found in all three types of CRISPR-Cas immune systems, which indicates that they are involved in spacer acquisition. Mutation studies confirmed this hypothesis, showing that removal of cas1 or cas2 stopped spacer acquisition, without affecting CRISPR immune response".*

How they operate in terms of evolution as induced metamorphosis is further described as:

> *"The basic model of CRISPR evolution is one where newly incorporated spacers drive phages to mutate their genomes to avoid the bacteria immune response, creating diversity in both the phage and host populations. To fight off a phage infection, the sequence of the CRISPR spacer must correspond perfectly to the sequence of the target phage gene. Phages can continue to infect their hosts given point mutations in the spacer…CRISPR was proposed to be responsible for the generation of adaptive immunity in microbes… CRISPR was first shown to work as a genome engineering/editing tool in bacterial cell culture in 2012 … [they have been described as being involved in] genome editing in human and mouse cell culture using CRISPR/Cas Systems (Seruggia and Montoliu, 2014) … [it has been] found that bacteria respond to an invading phage by transcribing spacers and palindromic DNA into a long RNA molecule. …CRISPRs are widely distributed among bacteria and archaea and show some sequence similarities. However their most notable characteristic is their repeating spacers and direct repeats"* (Wikipedia, 2016).

Hence, CRISPRs actually appear as inverted repeats rather than palindromes, which in §10 we described their formation of local Möbius strips or Klein Bottles. In terms of them, genomes appear to be resonance systems, which in the case of the mitochondrial human genome was described in fig. 8.III, with the subsequent presentation of the harmonics.

The CRISPR system responds directly to the environmental cue by introducing a genetic change into the organism that is

immediately adaptive to the environmental cue; thus its Lamarckian character.

Again, the Hyper Klein Bottle Logic embodies such an environmental adaptation, and the basis for error-immune digital codification.

This is consistent with the notion that transposons are the drivers of evolution (Kazazian, 2003; Larionov, 2008).

Finally the remarkable disparity of viruses outnumbering bacteria as environmental agents point out to the importance of antivirus systems, such as the CRISPRs, as central to the evolution of bacteria and archaea (Koonin and Wolf, 2012).

Yet, this still points to a further role of heterarchies in biological evolution. Indeed the notion of a Tree of Life as early envisaged by Darwin, was an outcome of the binary replication of the genetic material.

However, it is precisely the study of the phylogenomics of microbes and virus, the simplest of all organisms which are known to have dominated the biosphere, that has led to conclude that the case is of networks, the so-called Forests of Life, rather than the Trees of Life which would be mere statistical trends (Koonin and Wolf, 2012).

That these networks are self-reentrant heterarchies is apparent from the destruction of the biosphere as currently practiced by the human species.

Moreover, a non-dual logophysics is at play is posited thus:

> *" We now realize that evolution of life is to a large extent shaped by the interaction (arms race but also cooperation) [not the dual logic – my emphasis] between genetic parasites (viruses and other selfish elements) and their cellular hosts, Viruses and related elements, with their distinctive life strategy, informational parasitism, actually dominate the biosphere both physically and genetically, and represent one of the two principal forms of life that as intrinsic to the history of the biosphere as cells are."* (Koonin and Wolf, 2012).

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 (Lynch, 2007a, 2007b; Koonin, 2012).

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.

13.3 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 information 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 Montagnier 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" (Montagnier, 2015).

We find again, the issue of mimesis or induction, of a metaform –as a shape of information, acting as the logophysical agency at some level being reproduced at another level of organization. As revealed by the studies on ciliate colonies, the manifestation of a natural intelligence and mimetic reproduction of vortices appears to be the case (Ben Jacob, 2003).

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 (Sokolov, 1973).

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 unconsidered due to the disconsideration of an ontology other than duality, that liquid crystals develop singularities (Bouligand, 1987, 1999), 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 in-formation.

Just like light waves, liquid crystals develop Möbius strip vortical structures (Bouligand, 1978a, 1978b, 1999; Mirkin, 1996; Musevic, 2006; 2013).

But liquid crystals by 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. 3.II.C; (Machon and Alexander, 2013).

Yet, as shown in Rapoport (2013), 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 (Pollack, 2013), is conceived to be the very signature of the surgence of life (Voeikov, 2001).

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* (Machon and Alexander, 2013; Melle, 2013; Musevic, 2006, 2013).

Thus, Möbius strips and knotted defects, pervasive to both organic chemistry (catenanes, rotaxanes, molecular motors, etc.) (Bonchev and Rouvray, 2010; Flapan, 2010; Forgan, 2011) 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 (Chow, 2010).

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, as in the previous references.

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, though no genomes are involved- 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 na-

ture, 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 (Lima de Faria, 1988).

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 Rapoport (2013; 2014).

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 (Bousso, 2002).

In this work and in Rapoport (2013), reiteratively, we have identified the dimension 2, as *the* phenomenological dimension of Nature.

In particular, this appears to be the case of olfaction, vision and the haptic sensory modes, the topographic maps for the last two being the Klein Bottle as well as the perception of music having this topology. Yet, the Klein Bottle as a surface is two-dimensional, yet in a highly non-Cartesian sense.

This is not only so because it appears as the dimension of the experience of the world as we act upon it *as if* Exterior, rather than of the world *as* Exterior.

It is not the dimension of objectivity, in the Cartesian paradigm of which physics has made its knowledge of as Exterior and detached from the Interior.

This take has been kept by quantum mechanics, maintained in positing the observer, whose multiplicity of states (of the observer and of the world) is reduced to a *single* one, for each observer, i.e. Boolean logic, reduced to a single state.

That is, the Exterior world and its Interior representation reduced to a single state, which Günther identified as the ultimate reduction of dual logic to a single monocontexture with a single logical value, that of truth (Günther, 1962; Rapoport, 2014b).

The image-schema for this, CONTAIN, alternates oscillating between ascribing the true state from Inside or as if independently existing environmental Outside, the God-eye perspective (Lakoff & Johnson, 2003).

As already argued, the metaphoric "selection pressure" is an outcome of this dualistic logophysics, at times as reified Potentia, and is construed as mandatory in a self-explanatory mode, rather seductive, for that matter.

The dimension two here intimated is the one which we as actors-participants *enact* the world and its multiple cognitive representations, and thus is entwined with meaning.

This is so due to the self-penetration of the Klein Bottle, which is related to depth, as the primal dimension, the 'dimension of dimensions' as Merleau Ponty put it (1965), which is not conflatable with a Cartesian dimension. For the latter, the non-relational formula of object-in-space-and-time-before-subject (Rosen, 2006) relates to the CONTAIN image-schema as such it has both the *ex*tensional character of dimensions as in physics and in accordance with CONTAIN, and a constitutive dimension which still in accordance with this image-schema can be qualified as *in*tensional (Rosen, 2008).

Yet, as we have seen in discussing the TIME-operator related to the non-orientability and its multifacetic role of recreation upon blow-up of non-linear systems, it is a creative dimension of non-linear structure – spatial and cyclical time-processes - very much like Musès pondered that time is (Musès, 1985).

Still it operates as an habilitator of cognitive processes such as finite-computations, and more fundamentally still as a protoform for semiosis.

Indeed, the depth dimension is not objectifiable if not through TIME, as much as the self-penetration of the Klein Bottle is imaginal, rather than material, but for ideally elastic objects and producing torsion dislocations otherwise, or remarkably in the case of organisms having a hard exoskeleton such as conchoids which elicit a reentrant non-linear structure.

TIME acts supporting non-linearity both in spatial and temporal organization, and through the manifold self and hetero-reentrant processes, be them cognitive, perceptual, physical in the ample sense, physiological, or their fusion.

However, this imaginal character *is* reified, and emplaces the Exterior world, yet not of unrelated objects each Exterior to the others as in Cartesian space, but one of relatedness.

It also structures the body as the embodied mind, as manifests in the over-laying of recursive foldedness already in embryological development, in the dynamical structure of the genome, in the fusion of chiralities, in the architecture of the anatomy trains of connective tissue crucial to body integration, in the anatomy of the heart, and sustains the unity of action and perception, still extending to intentionnality.

Merleau-Ponty further posited that time is intertwined with depth. Yet, the primal dimension of depth is also entwined with memory (Mazis, 1988), the logical and emotional, perceptual, cognitive and imaginal, past and present, personal and impersonal, semiotical all the way through, and thus it is intertwined plurality.

Depth is the articulating and proto-dimension of the heterarchical HyperKlein Bottle, not of the extensional physical space of dual logophysics, and far more complex –in the topological sense- than the Klein Bottle considered so far (Rosen, 2006, 2008).

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, an individual appears to participate in the construal of the visual metapattern rather than being somewhat controlled by the genomic metapattern as is the case of genomes, although a symmetrization of this latter relation may follow from (Gariaev, 2001; Maslow and Gariaev, 1994).

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 (Carlsson, 2008, 2009).

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 (Rapoport, 2013).

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" (Albrecht-Buehler, 2006), they are the expression of this logophysics which actually *ensure heredity as a memory which is encoded in the self-referential generation of the geno-matrices, 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 incurporated 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.

As already commented, the immune system was identified 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", as placed in terms of CONTAIN (Forsdyke, 2011).

This is a kind of logophysical checksum process, which surmounts the dualistic divide between organism and environment.

13.4 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 (2009).

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 between.

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 (Chénais, 2013).

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 (Wright, 2014).

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" (Perez, 2009).

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]"* (Perez, 2009).

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 (Koonin, 2012).

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" (Lima de Faria, 2003).

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 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"* (Brown, 2002), quoted in Lima de Faria (2003).

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" (Saini, 2013), the multiplicity of identity as a signature of non-duality already discussed.

These authors in a recent review conclude: *" 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".*

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, and as highlighted by Petoukhov, this fractal generation mimics heredity (Petoukhov, 2015).

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 (Petoukhov and He, 2010; He and Petoukhov, 2011).

Cellular automata have a self-referential generation.

The most known example, is the Fibonacci series, which is the basis for the so-calledHarmonic Mathematics (Stakhov, 2009), as well as for the complete generation and identification of the prime numbers (Johansen, 2010, 2012, 2014).

Stephen Wolfram, upon revealing the amazing intricateness of the patterns that these cellular automata create by self-referential iteration of a "seed" and a set of simple rules –as is the case of the genomatrices (Petoukhov and He, 2010), surmised that a "New Kind of Science" was possible (Wolfram, 2002).

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 intricacy 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 Perez (2009), computes automatically the 64 codon population numbers (Perez, 2010, 2013).

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 (Kauffman, 2002), as an algorithmic recursion tends to produce it . 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.

This was the basis for the pioneering work on neural Fibonacci networks due to Perez (1988, 1990).

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 (Johansen, 2010, 2012, 2014), plays a crucial role with respect to harmonics. Indeed, would systems, such as the genome, operate through a 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" (Merrick, 2012); it does so providing coherence in time and in space; see note no. 32.

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 (Boeyens, 2010).

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 in Rosen (2008); see note no. 33. 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 electro-encephalograms (Pletzer, 2010; Weiss and Weiss, 2003).

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 (Mae Wan Ho, 1998, 2012).

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.ù

A remarkable computational model of growth which reproduces a fractal are the L-systems, after Aristid Lindemayer, who pioneered the approach (Green, 2000).

Of particular interest is the case of the networks of Purkinje cells in the cerebellum, and their relations to the fractality of genomes (Pellionisz, 2003).

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"* (Koonin, 2012).

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, $\Phi^{1/3}$),etc. (Perez, 2009).

Yet, the role of the "genomic" numbers appears to extend from its role as providing overall coherence of genomes. While "junk" –or "selfish"- DNA (see note no.26) as transposons, play a crucial role in the algorithmic complexity, non-adaptive punctuated evolution and mainte-nance of genomes (Koonin, 2012), 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..." ;* for a discussion of this and the possibility of an extension to exobiology see Perez (2015a).

Yet, this produces a remarkable relation between form and substance as noted by Perez, or still, shape as topology and substance, which may also carry to full genomes and individual chromosomes, and still further to proteomics .

In synthesis, self-reference together with hetero-reference as Hyper Klein Bottle, appear to be universal generating principles.

Their non-dual logophysics appear to produce and reproduce the different yet integrated levels of self-organization of nature, either logical, physical, biological, chemical, cognitive, semeiotic, 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, respectively see Rowlands (2007) and note no.34 below, while for the relation of torsion geometry to quantum mechanics see Rapoport (1997, 1998, 2005a, 2005b, 2007a, 2007b).

Acknowledgments

My gratitude to Dr. Jean-Claude Perez, Prof. Tidjani Negadi, Prof. Sergey Petoukhov and Prof. Luc Montagnier, for

their kind interest in my work. I am especially grateful to Prof. Stein Johansen for discussions on algorithmic complexity, and for posing out several queries on evolution which moved me to elaborate them in the present contribution. To an anonymous reviewer which posed several queries and suggestions for improvement I express my deep gratitude as well. This work would have been impossible to materialize without the loving support of Sonia.

Conflicts of Interest

The author declares no conflict of interest.

References

Abudayyeh O et al. C2c2 is a single-component programmable RNA-guided RNA-targeting CRISPR effector. Science. Online First: June 2, 2016. DOI:10.1126/Science.aaf5573.

Achaz G, Coissac E, Netter P , Rocha E . Associations Between Inverted Repeats and the Structural Evolution of Bacterial Genomes. Genetics 2003 Aug; 164(4): 1279–1289.

Adami C, Ofria C and Collier T. Evolution of biological complexity. PNAS, April 25, 2000; 97 , 9: 4463–4468. , doi: 10.1073/pnas.97.9.4463.

Adami C. What is complexity? BioEssays 2002; 24:1085–1094. PMID:12447974.

Ahmed NU, Rao KR. Orthogonal transforms for digital signal processing. Springer Verlag: New York, NY, USA, 1975.

Albalat R and Cañestro C.Evolution by gene loss.Nature Rev Genetics 2016, 1. www.nature.com/nrg.

Albrecht-Buehler G. Asymptotically increasing compliance of genomes with Chargaff's second parity rules through inversions and inverted transpositions. Proc Natl Acad Sci USA 2006; 103:17828–17833.

Albrecht-Buehler G. Inversions and inverted transpositions as the basis for an almostuniversal " format" of genome sequences. Genomics 2007; 90 : 297 – 305.

Annett M. Left, right, hand, and brain. Lawrence Erlbaum: New Jersey, USA, 1985.

Bansal M. DNA structure: Revisiting the Watson–Crick double helix. Current Science 2003; 85, 11, 10 December.

Barbieri M. Introduction to Biosemiotics: The New Biological Synthesis. Springer Verlag, Berlin, 2007.

Barrangou R et al. CRISPR provides acquired resistance against viruses in prokaryotes. Science 2007; 315(5819):1709–1712.

Bates A and Maxwell A. DNA Topology; Oxford University Press: Oxford, UK, 2005.

Bateson G. Steps to an Ecology of Mind. Aronson, London,1972.

Bauer T, Banzer P, Karimi I, Orlov S, Rubano, A, Marrucci L, Santamato E, Boyd RW, Leuchs G. Observation of optical polarization Möbius strips. Science 2015; 27 February: 347; 6225 pp. 964-966. Doi: 10.1126/science.1260635.

Beltrami E. What is Randomness?: Chance and Order In Mathematics and Life. Springer, 1999.

Ben Jacob, Eshel. Bacterial self-organization: co-enhancement of complexication and adaptability in a dynamic environment. Phil Trans R Soc Lond A 2003; 361, 1283-1312.

Berezin AA, Gariaev P, Gorelik VS, Reshetniak SA and Shcheglov VA. Is it possible to create laser based on information biomacromolecules? Laser Physics 1996; 6: 1211-1213.

Betran E, Demuth J and Williford A. Why Chromosome Palindromes? Inter Journal of Evol Biol 2012, Article ID 207958, 14 pages; doi:10.1155/2012/207958.

Biegeleisen K. Topologically Non-linked Circular Duplex DNA,Bull Math Bio 2002; 64: 589–609.

Binhi V. Magnetobiology: Underlying Physical Problems. Academic Press, New York, 2002.

Binz E, Pods S and Schempp W. Heisenberg groups—the fundamental ingredient to describe information, its transmission and quantization. J Phys A: Math. Gen 2003;36: 6401-6421.

Blekhman I. Vibrational Mechanics: Nonlinear Dynamic Effects, General Approach, Applications. World Scientific, Singapore, 2000.

Boeyens JC. New Theories for Chemistry. Elsevier, Amsterdam, Holland 2005.

Boeyens JC. Chemical Cosmology;.Springer: Berlin, Germany,2010.

Bohm D . Time, the implicate order, and pre-space, In: Physics and the Ultimate Significance of Time, David R. Griffin ; editor; State University of New York Press, pp. 177–208; 192, 1996.

Bohm, D and Peat FD. Science, Order and Creativity. Routledge & Kegan, London, UK, 2000.

Bouligand Y. Liquid Crystals and their Analogs in Biological Systems. In: Liquid Crystals. Liebert L, editor; Academic Press, New York, NY, USA, pp 259-293, 1978.

Bouligand Y. Defects and Textures. In: Physical Properties of Liquid Crystals; Demus,D, Goodby J, Gray G, Spiess H, Vill V; editors, Wiley VCH: Weinheim, Germany, 1999.

Bonchev D and Rouvray DH. Chemical Topology; Gordon & Breach: London, 2010.

Bousso R . The holographic principle. Reviews of Modern Physics 2002;74 (3): 825–874. arXiv:hep- th/0203101.

Brooks D. The Concept of Levels of Organization in the Biological Sciences. Ph.D. thesis. Bielefeld Univ., 2014.

Brown AT. Genomes. Wiley-Liss: Oxford, UK, 2002.

Burdick D. Circular DNA: Double Helix or Moebius strip? Naturwissenchaften 1971; 57: 245. doi:10.1070/RC1973v042n06ABEH002636 .

Carlsson G, Ishkhanov T, de Silva V and Zomorodian A. On the Local Behavior of Spaces of Natural Images .Inter Journal of Comp Vision January 2008; 76, Issue 1: 1-12 .

Carlsson G. Topology and data. Bull AMS 2009; 46, 2: 255-308.

Central Dogma of Molecular Biology. In http://openwetware.org/wiki/IGEM:IMPERIAL/2007/Tutorials/Guide_for_Engineers/Central_Dogma_of_Molecular_Biology.

Chargaff E, Lipshitz R and Green C. Composition of the deoxypentose nucleic acids of four genera of sea-urchin. J Biol Chem 1852; 195 (1): 155–160. PMID 14938364.

Chénais, B. Transposable elements and human cancer: a causal relationship? Biochim Biophys Acta. 2013; Jan;1835(1):28-35. doi: 10.1016/j.bbcan.2012.09.001.

Chow MHK, Yan TH, Bennett MJ, Wong J. Liquid Crystal chromosomes, birefringence and DNA, Eukaryotic Cell (2010); 9, 10: 1577-1587.

Chromosomes http ://hgdownload.cse.ucsc.edu/goldenPath/hg16/chromosomes/

Cosic I. The Resonant Recognition Model of Macromolecular Bioactivity: Theory and Applications. Birkhauser, Basel, 1997.

Crick F, Wang J and Bauer W. Is DNA really a double helix? J. Mol Bio 1979; 9: 449-461.

Editorial. Systems biology and the virtual physiological human. Molecular Systems Biology 5; Article number 292; doi:10.1038/msb.2009.51.

Davydov AS. Solitons in Molecular Systems, Kluwer, Dordrecht,1981.

Dawkins R . The Blind Watchmaker: Why the Evidence of Evolution Reveals a Universe without Design New York: W. W. Norton & Company, Inc.; 1986.

Dawkins R. The selfish gene. Oxford University Press; Oxford, 1976.

Del Giudice E, Preparata G and Vitiello G. Water as a free electric dipole laser. Phys Rev Lett 1988, 61, 1085–1088.

Deutsch D. Paradoxes of musical pitch. Scientific American 1992; 267: 88-95.

Dershowitz N and Jouannaud J-P. Rewrite Systems. In Handbook of Theoretical Computer Science Volume B: Formal Methods and Semantics. van Leeuwen J (ed), North-Holland,Amsterdam, pages 243-320, 1990.

Distin, K. Cultural Evolution. Cambridge University Press, Cambridge, 2011.

Duerr HP. Dreamtime: Concerning the Boundary between Wilderness and Civilization. Blackwell, London,1985

Dykes R and Rues W. What Makes a Map In Somatosensory Cortex? In: Cerebral Cortex Vol. 5 Sensory- Motor Areas and Aspects of Cortical Connectivity. Jones E and Peters A; editors,Plenum Press: New York, NY,1986.

Flapan E. When topology meets chemistry; Cambridge Univ Press: Cambridge, 2010.

Freund T. Multi-twist optical Mobius strips. Optics Letters 2010; 35, Issue 2: 148-150. doi: 10.1364/OL.35.000148.

Eisen J, Heidelberg JF, White O and Salzberg S. Evidence for symmetric chromosomal inversions around the replication origin in bacteria. Genome Biology 2000, 1(6):research0011.1–0011. http://genomebiology.com/2000/1/6/research/0011.

Fadeyeva T, Shvedov V, Izdebskaya Y, Volyar A, Brasselet E, Neshev D, Desyatnikov A, Krolikowski W and Kivshar Y. Spatially engineered polarization states and optical vortices in uniaxial crystals. Optics Express. 10 May 2010; 18, 10: 10848.

Fedoroff N. Transposable Elements, Epigenetics, and Genome Evolution. Science 2012; 338; 9.

Fedoroff N. Introduction. In Plant Transposons and Genome Dynamics in Evolution. Fedoroff, N.V. , editor; Wiley Blackwell: Iowa (USA), pp.xiii-xvii, 2013.

Fedorov A, Roy S, Fedorova L, Gilbert W. Mystery of intron gain. Genome Res 2003; 13: 2236-2241.

Fedorov A and Fedorova L. An Intricate Mosaic of Genomic Patterns at Mid-range Scale. In Advances in Genomic Sequence Analysis and Pattern Discovery. Elnitski L, Piontkivska H and Welch LR (ëds).World Scientific, Singapore, 2011.

Freedman D and van Niewenhuizen P. Scientific American 1978,238, 126.

Focossi D. http://www.ufrgs.br/imunovet/molecular_immunology/dogma.htm; accessed May 31, 2015.

Forsdyke D. Bioinformatics, Symmetry observations in long nucleotide sequences: a commentary on the Discovery Note of Qi and Cuticchia. Bioinformatics 2002; (18) 1:215-7.

Forsdyke DR and Bell SJ. Purine loading, stem-loops and Chargaff's second parity rule: a discussion of the application of elementary principles to early chemical observations. Appl Bioinfor 2004; (3) 1:3-8.

Forsdyke D. Evolutionary Bioinformatics. Springer, second edition. Berlin, 2011.

Forgan R, Sauvage J-P and Fraser Stoddar J. Chemical Topology: Complex Molecular Knots, Links, and Entanglements. Chem Rev 2011; 111, 5434–5464. dx.doi.org/10.1021/cr200034u.

Frankin S and Vondrisk T.Genomes, Proteomes, and the Central Dogma.Circulation: Cardiovascular Genetics 2011; 4: 576. doi: 10.1161/CIRCGENETICS.110.957795.

Frohlich H and Kremer S. Coherent Excitations in Biological Systems; Springer-Verlag: Berlin, 1983.

García-Bellido A. Symmetries throughout organic evolution. Proc Natl Acad Sci USA December 1996; 93: 14229–14232.

Gariaev P, Kaempf U, Marcer P, Tertishny G, Birshtein B, Iarochenko A and Leonov K. The DNA-wave Biocomputer. Inter J. Comput Anticip Sys 2001;10: 290-310. Liege, Belgium.

Gariaev P, Marcer P and Schempp W.A mathematically specified template for DNA and the Genetic Code in terms of the physically realisable processes of Quantum Holography. Proc. Symposium "Living Computers" 9th March, University of Greenwich, Marcer P, Fedorec (editors); 1996; 45-63.

Gariaev P, Vasiliev AA and Berezin AA. Holographic associative memory and Information transmission by solitary waves in biological systems. SPIE, The International Society for Optical Engineering, CIS Selected Papers, Chip Measuring and Data Processing Methods and Devices 1994; 1978: 249-259.

Ghyka M. The Geometry of Art and Life. Dover, New York, 1952.

Goertzel B. Chaotic Logic: Language, Thought, and Reality from the Perspective of Complex Systems Science. Springer Science, Berlin, 2013.

Gordon R. The Hierarchical Genome and Differentiation Waves. World Scientific , 1999.

Goriely A. Integrability and Nonintegrability of ordinary differential equations. World Scientific: Singapore, 2001.

Goriely A and Tabor M .Nonlinear dynamics of filaments II: Nonlinear analysis. Physica D 1997; 105 : 20-44.

Goriely A, Robertson-Tessi M, Tabor M and Vandiver R. Elastic growth models. In Mathematical Modelling of Biosystems, 1-45, Mondaini R and Pardalos P (eds), Springer, 2008.

Green D. Self-organisation in complex systems. In: Complex Systems,Bossomaier T, eds.,Cambridge University Press, Cambridge, 2000.

Gregory RT. Synergy between sequence and size in large scale genomics.Nature Reviews, Genetics, 2005; 6: 699-708. doi:10.1038/nrg1674.

Günther G. Cybernetic ontology and transjunctional operations. In Yovits, M.C., Jacobi, G.T. and Goldstein, G.D., Eds., Self-organizing Systems, Spartan Books, Washington DC, 313-392, 1962.

Han D, Pal S, Liu Y and Yan H. Folding and cutting DNA into reconfigurable topological nanostructures. Nat Nanotech 2010; 5, 10: 712–717 . doi: 10.1038/nnano.2010.193.

He M and Petoukhov SV.Mathematics of bioinformatics: theory, practice, and applications, John Wiley & Sons Inc , New York, NY, 2011.

Herges R. Topology in Chemistry: Designing Möbius Molecules. Chem Rev 2006; 106 (12): 4820–4842.

Hiley B and Pylkkänen P. Active information and cognitive science – A reply to Kieseppä, Brain, Mind and Physics, Pylkkänen P et al; editors, IOS Press, 1997.

Hiley B. Process, Distinction, Grupoids and Clifford Algebras: an Alternative View of the Quantum Formalism. In http://www. arXiv:1211.2107. Accessed July 02, 2015.

Ho MW . The Rainbow and the Worm, the Physics of Organisms, Singapore; River Edge, NJ: World Scientific, 1998.

Ho MW. Living Rainbow H2O, Singapore; River Edge, NJ: World Scientific, 2012.

Ho MW. Illuminating Water and Life. Entropy 2014; 16: 4874-4891; doi:10.3390/e16094874

Hwang U, Laming MA (2012) Chandra X-Ray Survey of Ejecta in the Cassiopeia A Supernova Remnant. Astrophys. J. 746 . doi:10.1088/0004-637X/746/2/130.

Isaeva V, Kasyanov N and Presnov E. Topology in Biology: Singularities and Surgery Transformations in Metazoan; Development and Evolution. Applied Mathematics 2014; 5, 17:2664-2674. doi: 10.4236/am.2014.517255.

Jablonka E and Lamb, JM. Evolution in Four Dimensions: Genetic, Epigenetic, Behavioral and Symbolic Variation in the History of Life. MIT Press, Cambridge, Mass.,2005.

Jockusch H and Dress A. From Sphere to Torus: A Topological View of the Metazoan Body Plan. Bull Math Biol 2003, 65: 57–65.

Jenny H. Cymatics: A Study of Wave Phenomena & Vibration , 2001, 3rd ed. Macromedia Press.

Johansen, SE. Outline of Differential Epistemology. Translation of the Norwegian edition, University of Trondheim, Trondheim, Norway, 1991; to appear.

Johansen SE. Complete Exposition of Non-Primes Generated from a Geometric Revolving Approach by 8x8 Sets of Related Series, and thereby ad negativo Exposition of a Systematic Pattern for the Totality of Prime Numbers'', Journal of Dynamical Systems and Geometric Theories 2010; 8 (2): 101-171.

Johansen SE. Unveiling of Geometric Generation of Composite Numbers Exactly and Completely. Applied Mathematics & Information Sciences 2012; 6(2): 223-231.

Johansen SE. Generation of Exact and Complete Pattern of Prime Numbers vs. Composite Numbers as Anticipating and Computational Prime Numbering System. Generation of Exact and Complete Pattern of Prime Numbers vs. Composite Numbers as Anticipating and Computational Prime Numbering System. International Journal of Computing Anticipatory Systems 2014; vol. 26.

Jordan IK, Rogozin IB, Glazko GV and Koonin EV. Origin of a substantial fraction of human regulatory sequences from transposable elements. Trends Genet 2003; 19 (2): 68–72. doi:10.1016/S0168-9525(02)00006-9.

Joyce GF and Orgel L. Prospects for understanding the origin of the RNA world. In The RNA World Gesteland RF, Atkins JF, Cold Spring Harbor, New York: Cold Spring Harbor Laboratory Press: 1-25, 1993.

Jürgen B.The contribution of RNAs and retroposition to evolutionary novelties. Genetica 2003; 118 (2–3): 99–116 doi:10.1023/A:1024141306559.

Kaehr R and von Goldammer E. Again Computers and the Brain. J Mol Electronics 1988, 4: S31-S37.

Kaehr R and von Goldammer E. Models of Brain Functions (Cotterill R, ed.), Cambridge University Press, 1989, p.483-497.

Kaehr R and von Goldammer E. Problems of Autonomy and Discontexturality in the Theory of Living Systems . In: Analyse dynamischer Systeme in Medizin, Biologie und Ökologie: 4. 4. Ebernburgerer Gesprach Bad MOnster, 5.-7. April 1990. Springer, 1991.

Kamikawa R, Shiratori T, Ishida K, Miyashita H and Roger A. Group II Intron-Mediated Trans-Splicing in the Gene-Rich Mitochondrial Genome of an Enigmatic Eukaryote, Diphylleia rotans. Genome Biol Evol 2016; 8(2):458–466. doi:10.1093/gbe/evw011.

Kari L and Landweber LF. Biocomputing in ciliates, in: M. Amos (Ed.), Cellular Computing, Oxford University Press, Oxford, 2003.

Karkas JD, Rudner R and Chargaff E. Separation of B. subtilis DNA into complementary strands. II. Template functions and composition as determined by transcription by RN polymerase. Proc NAS USA 1968; 60, 915-920.

Kauffman L. De Morgan algebras, completeness and recursion. In: Proceedings VIIITh International Symposium in Multiple Valued Logics. IEEE Computer Society Press 1978;: 82-86.

Kauffman L. Imaginary values in mathematical logic. Proceedings of the Seventeenth International Conference onMultiple Valued Logic, May 26-28 (1987), Boston MA, IEE Computer Society Press 1987: 282-289.

Kauffman L. I am a Fibonacci Form. Cybernetics And Human Knowing 2002; 11, 3: 101-106.

Kauffman L. Eigenform. Kybernetes 2005; 34.1 & 2: 129-150. DOI 10.1108/03684920510575780.

Kazazian HH. Mobile elements: drivers of biological evolution. Science 2004, 303, 1626-1032.

Keller EF A feeling for the organism: the life and work of Barbara McClintock. New York,NY: W.H. Freeman, 1983.

Khrennikov A. Ubiquitous Quantum Structure: from Psychology to Finances. Springer, 2010.

Kong SH, Fan W-L, Wen-Lang, Chen,H.-D, Hsu, H-T, Zhou N, Zheng B, Lee,H.-C Inverse Symmetry in Complete Genomes and Whole-Genome Inverse Duplication. PLoS One, 2009; November, 4 , 11 | e7553. doi:10.1371/journal.pone.0007553.

Koonin E and Wolf Y. Evolution of microbes and viruses: a paradigm shift in evolutionary biology? Frontiers in Cellular and Infection Microbiology, 2012;September, 2, 119.1-15.

Koonin EV.The Logic of Chance: The Nature and Origin of Biological Evolution. FT Press Science; New Jersey, USA, 2012.

Kozinski AW, Kozinski PB and James R. Molecular Recombination in T4 Bacteriophage Deoxyribonucleic Acid. J of Virology, Aug. 1967; 1: 758-770.

Lakoff G and Johnson M. Metaphors we live by.The University of ChicagoP. , Chicago (IL),2003.

Larionov S, Loskutov A and Ryadchenko E. Chromosome evolution with naked eye: Palindromic context of the life origin. CHAOS 2008, 18, 013105. DOI: 10.1063/1.2826631.

Legéndy C. Circuits in the Brain: A Model of Shape Processing in the Primary Visual Cortex. Springer Science, Berlin,2009.

Levitating superconductor on a Möbius strip http://www.youtube.com/watch?v=ooIjPAU269A, 2013. Accessed April 6, 2016.

Lima de Faria A. Molecular Evolution and the Organization of the Chromosome". Elsevier, Amsterdam, 1983.

Lima de Faria A. Evolution without Selection. Form and Function by Autoevolution. Elsevier: New York, NY, 1988.

Lima de Faria A. Biological Periodicity: Its Molecular Mechanism and Evolutionary Implications. JAI Press Inc., Greenwich, Connecticut, 1995.

Lima de Faria A. One Hundred Years of Chromosome Research and What Appears to be Learned. Kluwer; Dordrecht, Holland, 2003.

Lima de Faria A. Praise of Chromosome "folly": Confessions of an Untamed Molecular Structure; World Scientific: Singapore, 2008.

Lima de Faria A.The molecular origins of brain and body geometry. Springer, Berlin, 2014.

Lynch M. The frailty of adaptive hypotheses for the origins of organismal complexity. PNAS May 15, 2007 ;. 104, suppl. 1: 8597–8604. doi10.1073pnas.0702207104.

Lynch M. The Origins of Genome Architecture. Sinauer, Sunderland, MA, 2007 (b).

Machon T, Alexander G. Knots and nonorientable surfaces in chiral nematics. PNAS 2013; August 27,110;35:14174–14179. doi: 10.1073/pnas.1308225110

Mantegna R, Buldyrev S, Goldberger A, Havlin S, Peng C, Simons M and Stanley H. Linguistic features of non- coding DNA sequence. Phys Rev Lett 1994; Dec 5;73(23):3169-72.

Marcer P and Schempp W. Model of the Neuron Working by Quantum Holography, Informatica 1997, 21, pp. 519-534.

Maresin VM and Presnov E. Topological approach to embryogenesis. Jour Theor Biol. 1985; 114, 3:387-398.

Maslow MU and Gariaev P. Fractal Presentation of Natural Language Texts and Genetic Code. 2nd International Conference on Quantitative Linguistics", QUALICO '94, Moscow, September 20-24, 1994; 193-194.

McCulloch WS. A heterarchy of values determined by the topology of nervous nets. Bull Math Biophys 1945, 7: 89-93.

McKenna A et al. Whole-organism lineage tracing by combinatorial and cumulative genome editing. Science 2016; 353, Issue 6298, DOI: 10.1126/science.aaf7907.

McLaughlin R.W.et al. Are There Naturally Occurring Pleomorphic Bacteria in the Blood of Healthy Humans?Jour Clin Microbiology. 40 (12). doi:10.1128/JCM.40.12.4771-4775.200.

Meinherich U. Amino Acids and the Asymmetry of Life Caught in the Act of Formation. Springer Verlag: Berlin, Germany, 2008.

Melle M, Schlotthauer S, Hall, Diaz-Herrera E, Schoen M. Disclination lines at homogeneous and heterogeneous colloids immersed in a chiral liquid crystal. Soft Matter 2014; 10: 5489–5502.doi: 10.1039/C4SM00959B.

Merrell F. Peirce. Peirce, Signs, and Meaning. University of Toronto Press, Toronto, Canada, 1997

Mezey P (1993) Shape in Chemistry: An Introduction to Molecular Shape and Topology. VCH: New York, NY, USA.

Mirkin C, Letsinger R, Mucic R and Storhoff J. A DNA-based method for rationally assembling nanoparticles into macroscopic material. Nature 1996, 382, 607-609.

Mislow K. Molecular Chirality. In: Topics in Stereochemistry, vol.22.Denmark S; ed. Interscience /John Wiley: New York, NY, 1999.

Mitchell E. Quantum Holography: A Basis for the Interface Between Mind and Matter, Bioelectromagnetic Medicine, Marcel Dekker, New York, 2003.

Mitchell D and Bridge R. A test of Chargaff's second rule, BBRC, 2006; 340, 90-94.

Mitchell T. http://www.therosslynmotet.com/, accessed in May 28, 2015.

Molinari S. et al (2011) A 100-Parsec Elliptical and Twisted Ring of Cold and Dense Molecular Clouds Revealed by Herschel around the Galactic Center. The Astrophysical Journal Letters 735 (2), L33.

Montagnier L, Jamal A, Ferris S.Montagnier JL and Lavallee. Electromagnetic Signals Are Produced by Aqueous Nanostructures Derived from Bacterial DNA Sequences. Interdiscip Sci Comput Life 2009; Sc 1-10.

Montagnier L, Aissa,J, Del Giudice E, Lavallee C, Tedeschi A, Vitiello G. DNA waves and water. Journal of Physics: Conference Series 306 , 2011, 012007. doi:10.1088/17426596/306/1/012007.

Montagnier L, Del Giudice E, Aissa J, Lavallee, C, Motschwiller S, Capolupo M, Polcari A Romano P, Tedeschi A and Vitiello G. Transduction of DNA information through water and electromagnetic waves; arxiv.org/abs/1501.01620.

Morin, Edgar, Method: Towards a Study of Humankind, Vol. 1: The Nature of Nature. Peter Lang Publishing, New York, NY, 1992.

Musevic, I. Nematic colloids, topology and photonics. Phil Trans R Soc A 2013; 371: 20120266. http://dx.doi.org/10.1098/rsta.2012.0266.

Musevic I; Skarabot,M.;Tkalec,U.;Ravnik,M.;Zume,S..Two -Dimensional Nematic Colloidal Crystals Self-Assembled by Topological Defects. Science, 2006, 313, August 18,954-956.

Neelekanta P; Arredondo T, De Groff D (2003) Redundancy Attributes of a Complex System: Application to Bioinformatics. Complex Systems 14: 215–233.

Negadi TA. Quantum-Like" Approach to the Genetic Code. Neuroquantology; 2011, 9: 785-798.

Négadi TA. The Genetic Code Invariance: When Euler and Fibonacci Meet. Symmetry: Culture and Science; 2014, 25, 3: 261-278.

Neuman Y.Reviving the Living: Meaning Making in Living Systems, Elsevier, Amsterdam, Holland, 2008.

Nielsen M and Chuang I. Quantum Computation and Quantum Information. Cambridge University Press: Cambridge, 2011

Noble D. Physiology is rocking the foundations of evolutionary biology. Exp Physio 2013; 98.8: 1235–1243.

Ohno S. The grammatical rules of DNA language: messages in palindromic verses. In: Evolution of Life, Springer-Verlag , Berlin. Osawa S, Honjo T, editors. Springer-Verlag : Berlin, pp. 97-108, 1991.

Ohno S. Evolution by Gene Duplication. Springer Verlag,Berlin,1992.

Oyama, S. Evolution's eye: A Systems View of the Biology-Culture Divide. Duke University Press,Durham and London, 2000.

Pellionisz, A.J.; Graham, R.; Pellionisz, P.A.; Perez, J.-C. Recursive Genome Function of th Cerebellum: Geometric Unification of Neuroscience and Genomics. Handbook of the Cerebellum and Cerebellar Disorders. Manto, M.; Gruol, D.L.; Schmahmann, J.D.; Koibuchi, N.;Rossi, F.; editors, Springer, Berlin, 2013.

Pellionisz, A:J.; The Principle of Recursive Genome Function. Cerebellum (2008) 7:348–359 DOI 10.1007/s12311-008-0035-y.

Penner C, Knudsen R, Miuf M and Andersen C. An Algebro-Topological Description of Protein Domain Structure. PLoS ONE | www.plosone.org 1 May 2011; 6 , e19670. DOI: 10.1371/journal.pone.0083788.

Perez, JC. La révolution des ordinateurs neuronaux, Hermes; Paris, 1990.

Perez, JC. De nouvelles voies vers l'intelligence artificielle (pluri-disciplinarité, auto-organisation et réseaux neuronaux); Masson: Paris , 1988 and 1989.

Perez JC. Codex Biogenesis: Les 13 Codes de l'ADN. Marco Pietteur: Embour, Belgique,2009.

Perez JC. Codon populations in single-stranded whole human genome DNA are fractal and fine tuned by the golden ratio 1.618, Interdiscip Sci Comput Life Sci 2010; 2: 1–13.

Perez JC. The "3 Genomic Numbers" Discovery: How Our Genome Single-Stranded DNA Sequence Is "Self-Designed" as a Numerical Whole. App Math 2013; 4, 37-53.http://dx.doi.org/10.4236/am.2013.410A2004.

Perez, J.-C. Deciphering Hidden DNA Meta-Codes -The Great Unification & Master Code of Biology. J Glycomics Lipidomics 2015a, 5:2 http://dx.doi.org/10.4172/2153-0637.1000131.

Perez JC. First music of DNA. https://sites.google.com/site/thefirstmusicofgenes/home; accessed December 2015(b).

Petoukhov S. Genetic Code and the Ancient Book of Changes. Symmetry: Culture and Science 1999, 10, 3-4: 211-226.

Petoukhov S. Matrix genetics, part 2: the degeneracy of the genetic code and the octave algebra with two quasi-real units (the "Yin-Yang octave algebra"). arXiv:0803.3330; 2008.

Petoukhov S and He M. Symmetrical Analysis Techniques for Genetic Systems and Bioinformatics: Advanced Patterns and Applications, IGI Global, Hershey,NY, 2010.

Petoukhov S. Symmetries in Genetic Information and Algebraic Biology. Symmetry: Culture and Science 2012; 23, 3-4, 225-448.

Petoukhov SV (2012) Symmetries of the genetic code, hypercomplex numbers and genetic matrices with internal complementarities. Symmetry: Culture and Science, 23, 3-4: 275-301.

Petoukhov S. The system-resonance approach in modeling genetic structures. BioSystems 2016,139: 1–11. http://dx.doi.org/10.1016/j.biosystems.2015.11.001

Petsko G. Dog eat dogma. Genome Biology 2000; 1(2) :comment1002.1–1002.2.

Pevsner J. Bioinformatics and Functional Genomics. Wiley-Blackwell: London, 2013.

Pletzer B, Kerschbaum H and Klimesch W. When frequencies never synchronize: The golden mean and the resting EEG. Brain Research 2010; 1335: 91-102 . doi:10.1016/j.brainres.2010.03.07

Pollack G (2013) The Fourth Phase of Water: Beyond Solid, Liquid, and Vapor; Ebner and Sons: Seattle, Washington; USA.

Power D,Watson R, Szathmáry E, Mills R,Powers S,DoncasterP and Czapp B.What can ecosystems learn? Expanding evolutionary ecology with learning theory. Biology Direct 2015 10:69; DOI 10.1186/s13062-015-0094-1.

Prabhu V. Symmetry observations in long nucleotide sequences. Nucleic Acids Research 1993; 21: 2797-2800.

Prunell AA. Topological Approach to Nucleosome Structure and Dynamics: The Linking Number Paradox and Other Issues. Biophysical Journal 1998; 74, May, 2531–2544.

Rabounski D and Borissova, L. General Relativity Theory Explains the Shnoll Effect and Makes Possible Forecasting Earthquakes and Weather Cataclysms. Progress in Physics, 2014, 10,2,63-70.

Rakočević M. Genetic code as a coherent system. Neur Quant 2011; 9,4,821-841.

Ramy K, Aziz, Breitbart M, Edwards RA. Transposases are the most abundant, most ubiquitous genes in nature. Nucleic Acids Research 2010; 38,13, 4207–4217. doi: 10.1093/nar/gkq140.

Rapoport DL and Sternberg S. On the interactions of spin with torsion. Annals of Physics1984;

158, 2: 447–475. doi:10.1016/0003-4916(84)90128-3.

Rapoport DL and Tilli M. Scale Fields as a Simplicity Principlicity. In Proceedings of the Third Workshop on Hadronic Mechanics, vol. II (Patras, 1986); Janussis A, editor, Hadronic J.Suppl. 2 (1986) 682-778.

Rapoport DL. Stochastic processes in conformal Riemann-Cartan-Weyl gravitation. Int J Theor Phys 1991, 30, 11: 1497-1515. DOI 10.1007/BF00675614.

Rapoport DL. Riemann-Cartan-Weyl quantum geometry. II Cartan stochastic copying method, Fokker-Planck operator and Maxwell-de Rham equations. Int Jour of Theor Phys 1997; 36, 10: 2115-2152. DOI 10.1007/BF0243594.

Rapoport DL. Riemann-Cartan-Weyl geometries, quantum diffusions and the equivalence of the free maxwell and Dirac-Hestenes equations. Advances in Applied Clifford Algebras , 1988; 8 (1):129-146 . DOI: 10.1007/BF03041930.

Rapoport DL. Covariant non-linear non-equilibrium thermodynamics and the ergodic theory of stochastic and quantum flows. In: Instabilities and Nonequilibrium Structures vol VI, Tirapegui E, Martínez J and Tiemann R .editors, Springer Verlag, 2000. http://link.springer.com/chapter/10.1007%2F978-94-011-4247-2_19

Rapoport DL (2002a). Random diffeomorphisms and integration of the classical Navier—Stokes equations. Rep Math Phys 49, 1, February 2002: 1–27. doi:10.1016/S0034-4877(02)80002-7

Rapoport DL (2002b). On the geometry of the random representations for viscous fluids and a remarkable pure noise representation. Rep Math Phys, October 2002: 211–250. doi:10.1016/S0034-4877(02)80055-6

Rapoport DL (2003a). Random symplectic geometry and the realizations of the random representations of the Navier-Stokes equations by ordinary differential equations. Random Oper and Stoch Eqs. 2003,11, 4: 371–401. DOI: 10.1515/156939703771891888.

Rapoport DL (2003b). Martingale problem approach to the representations of the Navier-Stokes equations on smooth-boundary manifolds and semispace. Random Oper and Stoch Eqs. 2003, 11, 2: 109–136

Rapoport DL.(2005a) On the unification of geometric and random structures through torsion fields: Brownian motions, viscous and magnetic fluid-dynamic. Found Phys 2005; (35) 7: 1205-1244.

Rapoport DL. (2005b) Cartan–Weyl Dirac and Laplacian Operators, Brownian Motions: The Quantum Potential and Scalar Curvature, Maxwell's and Dirac-Hestenes Equations, and Supersymmetric Systems. Found Phys 2005, (35) 8: 1383-1431.

Rapoport DL.(2005c) Stochastic Geometry Approach to the Kinematic Dynamo Equation of Magneto-hydrodynamics. In Trends in Partial Differential Equations of Mathematical Physics. Rodrigues J, Seregin G and Urbano J (Eds.), Birkhauser, 2005, 225-241. DOI 10.1007/3-7643-7317-2_17.

Rapoport DL. Torsion Geometries, their Brownian Motions, and the Time Variables, Found Phys2007;(37)4-5:813-854.

Rapoport DL. On the state-space and spacetime geometries of geometric quantum mechanics, In: Foundations of Probability and Physics IV, Proceedings of the Conference, Center for Interdisciplinary Mathematics and its applications, Univ. of Vaxho, Sweden, Khrennikov A and Adenier G, American Institute of Physics Conference Series Springer, 2007.

Rapoport DL. Torsion Fields, Cartan-Weyl Space-Time and State-Space Quantum Geometries, their Brownian Motions, and the Time Variables, Found Phys 2007; (37) 4-5, 813-854.

Rapoport DL .Torsion Fields, the Extended Photon, Quantum Jumps, the Eikonal Equations, the Twistor Geometry of Cognitive Space and the Laws of Thought. In: Ether, Spacetime and Cosmology vol. 3: Physical Vacuum, Relativity and Quantum Mechanics. Duffy M, and Levy J, editors; Apeiron Press: Quebec, Canada, pp. 389-457, 2009.

Rapoport DL (2010a). Torsion, propagating singularities, nilpotence, quantum jumps and the eikonal equations. In: Computing Anticipatory Systems, Proceedings CASYS'09 , Dubois DM, ed., American Institute of Physics Conf. Series 1303. Springer, Berlin, 2010.

Rapoport D (2010b). Self-reference, the Moebius and Klein Bottle surfaces, Multivalued Logic and Cognition. Inter J Comput Anticip Syst 2010; 23: 103-113.

Rapoport DL (2011a). Surmounting the Cartesian Cut Through Philosophy, Physics, Logic, Cybernetics and Geometry: Self-reference, Torsion, the Klein Bottle, the Time Operator, Multivalued Logics and Quantum Mechanics. Found Phys 2011; 41, 1: 33-76.

Rapoport DL (2011b) Surmounting the Cartesian Cut: Klein Bottle Logophysics, The Dirac Algebra and the Genetic Code. NeuroQuantology 2011, 9, 4, Special issue: Classical and "Quantum-like" Views of the Genetic Code.

Rapoport, DL (2011c) On the Fusion of Physics and Klein Bottle Logic in Biology, Embryogenesis and Evolution. NeuroQuantology 2011; 9, 4:842-86.

Rapoport DL (2011d). Torsion Fields, the Extended Photon, Quantum Jumps, The Klein Bottle, Multivalued Logic, the Time Operator,

Chronomes,Perception, Semiosis, Neurology and Cognition. In Focus in Quantum Mechanics,Hathaway D, Randolph E, editors; Nova Science,NY,2011.

Rapoport DL. Klein Bottle logophysics a unified principle for non-linear systems, cosmology, geophysics, biology, biomechanics and perception. Journal Phys: Conf. Ser 2013; 437, 012024.doi:10.1088/1742-6596/437/1/01202.

Rapoport DL (2014a). Surmounting the Cartesian Cut: Torsion, Klein Bottle,Stereochemistry, the Biomechanics of the Cell Splitter in Embryogenesis and Bauplans. Int J Comp Anticip Sys 2014;29:225-246.

Rapoport DL (2014b). Hyper Klein Bottle Logophysics Ontopoiesis of the Cosmos and Life. In: Phenomenology of Space and Time: The Forces of the Cosmos and the Ontopoietic Genesis of Life: Book Two, Tyminieckia, A, editor, Volume 117 of the series Analecta Husserliana275-350.

Rich A. DNA comes in many forms. Gene Volume 1993;135, (1–2), 15: 99-109. doi:10.1016/0378-1119(93)90054-7.

Rodley G. Reconsideration of some results for linear and circular DNA. J Biosci 1995;,20, 2: 245-257.

Rowlands S. Coherent excitations in blood. In: Coherent Excitations in Biological Systems; Frohlich H and Kremer S; eds. Springer-Verlag: Berlin, 1983.

Root-Bernstein R. Causality, Complementarity, Evolution and Emergent Properties. In New Frontiers of Cancer Causation, Iversen O (ed), CRC Press, Boca Raton (FL), 1993.

Root-Bernstein R and Dillon P. Molecular Complementarity I: the Complementarity Theory of the Origin and Evolution of Life. J Theor Biol, 1997; 188: 447–479.

Root-Bernstein R. A Modular Hierarchy-Based Theory of the Chemical Origins of Life Based on Molecular Complementarity. Accounts Chem Research 2012; 45, 12: 2169–2177.

Rosen R. Essays on Life Itself. Columbia University Press, New York, 2000.

Rosen R. Anticipatory Systems: Philosophical, Mathematical and Methodological Foundations. Pergamon Press, first edition, 1985, Springer Verlag, second edition,2012.

Rosen S. Science, Paradox, and the Moebius Principle: The Evolution of a "Transcultural" Approach to Wholeness. State University of New York Press, 1994.

Rosen S. What is radical recursion? SEED Journal 2004; 4, 1:38-57.

Rosen S. Topologies of the Flesh: A Multidimensional Exploration of the Lifeworld. Ohio Univ. Press, Illinois, 2006.

Rosen S. The Self-evolving Cosmos: A Phenomenological Approach to Nature's Unity in Diversity. Series on Knots and Everything 18, World Scientific: Singapore, 2008

Rowlands P. From Zero to Infinity: The Foundations of Physics. World Scientific, Singapore, 2007.

Royal Academy of Sciences, Sweden. https://www.nobelprize.org/nobel_prizes/chemistry/laureates/2016/advanced-chemistryprize2016.pdf.

Ruane G, Swartzlander A, Slussarenko S, Marruccie L and Dennis M. Nodal areas in coherent beams.Optica 2015; (2) 2: 147-150. doi: 10.1364/OPTICA.2.000147.

Rzepa H. Möbius Aromaticity and Delocalization. Chem Rev 2005; 105 (10), pp 3697–3715.

Saini N, Zhang Y, Usdin K and Lobachev K. When secondary comes first -The importance of non-canonical DNA structures. Biochimie 2013; 95, 117e123. http://dx.doi.org/10.1016/j.biochi.2012.10.005.

Sasisekharan GV, Pattabiraman N and Gupta G. Some implications of an alternative structure for DNA Proc Natl Acad Sci USA 1978;75, 9; 4092-4096.

Schempp W. Quantum Holography, Synthetic Aperture Radar Imaging and Computed Tomographic Imaging. In: Quantum Measurements in Optics NATO ASI Series Volume 282, Springer Verlag, Berlin, Germany, 1992, 323-343.

Schempp W. Quantum holography and neurocomputer architectures. In: The Physical Nature of Consciousness. Van Loocke P (editor), John Benjamins, Amsterdam 2001.

Seruggia D and Montoliu L. The new CRISPR-Cas system: RNA-guided genome engineering to efficiently produce any desired genetic alteration in animals. Transgenic Res 2014 Oct;23(5):707-16.

Shanon B. The Antipodes of the Mind. Oxford Univ. Press, Oxford, 2003.

Shapiro J. Evolution: A View from the 21st Century. FT Science Press, New Jersey, 2011.

Shih AC, Lee DT, Chin, C-F, Liao, H and Li WH .Palindrome Patterns in Genomes. Technical Report No. TR-IIS-04-019. Institute of Information Science, Academia Sinica, Taiwan; 2004,http://www.iis.sinica.edu.tw/LIB/TechReport/tr2004/threebone04.html.

Shnoll SE. Cosmological Factors in Stochastic Processes. American Research Press: Rehoboth,NM,USA,2012.

Shnoll SE . On the Cosmophysical Origin of Random Processes Open Letter to the Scientific Community on the Basis of Experimental Results Obtained During 1954–2014. Progress in Physics2014;10,4:207-208.

Solà-Soler J. Phi and Music in DNA. In http://www.sacred-

geometry.es/?q=en/content/phi-and-music-dna.AccessedJune01,2015.

Spencer-Brown G. The Laws of Form. Allen and Unwin, London, 1969; Bohmeier Verlag, Leipzig,5thinternationaledition,2008.

Spinoza B. Ethics, part 3, prop. 6. Curley, E., ed., Penguin Classics: New York, NY, 2005, 144–146.

Stakhov A. Mathematics of Harmony. World Scientific; Singapore, 2009.

Stergachis A, Haugen E, Shafer A, Fu, W, Vernot,V, Reynolds A, Raubitschek A, Ziegler S, LeProust E, Akey J, Stamatoyannopoulos J. Exonic Transcription Factor Binding Directs Codon Choice and Affects Protein Evolution. Science 13 December 2013, 342, no. 6164: 1367-1372.doi:10.1126/science.1243490.

Stern A. Matrix Logic and Mind: A Probe Into a Unified Theory of Mind and Matter. Elsevier, Amsterdam, 1992.

SternA. Quantum Theoretic Machines. Elsevier: Amsterdam,2001.

Stettler I, Weber H, Koller T and Weissmans C. Preparation and Characterization of Form V DNA, the Duplex DNA Resulting from Association of Complementary, Circular Single stranded DNA. Jour Mol Bio 1979;131:21-40.

Summers W. Phage and the Early Development of Molecular Biology. In The Bacteriophages Calendar R et al (ed.). Oxford University Press; 2 edition, 2005.

Suzuki D and Griffiths A. An Introduction to Genetic Analysis. W.H.Freeman & Co Ltd., San Francisco,1976.

Swigon D. The mathematics of DNA structure, mechanics, and dynamics. In: Mathematics of DNA Structure, Function and Interactions; Benham C, Harvey S,Olson W, De Witt L,

Swigon D,editors;Springer:Berlinm2009,293-320. Swindale N. Visual Cortex: Looking into a Klein Bottle, Current Biology 1996; 6, 7:776–779.

Swindale N and Bauer H. Application of Kohonen's self-organizing feature map algorithm to cortical maps of orientation and direction preference. Proc R Soc Lond B 1998; 265: 827-838.

Sykes B. Mitochondrial DNA and human history. The Human Genome. Wellcome Trust. (10 September 2003 Retrieved 5 February 2012).

Takeda M and Nakahara M. Protean Genome; ResearchSignpostPubls.:Kerala,India,2013.

Tanaka S. Theory of self-organization of cortical maps: mathematical framework. Neural Networks 1990, 3, 625:640. doi:10.1016/0893-6080(90)90053-N.

Tanaka S. Topological analysis of point singularities in stimulus preference maps of the primary visual cortex. Proc R Soc Lond [Biol] 1995; 261: 81–88.

Tanaka S. Information representation and self-organization of the primary visual cortex. In Natural and Artificial Computation: Proceedings of the 5th NEC Research Symposium; Waltz E (ed.), SIAM,1996,93-123.

The ENCODE Project Consortium. An integrated encyclopedia of DNA elements in the human genome.Nature 2012; 489; accessed 6 September 2016.

Thompson D'AW. On Growth and Form;.Cambridge University Press: New York, 1945 .

Thouless D. Topological Quantum Numbers in Nonrelativistic Physics. World Scientific, Singapore, 1998.

Todeschini R and Consonni V. Handbook of Molecular Descriptors. Wiley-VCH, New York,2000.

Tørring T, Voigt N, Nangreave J,Yan H, Gothelf K. DNA origami: a quantum leap for self-assembly of complex structures. Chem Soc Rev 2011; 40, 12:5636_5646.doi:10.1039/c1cs15057j.

Trifonov EN. The multiple codes of nucleotide sequences. Bull Math Biol 1989, 51(4):417-32.

Trifonov EN. Cracking the chromatin code: Precise rule of nucleosome positioning. Physics of Life Reviews 2011;8: 39–50.Trifonov EN. Codes of biosequences. In: The Codes of Life, Barbieri M. (ed.), Springer,2008, pp.3-12.

Van Driel R and Otte AP. Nuclear Organization, Chromatin Structure, and Gene Expression. Oxford University Press, Oxford, 1997.

Van Noort V, Worning P, Ussery DW, Rosche W and Sinden R. Strand misalignments lead to quasipalindrome correction. Trends in Genetics 2013; 19:365-369.Varela F. A calculus for self-reference. Int Jour of Gen Sys, 1975, 2(1):5–24.

Varela F. Principles of Biological Autonomy. Elsevier/North-Holland: New York, 1979.

Voineagu I, Nayanaran V, Lobachev K and Mirkin S.Replication stalling at unstable inverted repeats: Interplay between DNA hairpins and fork stabilizing proteins. PNAS July 22 2008; 105, 29: 9936–9941. http://dx.doi.org/10.1016/j.biochi.2012.10.005.

Volodyaev I and Beloussov L. Revisiting the mitogenetic effect of ultra-weak photon emission. Frontiers in Physiology, 2015; 6, Article 241. doi: 10.3389/fphys.2015.0024.

Waldon D. CRISPR memories of RNA. Nature Reviews Genetics 2016; 17:192–193.
doi:10.1038/nrg.2016.31.

Watson J and Crick F. Structure for Deoxyribose Nucleic Acid. Nature 1953; 171: 737-.

Weiss H and Weiss V. The golden mean as clock cycle of brain waves. Chaos, Solitons and Fractals 2003; 18, 643-652.

Werner C and Whitsel BL. Topology of the body representation in the somatosensory area 1 of primates,I. Neurophysiol 1968; 31:856-869.

Werner G. The topology of the body representation in the somatic afferent pathway. In: The Neurosciences, Second Study Program. Schmitt FO, Quarton CC, Melnechuk T, Adelman G; editors, Rockefeller University Press: New York, NY, 1970, pp 605-617.

Wikipedia. CRSPR. https://en.wikipedia.org/wiki/CRISPR; accessed April 28, 2016.

Wikner R. Extrachromosomal Elements in Lower Eukaryotes. Plenum Press, NY, 1986.

Wright J, Bourke P and Favorov O. Möbius-strip-like columnar functional connections are revealed in somato-sensory receptive field centroids. Frontiers in Neuroanatomy. October 2014; 8 ;Article 119 . Doi: 10.3389/fnana.2014.00119.

Wolfram S. A New Kind of Science; Wolfram Media: Champaign, Il, USA, 2002.

Lin Y (Guest Editor). Mystery of Nonlinearity and Lorenz's Chaos. A special double issue of Kybernetes: The International Journal of Systems and Cybernetics,1998; 27, 6 & 7: 605 – 854.

Lin Yi. Systemic Yoyos: Some Impacts of the Second Dimension. CRC Press, Boca Raton, Fl USA, 2002.

Wu Y and Lin Y. Beyond Structural Quantitative Analysis: Blow-ups, Spinning Currents and Modern Science. World Scientific, Singapore, 2002.

Yakushevich L. Nonlinear Physics of DNA, Wiley (Chichester) 1998; second edition 2004.

Ycas M. The biological code. North-Holland: Amsterdam,1969.

Yoshikazu K, Okazaki R. Mechanism of DNA chain growth: XIII. Evidence for discontinuous replication of both strands of P2 phage DNA. J Mol Biol 1975; 94, 2: 229-241.

Zenkin A. Scientific Intuition of Genii Against Mytho-'Logic' of Cantor's Transfinite 'Para-dise'. Philophia Scientiæ 2005; 9-2 | 2005. http://philosophiascientiae.revues.org/532 ;
DOI : 10.4000/philosophiascientiae.532.

Zenkin A. Ten Fatal Mistakes of the Cantor's Proof of the Real Numbers Uncountability (fragment of a letter to the Editor-in-Chief, Bulletin of Symbolic Logic.; 2000. http://www.ccas.ru/alexzen/papers/10_mistakes.html; accessed April 04,2016.

Zheng J, Birktoft J,Chen Y, Wang T, Sha R, Constantinou P,Ginell G,Mao G and Seeman N. From Molecular to Macroscopic via the Rational Design of a Self-Assembled 3D DNA Crystal. Nature, September 3 2009; 461(7260):74–77.doi: 10.1038/nature08274.

Notes

(we continue with the numbering of the previous Parts)

21. The topological model for DH replication and transcription by superhelix creation for "circular" DNA, assumes a 360° twist at a site of cutting of a ribbon, 180° turn for each of two points, then rejoined. Thus, it mimics thus one turn of a DH rather than a 180° 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 in Bates and Maxwell (2005).The rejoined ribbon then cut longitudinally, alike to cutting along the mid-red line in Fig.4.II, 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. 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.

22. As we already discussed, the Fibonacci sequence is a HyperKlein Bottle with double reentrance of a distinction (simpler than Fig. 4.II.B), a topological meta-algorithm which yields an output from the double reentrance of itself in two levels (Kauffman, 2002); it is the "fundamental reality "atom" of information" as already established by Johansen (1991). 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 (Johansen, 2010, 2012). 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.

23. The DNA transposon is excised from its position via transposase,and reintegrated el-sewhere 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

reintegration and are thought to add to the difficulties in recognizing transposons.

24. 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 (Goriely, 2008). This suggests that single stranded DNA and RNA is at the roots of other more contorted genomic geometries, and particular the double helix.

25. Bohm's original conception superposed a dualistic logophysics with a metaphysics of wholeness –which later evolved to a theory of order and creativity (Bohm and Peat, 2000), 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 (Hiley and Pylkkänen, 1997), later extended to an informational "guiding" field; (Bohm and Peat, 2000). 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. However, the latter association of creativity to the participation of the subject closing a loop somewhat suggests the latter cybernetics (Hiley, 2015). 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 (Rapoport, 2011a) from which non-orientability is created (Rapoport, 2013), 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 (Hiley, 2015). Yet, the conceptual richness of Bohm's theory, deserves more space that the one we can afford in this article.

26. Thus, they are called "selfish" (Dawkins, 1976), rather than being associated to the Principle of self-reference, which is far beyond the cognitive setting for the author of that take.

27. Topological operations such as folding and their identifications as to produce the non-orientable surfaces have an imaginal (not to conflate with imaginary) nature which is that of agency, and is prior to their actual manifestation; see e.g. Fig. 2.II. More generally, mathematization is essentially imaginal, but as pledged by Spencer-Brown, Chaitin, Hellerstein, Wolfram and others, not all mathematics are equal with regards to its reification, although dualism is effective, by fracturization, in doing so. 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, particularly the Fibonacci meta-algorithm, upholded by Johansen as the ultimate ground for thought, which Shnoll proposed to be at the basis of the homonymous effect (Shnoll, 2012, 2014; Rabounski and Borissova 2014). 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, due to Stein E. 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 (Johansen, 1991). 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 semiotic operators which reify the algorithmic causality, while still they are the actual manifestations of this agency. In linguistic terms, these semiotic operators appear as injunctions, such as "cut", "paste","replicate", "recur", or still the instructions to build a mathematical structure (see caption of Fig. 1.II). One such semiotic operation is the computational representation of the principle of self-reference as recursion, which is a protoform of coherence. 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 (Johansen, 1991).

28. Already in the 1930s surged the quest to determine whether mutations followed as a response to environmental action, say the exposure of bacteria to the addition of lactose to their medium, in accordance with Natural Selection, or they became *known* as a consequence of the imposition of the selective growth condition. As Summers put it: "The outcome of this research would have profound implications [the formulation of the Central Dogma] not only for the science of genetics but also for a deeper understanding of evolutionary biology in general… M. Lewis examined the mutational change from the inability to ferment lactose to the ability to use this sugar source in the Escherischia coli strain mutabile. He concluded that the mutations to lactose utilization occurred prior to the selection, not as a consequence of exposure to the selective conditions" (Summers, 2005). What was also found

about the role of RNA in terms of the Central Dogma, led to identify the alien rather than the host as having the upper hand in terms of the outcome of the induced metamorphosis, as a distribution of identity. Summers: "Key experimental support for the role of RNA as an intermediary in such information transfer was the finding that in phage-infected cells, the base composition of newly synthesized RNA was much more like that of the phage DNA than the host DNA...Thus, it was concluded that phage gene function required the synthesis of RNA molecules that differed from those present in the uninfected cell, and that the RNA base composition, and hence its information content, was determined by the DNA of the phage" (Summers, 2007). No less remarkable was that "[T]he random nature of mutation and its very low frequency of occurrence suggested that it might be similar to, or governed by, a quantized, two-state process". The present imperative of dual logic, would immediately suggest itself as the case of this process of assimilation. However, we have repeatedly made the case for, the logophysics by which a host assimilates an alien is non-dual and associated to a HyperKlein Bottle. Upon the metamorphosis being completed, the metamorphosed host operates as a Klein Bottle; which in its Matrix Logic representation is indeed tantamount to a two-state quantum system (Stern, 2001; Rapoport, 2011a). The anticipative –prior to mutation- behaviour of the host with respect to the phage seems to indicate that these two formed a superposition state, which upon the Outside-Outside phage incorporated into the bacteria as an Inside-Inside through the superposition Outside-Inside and Inside-Outside states.This may be related to biochemical recognition in terms of harmonic resonance (Cosic,1997) associated to oscillations of electromagnetic fields of the host and phage genome. Root-Bernstein has proposed a theory for the origin of life and evolution in terms of the principle of molecular complementarity of shape, which in the case of enzymes he proposed to be embodied by the Möbius strip (Root-Bernstein, 1993). On the basis of this principle of complementarity which is topological due to the continuity of the coexistence of shapes up to the production of holes –though Root-Bernstein's definition is in another terms-, which we rather extend to a continuity up to Klein Bottle penetrations, he raised the topic whether the immune system has evolved to protect organisms from non-complementary shapes (Root-Bernstein, 2012). We have already seen the crucial role of non-orientability and molecular complementarity, in the present topological sense, both to genomics and evolution, and even development. In Root-Bernstein's theory, life and molecular complementarity are synonymous, and we have argued in §1.1 that the metaform of the latter is the Klein Bottle.

29. Lima de Faria argued for the role of metamorphosis in the ten-fold increase of hormones released in the blood of tadpoles as they emerge to a non-acquous environment. Thus metamorphosis appears following hormonal secretions produced upon environmental changes leading to vertebrates becoming terrestrial species (Lima de Faria,1988), as a series of topological metamorphosis to produce the novel terrestrial anatomy-physiology. We already discussed that the HyperKlein Bottle topology of genomes is that of embodied contextualization vis-à-vis environments. As noted by Goertzel, this metamorphosis is a kind of structural instability, whereby a small change in a processual network may produce major changes (Goertzel, 2013). In his lifework, Lima de Faria produced several such examples; yet is still most remarkable that both Bell Petigrew and Lima de Faria identified that biological shapes follow from those of material systems, as is the case already in crystals, where as we already said, shape is tantamount to the structural information of a torsion geometry. Lima de Faria further claimed that biological shapes are thus not created de novo, but even appear with some periodicity; thus he coined the term "biological periodicity" (Lima de Faria, 1995). Yet, he insisted that this ability of organisms to change with the environment is already present in minerals; say a rock salt crystal upon immersion in a solution of sodium chloride and urea changes its form. Similarly, "eye formation may be surpressed in fishes as the result of the presence of magnesium chloride in water (Lima de Faria,1995); furthermore "[A]n organism does not need to be initially exposed to a given environment to produce a form or function that fits into… display[ing] an "adaptation"to a type of environment to which… [they] have not been subjected. Still, tadpoles (i.e. frogs in the larval stage) live in water; however as they become adult frogs, they undergo notorious physiological and structural changes as they adopt a terrestrial life, with the reabsorption of the tail and of pulmonary respiration, and other major changes. Major structural transformations of plants also occur upon changing the environment, according to the ordered addition of components, both in atoms and molecules, reflecting thus the structure of the Periodic Table, which we recall is that of a Klein Bottle (Boeyens, 2010). As noted by Lima de Faria, this allows, in principle, to predict novel biological transformations. There is still another phenomenology of metamorphosis, as explored by cognition science (Shanon, 2003), ethnology and anthropology (Duerr,1985; Narby, 1999). It claims a quick *perception* of a metamorphosis of the self and the world, lived as if real novel capabilities in terms of a non-dual distributed identity and non-

dual logophysics. This is experienced in expanded or altered consciousness states and dynamical perceptual contexts.

30. Long before comparative genomics would appear, Lima de Faria observed: "There are two trends of thought that has been pernicious to the development of biology. The first is that the human species is unique. The second one is that complexity dominates the biological world " (Lima de Faria, 1983), quoted from Gordon (1999).

31. We already introduced an immune system with a local non-orientable topology which appears to produce a Lamarckian evolution. Already the immunological system related to the distribution of Self with respect to Thou, and its proliferation was identified as crucial to evolution (Ohno, 1992). He further suggested that at a neuronal level, the complementary attraction of cell surfaces proteins may have been crucial to the creation of neural networking, and thus to the enhancement of predictive capabilities which are somewhat characteristic of humankind. We already argued that instead of a mechanical shape complementarity, the principle for distant macromolecular recognition is that of bioresonance for which ordered water domains which as we already explained have a Möbius strip structure, play a crucial role in the transmission of these resonant oscillations. Indeed, the basic assumption is that this bioresonance operates through oscillations with characteristic frequencies of a putative field, believed to be of electromagnetic nature, and thus an example of the torsion field (Rapoport, 1987, 1997, 1998, 2005b, 2009a, 2010a, 2012c), which propagates through water. It is natural to propose that these characteristic frequencies should be related to the electromagnetic fields emitted and absorbed by genomes according to its own bioresonance system, which themselves generate and break down intermittently the ordered water domains.

32. 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 (Mitchell, 2015). Remarkable work on the music of DNA as follows from the genomic matrix due to Perez arranged as the Dragon curve (Perez, 2009, 2010, 2013) is Jordi Solà- Soler's (Jordi Soler, 2015), following the pioneering work of Perez (2015), and recently Petoukhov's work being currently presented (personal communication) following remarkable studies on harmonics, aesthetics, the proportions of the human body and genomic matrices (Petoukhov and He, 2010). Solà-Soler also concurs on identifying the essential role of Φ as providing coherence to genomes.

33. In this regard, Lima de Faria elaborated a theory showing that the developed morphology of vertebrates appears to follow an expanding circular geometry with stripes positioned in 90° to the axis of development. This conforms for the whole vertebrate bodies an orthogonal grid that can be conceived as produced by standing waves. Yet, this "geometry" of morphology has a molecular basis, particularly in the batteries of Hox genes (Lima de Faria, 2014). Developmental fields, as standing waves, and the genome, cooperate with the latter playing the role of a canalizer of symmetries, as elaborated by Lima de Faria (1988). However, as elaborated by Gordon and Björklund-Gordon, tissue differentiation appears to be related to sequences of contraction and expansion waves in the embryo of Axolotl, obeying the Fermat principle of minimal action (Gordon, 1999), which was further related to torsion geometry and non-orientability (Rapoport 2011c, 2014a).

34. With respect to the formalization of physics as a system of symbols which has a semantics, it is notable the Nilpotent Universal Rewrite System (NURS) due to Rowlands (2007). The most known rewrite system is the self-referential lambda calculus. NURS which provides for a symbolic representation of the four fundamental interactions of particle physics, is based on recursion (as an algorithmic operation of self-reference) and a principle of null action, nilpotence, which resembles Fuller's Synergetics which is fully geometrical-topological and non-dual. This theory is based on only two operators, one of creation and another one of conservation, operating on alphabets and subalphabets to generate the symbolic strings. Furthermore, they operate solidariously to produce zero, 0, thus the nilpotency. Yet, following the implicit take in the sciences that the problems with syntactic systems that arise from self-reference are done away by the dualistic ontology, NURS which operates through recursion is posited in terms of the dual logophysics (Rapoport, 2014b). However, Rowlands suggested that there is an analogy with Klein Bottle at the basic level of spinor fields –in terms of which NURS develops- and their 720º rotational symmetry which is very much the case of the Klein Bottle as discussed in Fig. 2.I in Part I; see also Figs. 2.II & 3.II in Part II. Actually there is more to this analogy . The representation of the NURS in terms of algebraic elements given by the positive quaternions and their minuses conjugates, $\mp 1, \mp i, \mp j$ and $\mp k$, for which the minuses are considered as duals of the pluses, are introduced in terms of the primal duality of the conservation and creation operators to achieve 0, and conceived in terms of Boolean algebra, which is the standard ontology in the theory of abstract rewrite systems (Dershowitz

and Jouannaud,1990), due to the binary nature of the rewrite relation. But already the complex numbers, generated by ∓1 and ∓**i** (**i** is the square roots of -1, i.e. **ii**= -1), upon its one-point compactification with the Riemann 2-sphere for its representation with infinity placed at the North Pole, embodies a closed loop; see Fig.2.I. It unifies the purely real and imaginary numbers, generated by ∓1 and ∓**i**, respectively, as presented in Fig. 2.I Centre. The whole development of the NURS hinges on the assumption of the separation of real and imaginary axis, rather than on the continuity to produce the 720° symmetry of spinors embodied in the closed-loop return to 0. In the setting of NURS, mass and time are real, while charge and time are imaginary; but as we shall see below, this separation is not the case, and actually the most mysterious physics is given upon their metamorphical integration, rather than their separation which is the implementation of dual ontology. Remarkably table 3.1 which describes the transition of two elements 0,E is identical to the Kein Bottle Logic of Fig. 2.III, until the nilpotence condition is imposed, which is tantamount to identify Outside-Outside with Inside-Inside; in doing so, we have a further reduction of Boolean logic to a single state, 0, which is the nilpotence condition. From there onwards, the nilpotence is associated to dualism. But the actual construal of the theory, is related to the disconnection of the real and imaginary axis of the complex plane, as if two separate axis, implicitly reconnected by the nilpotence condition by neglecting the non-orientability of the compactified complex plane. It is the non-orientable connection of them which is crucial to the non-linear dynamics of blown-up systems which are generic rather than exceptional. As already mentioned, this non-orientability at infinity is further crucial to the processes of renewal of these non-linear systems, such as the negative-entropy reentrance of entropy divergent non-linear thermodynamical systems at 0, as they reinitiate in a new phase (Rapoport, 2013; Wu and Lin, 2002; Lin, 1998, 2008). Nilpotence reappears in terms of the said calculus, yet fully associated to torsion and the relational paradigm; more of this in note no.6. Yet, what is peculiar to the NURS which is based on the Dirac equation of quantum mechanics, is that so far has not reproduced itself as a theory of electromagnetism based on Maxwell's equations, which as torsion fields equations are equivalent (Rapoport, 1998, 2005b). The latter is an equation for a spin-1 field, a boson, while the Dirac equation is for a spin-1/2 field, a fermion. Fermions abide to the Fermi's exclusion principle which is related to a dual ontology since two fermions cannot be in the same quantum state, unlike bosons as in Maxwell equatons which are related to a non-dual ontology since they may share the same quantum state. Actually, in the setting of the so-called supersymmetries, bosons and fermions are conceived as instances of a single kind of particle. Furthermore, they are intertransformable by multiplication by i. Represented on an helix, both bosons and fermions are conceived as having an associated Internal arrow vertically for bosons, horizontally for fermions (Freedman and Niewenhuizen, 1978). Thus, represented on the Riemann sphere as in Fig.2.I, again, TIME plays the role of a metamorphic transformation transforming bosons, say as identified by states on the real axis, to fermions, as states on the imaginary axis. As before, the 720° rotation returns an original state to itself: the identity transformation. At this primal level, Maxwell's electromagnetism is equivalent to quantum mechanics; in the latter non-commutativity is the crucial property as it appears in the Heisenberg relations. But then, the non-commutativity of torsioned spacetime is the common basis for both theories. Yet, the equivalence of both equations, for a massless electromagnetic field and a massive Dirac field, both being torsion geometries, shows that indeed the separation of the real and imaginary coordinates to distinguish between the constants of physics, is not the case. Indeed, this equivalence transforms the spin one-half field with a positive real number, the mass, to a massless (electromagnetic) field, which is both a real and imaginary parameter, or still, nor real nor imaginary, as it stands at the origin; the converse is also the case, both under a condition of electromagnetic potentials being restricted to the spin-plane (Rapoport,1998, 2005b). Mass appears to be associated to the kinetic energy of rotation in the spin-plane of the Dirac-Hestenes spinor-operator field which generates two-dimensional electromagnetic potentials (Rapoport, 1998, 2005b). Thus, at a quantum level, mass is not primal, nor related to linear motion, but to rotational motion, and to electric charge. Indeed, the most basic and mysterious physics is embodied by the relatedness of the fundamental "parameters" through intertransformations, rather than standing for separable parameters as in NURS.