Klein Bottle Logophysics, Topological Chemistry, The Genetic Code, Universal Rewrite System, Bauplans and the Surmountal of the Cartesian Cut.

Diego Lucio Rapoport

Univ.Nac. de Quilmes, Buenos Aires, Argentina; Email:diego.rapoport@gmail.com

Abstract: We reintroduce logophysics based on self-referential torsion fields and the Klein bottle (KB) logic, which unifies the objective and subjective realms. We apply it to biology, particularly allosterics and the genetic code. We reveal several topologies of the genetic code and its bioinformatics codification, in particular the hyper Klein bottle (HKB) surface. We relate it to the Universal Rewrite System, the Code of Nature, and Dirac algebra.We find that the double helix is unnecessary in this setting, and elaborate the ontology of 3D with regards to time, multistable perception, and a topological (lawless) form of Newton's Third Law. We present the key ideas for a logophysical theory for contextual evolution.

Keywords: Logophysics, Torsion, Klein Bottle, Quantum Tensegrity, Double Helix.

Introduction:Topological Stereochemistry, Allosterics & DNA

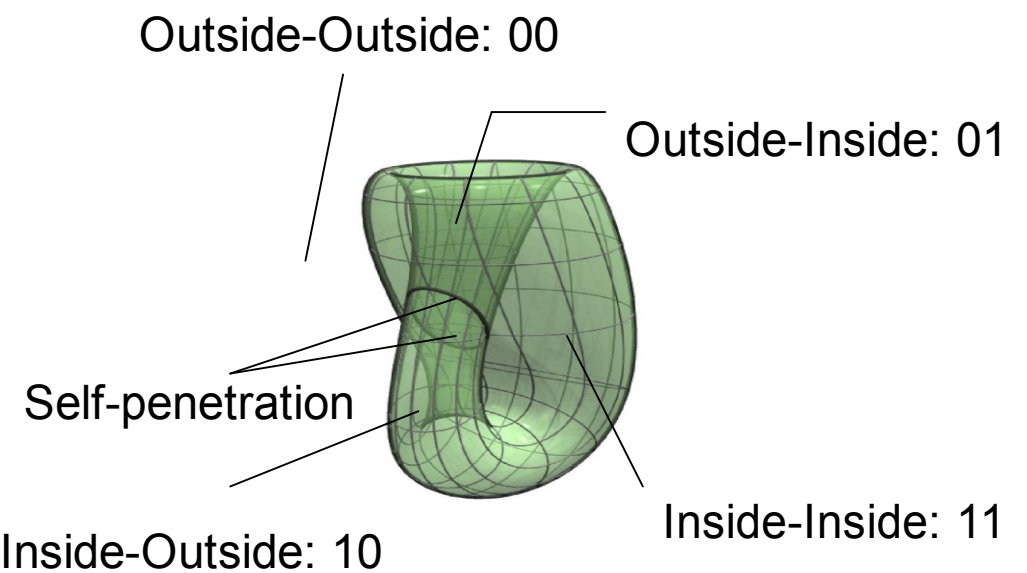
A logophysical theory surmounting the conception that separates the objective and subjective realms (*Cartesian Cut*), based upon Klein Bottle logic (**KBl**) and torsion fields was proposed in [22,23], and applied to cell biology and embryology [20]. The objective of this article is to extend this conception to the genetic code (**GC**) and its bioinformatic coding, and to the Nilpotent Universal Computational Rewrite System (**NUCRS**) [12,25], a unifying language for mathematics, physics and the **GC**. A crucial role was ascribed to topological stereochemical (molecular configurational) changes in chemistry and cell biology, in which the Moebius band (**MB**) and the **KB** (from now on we may not explicit a distinction between the surface and the logic as they are fused, as we shall see next), acting in the cell's membrane adhesion cites for i*ntegrines,* may be related to the logophysical onset of embryonic wave differentiation.These are crucial molecules for the self-organization and self-regulation of the cell through its quantum tensegrity structure that extends outside of the cell to the extracellular matrix, conforming thus an holonomic living matrix, in which quantum-topological superposition and holography are at the roots of cell biology [20]. The living matrix appears to act as a perceptual self-transforming system,in relation with the environment. Topological transformations of molecules and the cell's living matrix, are conceptually similar to the allosteric effect, which is regulatory, and is transmitted over a *distance* (alike entanglement, either topological or quantum, which in the **KBl** are related [22,23,40]) within a protein, by which the binding of an effector in one site will change the catalytic behaviour of an enzyme or the binding affinity of a binding protein in a different part of the biomolecule. Conformational changes, say enzyme-substrate, antibody-antigen,protein-protein complexes, of protein to **DNA**, are essential to the

mutual *recognition* of biomolecules.The classic example is haemoglobin where binding of oxygen to one of the four subunits arranged at the vertices of a tetrahedron around an axis of two-fold symmetry (alike the DNA single strand of the NUCRS), increases the affinity of the others; remarkably, haemoglobin undergoes a crucial topological transformations that allows it to phagocyte. Thus, Outside is turned Inside,as is the case of the living matrix and the KB [20]; since the human brain originates from the neural *ec*toderm, this generic interiorization establishes the individual's relation with the environment [23,48]. Thus, a KBI molecular topology, can produce quantum coherences by establishing a logophysical recognition in which interior and environment are unified, through quantum (particularly nilpotent) *logical* gates [22,23,40]; these topological changes produce biochemiluminisence (biophotons) [20]. We shall see below that the GC, stems from the logophysical recognition of these logical gates. Mechanical recognition is the case of enzymes in the key and lock model proposed by Emil Fischer, in which there is a perfect conformational complementarity; even here the matching is not an artefact of the parts (¨the whole is more than the sum of its parts¨, rather different!) but the KB holonomy of their logophysical integration. A dynamical modification to the lock and key model appeared, the induced-fit (IF) [15]: Since enzymes are flexible structures, the active site is continually *reshaped* by interactions with the substrate as the substrate interacts with the enzyme, alike to the behaviour of the cell's membrane with respect to the cytoskeleton and the extracelular matrix [20].Yet, while the IF was based upon geometrical and topological related (orientability) issues, the discovery of natively unfolded proteins, i.e. protein systems that perform their physiological role *without* the need of acquiring a well defined 3D structure [15], lead to enlarge the idea of 'structure' from a specific *geometrical* pattern to a dynamical *non unique* configuration [9]. These adaptable stereochemical modifications [29] point out to the biological importance of topological changes [20]. This is analogous to the link existing between the topological representation of a given network (its wiring diagram, corresponding to the crystal structure of the protein) and the dynamics of the network itself that are supported (but not barely coincident) with its topology [9], alike to the differentiation waves acting to the cell's tensegrity structure, on which the quantum wave propagation produces embryological development [20]. We notice the striking similarity with the modification of the living matrix with regards to the environment, which we interpreted in terms of the KBl [20]. In that work we contested the dualistic approach implicit to the rigid cathegorization of cell biology and phenotypical transformations derived from an Outside/Inside dual logic, which haemoglobin phagocytosis disproofs, yet is pervasive to biology, even in alledgedly radical revisions from classical physics [20]. Indeed, the KB has no separation between inside and environment, due to its self-containment; see Fig. 1 below. As a result, the substrate does not simply bind to a rigid active site; the aminoacid side chains which make up the active site are molded into the precise positions that enable the enzyme to perform its catalytic function, evidencing a design-oriented change which the present logophysical paradigm associates with the TIME operator [20,23]. IF may enhance the fidelity of molecular recognition in the presence of competition and noise via the conformational proofreading mechanism [9]; yet, what *we* interpret as ¨noise¨ might be interpreted as geometrically structured signaling [46], in a nested heterarchy of KBs [20,23]; this applies as well to evolution. Robustness of DNA and embryological differentiation, in spite of ¨noise¨, is the very signature of the KBl; its informational Hadamard matrix representation, central to quantum computation [22,23,40], is

the basis for error-correcting digital communications [18], and quantum self-correcting codes in the Matrix Logic of the **KBl** [22,40]. This robustness is apparent also in the **KB** topographic map of the sensorium [23] and in the *persistent homology* of shapes of higher-dimensional data of digital photographs of natural sceneries, when processed in terms of depth-enhancing (i.e. time operation; we shall retrieve this below!) filtering, that evidences a hidden **KB**, as a universal gestalt [10]. The topological embodiment of this coupling of an object (say, molecule, cell, etc) to the environment is difficult to identify since the integrity of these entities under study may change their structure beyond recognition; the same problem is encountered with molecules [29]. Yet, catenoid deoxyribonucleic acids in the mitochondria of several cells (catenanes are topologically-mechanically-interlocked molecular architectures, consisting of two or more interlocked macrocycles), are pervasive to organic chemistry and **DNA** [26]. A mechanism for the biogenesis of catenoid **DNA** on the basis of the **MB** [35] and for the construction of **MB DNA** were proposed [4]. If a **MB** twisted η times is cut along the midline, catenanes are formed whenever η is an even number; when η is unity, a single ring is obtained with a double circumference; other odd values of η yield various knots [5,7]. The *replication* of **MB DNA**, which is *equivalent to this slitting*, naturally yields catenoid & knotted macromolecules.Topological operations on **DNA**, are the core of cutting-edge synthetic nanobiology technologies [28] and in metamaterials [11]. Through topological and self-assembling operations upon **DNA** material, catenanes, rotaxanes and knots are produced [38], in which tensegrity structures having multivalued logic enantiomer configurations (as in Fig. 3 below), have a central role [22]. Hereon, we shall deal with the topologies and informatics of **DNA** in the setting of topological stereochemistry and the **KB.**

The Klein Bottle, Stereochemistry, the Genetic Code and Informatics

We depart from a logical-numerical representation of the **KBl** in Figure no. 1:



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. 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][c,d] = [ac,bd], [a,b]' = [b',a'], with (a')' = a , aa = a, a+a= a for all a= 0 or 1, and a' is the operation of 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 **ij** = **0,** so that **i** & **j** are non-trivial nilpotents. We have mapped the topological states of the **KB** into a 4-state de Morgan algebra which is not trivial since Outside, 0, is different to Inside, 1 [14]; this is a new representation for the **KBl**, from which Matrix Logics –that has quantum fuzzy and Boolean logics as subcases- is derived [22,41]. We notice that **i** and **j** are the *imaginary time-waves* [14,22] that appeared as imaginary logical values in the Calculus of Distinctions [30]; we here see explicitly their association with the **KB** self-penetration. In topological phenomenological philosophy [24], only three states were considered, the container (Outside-Outside) that no longer corresponds to the Cartesian exterior space where objects- the Inside-Inside- are contained in, which is the usual take on space, and the uncontained (**KB** neck) realizing the depth dimension of self-penetration, associated to time [22,23,24]. An identical 3-state logic was provided in [32], in which there is a single reentrance of the form on itself, the 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**. We relate this 4-state logic to the four letters, A, T (or U), G and C, of the **GC**, following a combinatoric-algebraic approach [18,19], by considering the 2x2 matrix (table)

	0	1
0	C 00 (0)	A 01 (1)
1	U 10 (1)	G 11 (2)

which we denote as [C,A;U,G], or still, **P***(*1). We have written in parentheses the decimal interpretations of the elements of the logic; while the pairs 00,01,10,11 will be interpreted in the following –for computational reasons- as binary numbers (with modulo 2 sum) rather than elements of the de Morgan algebra. We shall introduce another distinctions that will be crucial to the topological theory of the **GC**. We know from [22,30] that the invocation of a distinction, is tantamount to invoke through the self-entrance of a form produced by this distinction (as a boundary/cleavage, which as an operator we denoted as ') a **KB**, and in fact as we shall be considering three distinctions, we shall be bringing to manifestation an hyperKlein Bottle (**HKB**), as nested **KB***s*. They are produced by *three* subalphabets of the **GC** [33,18], introduced in terms of pairs of attributes and their lacking (¨antiattributes), described succintly in Fig.2 below and by the following subalphabets:

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

Subalphabet No. 2: amino-mutating or non-amino-mutating under action of nitrous acid HNO_2 [36]; the same division is given by the attributes "keto"or "amino" [34], so that 0 stands for a letter with amino-mutating property (amino), 1 a letter without it (keto), C= A = 0, G = U/T = 1.

Subalphabet No.3: 0 a letter with three hydrogen bonds, 1 a letter with two hydrogen bonds; C=G=0, A=U/T = 1; this is the usual subalphabet.

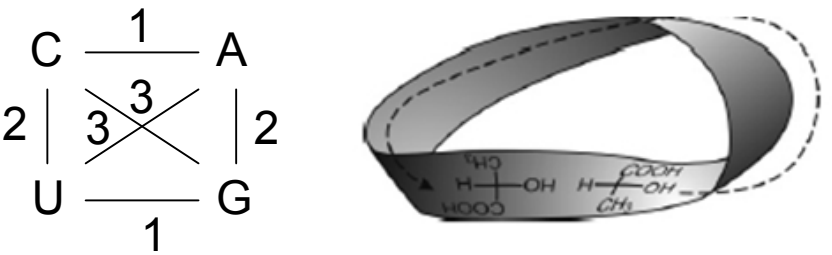
These distinctions introduces further *multivaluedness* in the topological codification of the **KBI**, –yet we shall not tag them with a symbol to distinguish which is the subalphabet they stand for- treating them as binary numbers so that we take 0 (Outside), 1 (Inside); their *multivaluedness with respect to the subalphabets* will manifest in the **KB** and **HKB** that will appear in the **GC**. 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 **KB** additional **KB** distinctions, an **HKB** as nested **KB**s, evidencing a *polysemic* and *polysemantic* character of the **GC** as an *heterarchy* composed by the **KB** associated to *different* subalphabets indicating the codification of distinct *characters*. This is illustrated in Fig.2 below. Recalling our previous discussions on the coexistence of orientable and non-orientable topologies for molecules (without breaking of any chemical bonds) [29], we shall see next that these subalphabets, produce the same coexistence, for the **GC.** We consider the 4x4 matrix, **P**(2) = [C,A;U,G](2), the two-fold tensor (Kronecker [8]) self-product of [C,A,U,G] , i.e. **P**(2) =[C**P**(1), A**P**(1);U**P**(1),G**P**(1)], the 4x4 matrix (table) of *all* 2plets

	C 00 (0)	A 01 (1)	U 10 (2)	G 11(3)
C 00 (0)	CC 0000 (0)	CA 0001 (1)	AC 0010 (2)	AA 0011 (3)
A 01 (1)	CU 0100 (4)	CG 0101 (5)	AU 0110 (6)	AG 0111 (7)
U 10 (2)	UC 1000 (8)	UA 1001 (9)	GC 1010 (10)	GA 1011 (11)
G 11 (3)	UU 1100 (12)	UG 1101 (13)	GU 1110 (14)	GG 1111 (15)

We finally compute the 3-fold tensor self-product, [C,A,U,G](3), i.e. the 8x8 matrix **P**(3) = [C**P**(2), A**P**(2) ; U**P**(2), G**P**(2)], of *all* triplets, which we present as the table:

	000(0)	001(1)	010(2)	011(3)	100(4)	101(5)	110(6)	111(7)
000 (0)	CCC(0) 00000 Pro	CCA(1) 000001 Pro	CAC(2) 000010 His	CAA(3) 000011 Gln	ACC (4) 000100 Thr	ACA(5) 000101 Thr	AAC(6) 000110 Asn	AAA(7) 000111 Lys
011 (1)	CCU(8) 011000 Pro	CCG(9) 011001 Pro	CAU(10) 011010 His	CAG(11) 011011 Gln	ACU(12) 011100 Thr	ACG(13) 011101 Thr	AAU(14) 011110 Asn	AAG(15) 011111 Lys
010 (2)	CUC(16) 010000 Leu	CUA(17) 010001 Leu	CGC(18) 010010 Arg	CGA(19) 010011 Arg	AUC(20) 010100 Ile	AUA(21) 010101 Met	AGC(22) 010110 Ser	AGA(23) 010111 Stop
011 (3)	CUU(24) 011000 Leu	CUG(25) 011001 Leu	CGU(26) 011010 Arg	CGG(27) 011011 Arg	AUU(28) 011100 Ile	AUG(29) 011101 Met	AGU(30) 011110 Ser	AGG(31) 011111 Stop
100 (4)	UCC(32) 100000 Ser	UCA(33) 100001 Ser	UAC(34) 100010 Tyr	UAA(35) 100011 Stop	GCC(36) 100100 Ala	GCA(37) 100101 Ala	GAC(38) 100110 Asp	GAA(39) 100111 Glu
101 (5)	UCU(40) 101000 Ser	UCG(41) 101001 Ser	UAU(42) 101010 Tyr	UAG(43) 101011 Stop	GCU(44) 101100 Ala	GCG(45) 101101 Ala	GAU(46) 101110 Asp	GAG(47) 101111 Glu
110 (6)	UUC(48) 110000 Phe	UUA(49) 110001 Leu	UGC(50) 110010 Cys	UGA(51) 110011 Trp	GUC(52) 110100 Val	GUA(53) 110101 Val	GGC(54) 110110 Gly	GGA(55) 110111 Gly
111 (7)	UUU(56) 111000 Phe	UUG(57) 111001 Leu	UGU(58) 111010 Cys	UGG(59) 111011 Trp	GUU(60) 111100 Val	GUG(61) 111101 Val	GGU(62) 111110 Gly	GGG(63) 111111 Gly

In the above figure 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 CAU is codified by the binary number 001010, where the first three digits 001 corresponds to the *No.1* assignment for CAU whilst the last three digits 010, corresponds to the *No.2* assignment; the decimal notation for the concatenation 001010 is 10. Remarkably, each pair codon-anticodon (and only such pair) has the sum of their decimal numbers equal to 63 (111111, in binary notation), say CAU which is 10 its anticodon GUA has the decimal number 53. We note that *No.3* transcriptions of C with G, and A with U(T), are completely determined by the other two subalphabets, as shown in Fig. 2 below, and correspond to the mutual transcriptions of Outside-Outside/ Inside-Inside, and of the time waves Outside-Inside/Inside-Outside, and they correspond to the binary-opposition attribute by which the former (latter) correspond to three (two) hydrogen bonds. This *genomatrix* has surprisingly rich symmetry properties which invite to topological interpretations, which we shall realize next. They further indicate relations with hypernumbers and 8-fold symmetries structures which also appear in Matrix Logic [40] and **NUCRS**, 5-fold Fibonacci structures (also essential to both **NUCRS** and torsion fields), chronomes [22,23], and in particular, a music translation of the **GC**, in an epochal unified approach [18,19]. 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. 2 below. We note that the columns correspond to the classical octets reflecting biochemical properties of elements of the **GC** [35]. Secondly, it is bisymmetric (with respect to *No.3*), i.e. symmetric with respect to both diagonals, say UUC which is the matrix element corresponding to 7th line and first column has the anticodon AAG in 7th line and 1st column. Hence, we have **MBs** with either chirality, produced by 180º rotation about the central vertical line and identification oppositewise, 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 band; say we have UUC, UUA, UGC & UGA superposed to AAG, AAU, ACG & ACU, respectively. This is the **MB** topologies of the genomatrix **P**(3). If we further consider now the (*No.2-wise)* column symmetry, we finally obtain a **KB** by further topological identification. Yet, it is more than a single **KB**, but four of them, produced by the superposed 1st/8th, 2nd/7th, 3rd/6th, 4th/5th columns, with the first element of each superposition inverted (the equivalent of **DH** antiparallelism) with respect to the second, yet embedded in a single **KB** given by the 64 triplets: an **HKB**. 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 **HKB** with four others embedded given now by the superposed rows 1st/8th, 2nd/7th,3rd/6th, 4th/5th, with the same inversion as before.



Figs. 2 & 3, respectively: In Fig.2 the lines stand for transcription and the subalphabet by which each operates is the number attached to it; it also provides the symmetries of genomatrixes for coding sequences of arbitrary length, and their topologies. Folding for topological identification according to these symmetries, say *No3.* yields **MB** of both chiralities, which followed by either *No.2* or *No.1* yields the **KB**; the combination of *No.1* with *No.2* yields a 2-torus In the right hand side of the **MB** Fig. 3, we have drawn the Fischer formula for D-lactic acid which if we continue on the surface to the ¨other¨side we obtain the L-form drawn displaced to the left for allowing its vision; for the genomatrix we have instead the four superpositions of either the pairs of opposed rows (columns) with say each first element opposed to the second drawn on the surface which is a quantum interface.For the Mendeleev table we have instead a superposition of each atom in ¨matter¨/ ¨antimatter¨-duplets, superposed on the **MB**, fig. 2.1 in [3]. The inversion of each element of a pair of rows or columns mandated by *No3*., plays the role of the antiparallelism in the **DH**.

We have thus found *two fractal* **HKB** structures in the genomatrix **P**(3), and recursively in **P**(n) = [C**P**(n-1), A**P**(n-1); U**P**(n-1), G**P**(n-1)], for arbitrary natural n, 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 **GC** arising from the **KBL**, and we also have a 2-torus by using *No1. & No.2;* as we can easily visualize from the definition of the tensor product, it produces the fractality which reproduces the original (i.e. n= 1) topological identification introduced in Fig.1.We remark again, this has surfaced from a *simultaneous double 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 *trascends* the usual approach to the genetic code as well as the combinatorial one [18,19]; these topologies apply as well to the codification of the sequences of n letters by 2n digits. The information content in each interior **KB** to the **HKB** 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 **GC** the same situation of polytopologies (we recall that also **DNA** is polygeometrical) that appears already in topological stereochemistry [29] which we claimed to be essential to cell biology and to embryological development, and a fortiori, to evolution [20]. 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, U, 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 *path* on either two fractal **HKB**, or a 2-torus, given by **P**(n). This construction does *not* require the assumption of the double helix (**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 **MB**.A **MB** model for *circular* genetic code was proposed [4], yet to our knowledge, this has not been the case for a **KB** structure [7]. These findings, appear to give further support to the unifying paradigm for chemistry [5], that claims that the topology of molecules, are crucial to their stereochemical configuration [29], which we have suggested to be crucial as well to allosterics, cell biology and embryological differentiation [20].A **KB** 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 **GC** claimed to be *unnecessary* for transcription for *closed* **DNA**[4], a particular case to the one here unveiled. We recall that the two strands that make up the **DH**, 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 **DH**. Consequently, **DH 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 **MB** is forbidden because the bonds required would violate the conservation of 5'-3' directionality [2]. All that said, this claimed to-be Nature's prohibition appears *not* to have been realized [36] remarking the preeminence of the topological being of stereochemistry, rather than the geometrical one. Starting with **DNA** material and through folding and ¨sticky ends¨ (i.e. single strands, consistently with the present findings and [4]), opposite chirality **MB**s have been produced [11] and through joining their sides the **KB** can be realized; paradoxically, the **DNA** model advocated by this authors is the **DH**. So in principle, a biochip that may embody the **KBL** as the logic for quantum computation with self-correcting codes [22,40], is reachable [37]. We note that the crossover effect present at the core of the **KB** and consequently in the **GC**, is at the basis of morpho-functional structures in the human organism, such as the crosswise connection of brain hemispheres with the left and the right halves of a human body, of chromosomes, the crosswise gestalt of optic nerves from eyes in the brain [1] and visual synchronization [23,42], etc. There is another **HKB** fractal structure for the genetic code that is produced departing from another matrix representation for the **KB**, namely consider the Hadamard matrix H(2) = [C,A,U,G] = [1, 1; -1, 1], H(4) and H(8), the 2 and 3-times tensor self-product of H, respectively,

$$\mathbb{H}(2) = \begin{bmatrix} 1 & 1 \\ -1 & 1 \end{bmatrix}; \quad H(4) = \begin{bmatrix} 1 & 1 & 1 & 1 \\ -1 & 1 & -1 & 1 \\ -1 & -1 & 1 & 1 \\ 1 & -1 & -1 & 1 \end{bmatrix}; \quad H(2^k) = \begin{bmatrix} H(2^{k-1}) & H(2^{k-1}) \\ -H(2^{k-1}) & H(2^{k-1}) \end{bmatrix}$$

This example shows that genomatrixes are *logical operators* of the Matrix Logic form of the **KBL**, some of which may be chosen to be nilpotent, representing creation and annihilation quantum field operators [22,40]; the third-order tensor product –disregarded in the previous presentations of the Matrix Logic form of the **KBL** - considered before, may serve as a basis for octonionic quantum mechanics and for a logical representation for *emotics*, due to the relation with a musical code for **DNA** [18].There is an algorithm which transforms **P**(3) into H(8) and from P(n) to H(2^n) [18,19], and thus from two different topological codifications arising from the **KB**, we obtain the same genomatrix representations of the **GC**. This appears to be related to the **GC**'s resistance to environmental hazards. Indeed, the Hadamard matrix approach yields mosaic fractal structures with 32 positive and 32 negative ones, which are associated to Rademacher functions (which only take +1 and -1 values) from the digital theory of signal processing. They are widely used in the theory of coding, being crucial to the robustness of transfer of digital information with regards to environmental ¨noise¨. Thus the **KB** provides for the basic codification and the robustness of the **GC** and a fortiori, that of embryological development.

Indeed, we return now to the codification of the differentiation waves in embryological development discussed in [20]. There are two kind of waves, corresponding to either contraction or expansion of the cell's light rays torsion tensegrity. Far from being these states single-valued corresponding to a Boolean pair, there is a **KBL** to them. The contraction wave is the concatenation of a contraction C, followed by a transition C→E, and finally a reentrance E →C, with the arrows standing for transformation, E stands for expansion. Likewise, the expansion wave is the concatenation of E, followed by E→C, and C →E. C is coded by 00, E by 11, C by 01, and E by 10. Indeed, the transitionary states correspond to the imaginary time waves of self-penetration of the cell through the boundary separating the two types, while C and E correspond, say to Outside-Outside and Inside-Inside, respectively, as in **P**(1). Thus the contraction state of differentiation is coded by the triplet CAU, and the expansion wave by its anti-codon, GUA, synthetizing Histidine and Valine, respectively. Both are essential for growth and repair of human tissues.

We return to the genomatrices and the relation with **KBL** operators. 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 mean; instead of letters A and U in this multiple we place 1/φ [18,19]. As a result, we obtain a chain with n links, where each link is φ or 1/φ; we recall that these numbers are the eigenvalues of the OR & NAND operators of the Matrix Logic derived from the **KBL**, so their appearence in the GC from the **KBL** is not accidental. Indeed, OR & NAND are represented by the 2x2 matrices [0;1,1,1] and [1,1;1,0], respectively, which coincide with [F(0), F(1);F(1),F(1)] and [F(1),F(1);F(0),F(1)], respectively, and the n-th usual 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] another logical gate for the **KBL**. This will give a representation of n-plets [18,19].

The Klein Bottle, the Genetic Code and the NUCRS

Having produced the 64 codons at the third stage of recursion by tensor self-multiplication, we proceed to examine the relations with the *Code of Nature (**CN**)* proposed for the **GC**, in the setting of the **NUCRS** [12,25]. This theory based on recursivity (algorithmic self-

reference), establishes a symbolic relation between the Dirac algebra of quantum mechanics (thus the 64 triplets are mapped into the 64 basis elements of this algebra) and the **GC**, which is further embodied in a fractal structure produced in terms of the Platonic solids(**PS**); thus, by following the construction of the **CA** and its association with the Dirac algebra we may establish, an isomorphic representation between the **KBL** construction and the **CA**. The latter's construction is produced recursively starting from the tetrahedron; see Fig. 4 below: At each of its vertices the four letters, A,C,G and T/U are positioned, centered in the latter for distinction, similarly to the sign distinction for it in the Hadamard representation above) This single tetrahedron is taken to represent single stranded **DNA** from which through a fractal recursive construction, the **GC** follows in terms of fractal concatenations of tetrahedrons (the latter appear in the tensegrity structure of cell water [16], crucial to cell biology [20]). Consequently, *all* the 64 triplet codons which are uniquely represented by the elements of the Dirac algebra can be positioned in the four triangle faces of the tetrahedron, which thus in principle contains the basis for the operation of **GC**, *whatever* its topology and geometry may be. We recall that the **KBL** generation of the **GC**, has placed in evidence that the transcription does *not* require the **DH** since the two **HKBs** found in **P**(3) *fully* represents the transcription for triplets, and further for n-plets by **P**(n). A usually unacknowledged property of the **PS** drawn in 2D projections centered in one of the vertices, is that their perception gives rise to the so-called *multistable perception*, i.e. two possible percepts connected in time and the depth dimension [22,23,24] arise, depending on the interpretation –provided by the other sides acting as *contextual* cues- of the center perceived as being in the hind or the fore; thus, time, as the primeval generating dimension, produces this double being coexisting in time. This projection was devised in organic chemistry by Emil Fischer, to represent enantiomers (i.e. dual under reflection, non-identical beings) in 2D, and in topological stereochemistry is associated to the **MB** [26] (see Fig. 3 below). (By the same principle we find a *non-dual* topological precursor of Newton's Third Law, to be presented below.) Perception *is* the issue at stake with regards to 2D representation of the stereochemistry (stereo means solid, 3D) of organic chemistry which produce a multivaluedness that a set of rules for ¨disambiguation¨ is convened to remove them [17]: Herewith, the two possible percepts that arise from the single **DNA** strand tetrahedron are to be rendered distinct (as in Fig. 3), which for the **NUCRS**, unbeknownst of this issue and of its one-ness ontology, with the aim to represent the *assumed* **DH** transcription operation of the **GC**, choses to represent them as a star (*double* interlocked) tetrahedron (see Fig.4 below), thus starting the construction of the **CA** and the transcription in the **GC**: This is the *duplication* of 3D (the appearence of momentum space) in the **NUCRS** and the **CA** bauplan of the **GC** , and entails a duplication of the **KB**, which becomes now a **HKB** with two nested **KBs**, each associated to one of the tetrahedrons; this duplication has a *common singularity* by which these **KBs** *reente*r the origin, T/U for DNA/RNA. The paradoxical perceptual effect of this duplication is the *frustration of the multivaluedness*, as shown in Fig. No.4. below, and the duality of the **NUCRS** and a fortiori, the **DH** and **CA**, are produced [12,25].

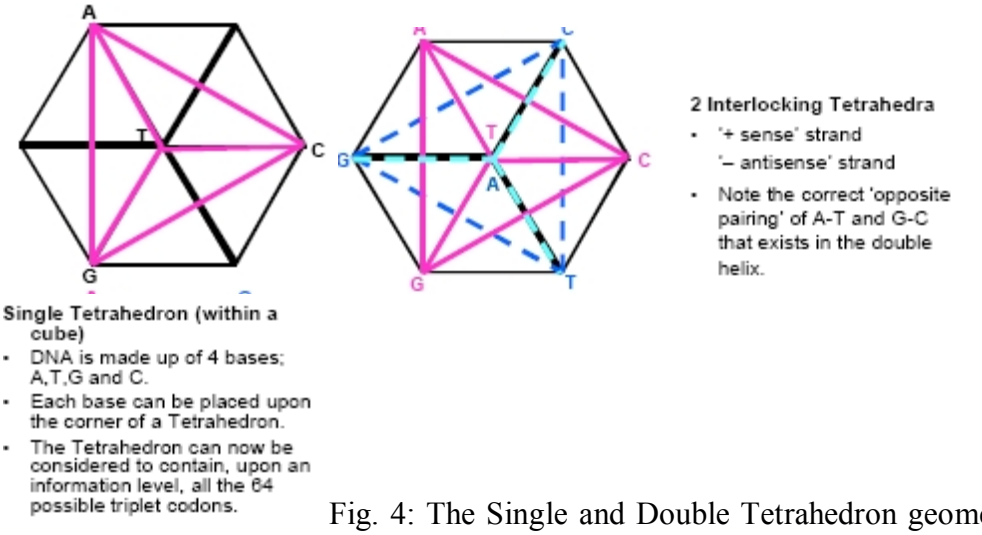


Fig. 4: The Single and Double Tetrahedron geometries of single and double stranded DNA, respectively (reproduced from [18]). The perception of the former produces two figures in time according to the contextual interpretation of T (or U) being either the Outside or Inside vertex of the cube. This generation produced by zooming on the centre is the T-centered non-dual (e)invagination of the **KB** map of the sensorium, and it is related to the existence of visual cues around T ([23] and references therein). In the **DT**, the zooming effect is frustrated and the perception in time becomes a spatial perception.

By setting A and T(U) superposed in the origin, subalphabet *No.3* is rendered as the identification of the Outside-Outside & Inside-Inside of two superposed **KBs** in their self-penetration singularity, consistently with the dual perception of the (e)-inversion of them through the singularity, and thus the mutual transcription of C with G is also fixed as the identification of the Outside-Inside and Inside-Outside states. Thus two states are produced, one being a single imaginary state by identifying both imaginaries, the other being the identification of, now, Outside & Inside: this is not the Cartesian Cut's reality. As for the 2D rendering of the **PS** and the ensuing fractal **GC** obtained in the **CA**, in the **NUCRS** 2D has a generative (in fact genetic as the **CA** shows) function which is the case already of the **KB** *surface*. A fortiori, **NUCRS** is based in the **HKB**, and in particular the *double* 3D space of this theory objectifies through the double-tetrahedron based generation of the **CA** & **GC**, the multivalued character of the **KBL** and its hyperextension to **HKB:** the operation of time on 2D creating a paradoxical 3space is transformed into double 3D, with the appearence of momentum space. The multistable perception of the initial single tetrahedron representation of the four letters of the **GC** is mapped as two different distinguishable gestalts, the star (interlocking two) tetrahedron, yet producing a codification of the 64 (*not* 128; no new objects are created by this, thus is not a fundamental ontological operation in the sense of creation of objects: *its ontology is representational amenable for computations*) codons already in the genomatrix , which we stress does not require the assumption of the **DH** (this assumption is implicit in [18,19], by which the interpretation of the bisymmetry of the genomatrix *is* done in terms of it). A fortiori, the triplets represented in the **CA** in the *third* order level star tetrahedron, which embeds the original pair of Fig.4 in a fractal structure are, in principle, transformable to our previous construction, yielding the same information

(64 triplet codons and 20 amino acids) than the *third* tensor product of [C,A,U,G], i.e. **P**(3). Yet, the latter's lack of assumption of the **DH**, a fortiori shows the *non necessity* of the **DH** in **CA**, would not be that a *duplication* of 3D is required by its alledged *fermionic* based character, in which the fermion and the Universe couple through algebraic nilpotence, self-referentially, in the Dirac algebra. In this coupling,the Universe is the context for the fermion; yet we remark that the content/context fusion of context is an essential operation of the **KB.** through the transitional states, i.e. time. Would we follow the suggestion in p. 491, [25], of identifying the singularity produced by the **KB** self-penetration, with the fermion (which thus becomes the fusion of the Inside-Outside & Outiside-Inside states, i.e. A with U), then the complement of the fermion - the Universe- for its algebraic self-annihilation returning to 0, requires the fusion of the other two states, completing thus the transcription rules of *No.3*. Thus, time, as the process and depth generative dimension embodied in the reentrance of the **KB** by self-penetration, the essential self-referential action, is objectified as a double 3D space and the **CA** and the **GC** materialize as well through the double tetrahedron. The construction of the **AUCRS** in terms of the Dirac algebra is quite remarkable since the Dirac equation for one-half spinors is *equivalent* to the Maxwell equation of electromagnetism for a spin-1 field (see [21] and references therein), and thus, in principle, the **AUCRS** can be introduced starting with spin-1, rather than ½-spin fermions. Indeed, on the **MB** we find a nondual topological protoform of Newton's Third Law, to manifest this duplication and halving of one-ness, unrestricted to spin. A normal vector to a point on the **MB** on ¨one¨side continuously moved to the ¨opposite¨ side points in the dual direction, and has equal magnitude; this requires no constraint, no ¨law¨, the claim of the latter is an unnecessary epistemology, due to the non-orientability!).While globally a single vector, alike to a codon/anticodon on the **MB** ¨sides¨, locally they are two vectors distinguished in/by time, through the motion of the former. Thus, 1-ness is the **MB** non-orientabilty, 2-ness its non-dual local manifestation, and returning back to the original ¨side¨, 2-ness becomes 1-ness (halving), yet through a dynamical history of 1-ness. This motion requires an a prior vortex producing the 180º turn (the two-fold operation of TIME operator [23]) to further return to 1-ness by self-identity (the identification of the opposites, one of them rotated and glued) and thus the **MB** is established, yet with *no singularity nor paradox*. These are indissolubly an issue of *self-penetration,* the **KB**, also produced by zipping two opposite chirality **MB**s. In the **AUCRS** the singularity is the fermion, interacting with the rest of the Universe to return to 0. In the current approach the **KB** completion of the **MB** by self-reference-penetration (rather than solely self-identification in the **MB**) is a massless spin 1 torsion light field which, as we have just shown, the global one-sidenedness implies that the singularity is *both* bosonic and fermionic; the computation of the singularities [48] have yielded a spin-1 twistor field representable as a pair of two spin ½ fields! Thus, the *discrete* symmetries in physics and the factor 2, distinguishing fermions from bosons –in **AUCRS** are traced back to dualities such as action-reaction (inexistent in the **MB** 1-ness), continuity/discontinuity [chap. XVI,25], which the **KB** is both due to the self-penetration-, ultimately producing the **DH**, which as we indicated already by slitting (i.e. halving) the **MB** **DNA** a catenane is produced, equivalently to transcription, though not the one envisaged here!) requires reassesment, since they arise from a topological *continuous* dynamics in the **MB**, yet continuous and discontinuous in the **KB**, eschewed by the assumption of duality. Instead, the **AUCRS** duplicates 3D, unacknowledged its **KBL** origin, as well as its self-referen-

ce unrestricted to algorithmic recursion, entailing the DH: Yet, the KBl construction of the GC produces topologically the transcription, without the DH. Thus, we conclude that the DH associated to fermions in the NUCRS & CN, is nothing else than a recourse to *materialize* time and self-penetration of the KB –the *material action* of self-reference, which appears to be the *origin for the fundamental discrete symmetries*-, through a spatial double 3D representation embodying the multivaluedness of the KBl and the transformations between bosons and fermions, and their unification (already embodied in the Dirac equation and the KB). It is in this time materialization, that the NUCRS finds its dualistic base further manifested in the relation with the GC established by the CN. This is associated to the breaking of the 8-fold full symmetry to the 5-fold symmetry in which mass and charge appear, as is case of the Dirac equation for a spin ½ field, or its massless Maxwell equation equivalent in which the mass of the electron is related to the rotational kinetic *energy* of the spin-plane of the spinor. With regards to the KBl & the ensuing polysemic codification of the GC, the DH is unnecessary; this reappears in the 2D hypercube representation of the genomatrix P(3): two images, in time, appearence of the 64 triplets,which would we wish to materialize as distinct, we would recourse to the construction of the CN, yet *nothing new* would appear from this bauplan, which the hypercube does not already represent *without duplication* of either 3 or 4D [19]. Indeed, the closed path in the hypercube joining the 64 triplets as vertices of a graph transversing each of them only once, but for the extremes, i.e. a Hamiltonian path, is *unique*. The reduction of the 64 Dirac algebra/codons to the 20 aminoacids, in the KBl construction of the GC, brings to the fore symmetry properties of P(3) [18], in which the TIME operator of the KBl manifests as chronomes [23]; we shall present this elsewhere.

Conclusions, On Evolution. A theory for the GC has been proposed departing from the KBl and its multivalued representations of the stereobiochemical structures of the GC, to yield two HKB –and a 2-torus- representations, which do not require the DH. This indicates the need for reconsideration of the transcription process, and instructs as to how to read topologically the bioinformatic data, which may yield unnoticed in-formation of genomes. This polytopological character of biochemistry, claimed to be a new paradigm for stereochemistry [5,29], may embrace allosteric recognition, in which KB-logical gates and biophotons establish quantum coherence [22,39,40]; these gates already appear to codify the GC. Thus, KB-*logophysics* removes from biochemistry (& biology), the need for anthromorphizations, due to the ontological cognitive being of the KBl, in physics (the measurement problema) and evolutionary theory,which are embodied in Anthropic Principles, through the ¨fine-tuning¨ of physical ¨constants¨which may turn out to be context dependent [43,46], variable, as early proposed by P.Jordan and Dirac. This variation of constraints reappears in the orthogenesis concept of directed regularities and homologies (*biological periodicities*,BP) in evolutionary theory [38,45]). We also gave a representation of embryological differentiation, identifying two aminoacids as relators of this process in action with the environment acting through the remaining aminoacids as discussed in [20]; evolution, with regards to the GC, appears to be driven by the interaction with the remaining triplets and of the environment. The KBl provides for the robustness to environmental action; it also generates a representation for the fusion of consciousness to the physical world [22,23,40]. Symmetry structures, especially 5 & 8-fold, that appear both in the GC

[18,19] and **NUCRS**, appear in the **BP** of evolutionary theory without selection [38,45]), and their interrelation with asym-metries (the **KB** synsymmetries [24]), proposed by Pierre Curie, express the fusion of form, logophysically the **KB** [42]. The suggested link of the **BP** to the Mendeleev table (**MT**), which is a **KB** derived from a Fibonacci 5-fold torsion *standing* wave generating the atomic num- bers when disposed on a plane (see Fig. 2.1 in [3], is through the role of atomic weights in defining the regularities of the **BP**, morphological and functionalwise [38], proposed by Va- lilov [44]. We may thus propose the novel idea that the periodicities of the taxonomy and functionality of biosystems, as an heterarchy embracing the physical plenum to the cosmo- logical scales, must also reflect the **HKBL** of *both* the **GC** and the **MT**, incorporating thus the heterarchical fusion of the self-determination of biological structures vis-à-vis the environ-ment. The latter far of being¨noise¨ -has torsion fields for their self-referential geometries [45]-, partakes in their constitutional self-reference already present at the diverse logophysi-cal levels. In this **bauplan** for evolution, the Fibonacci symmetry and its torsion fields, play a genetic role [20], already at the genesis of the **MT**. Yet, inasmuch the **MT** atomic weight periodicities are generated by a *standing time wave,* embodying the contextuality (pressure, density, etc.) for the formation of atoms [13], manifesting the TIME operator of the **KBL** [20,22,23], we conjecture to be the case for biosystems. Such an evolutionary **bauplan** in- corporates the environment also in the chemistry of the **BP**s, since atomic weights (particu-larly hydrogen, oxygen and carbon) are space dependent, a novel discovery [43]. The **HKB** heterarchy of evolution, embodies a fusion of context, content, form and function [43], crucial to consciousness and life [22,23,42,47]. This is not Darwinian selection, nor is the linear-time context-free evolution of creationists, due to never ending ever starting **KB** self-reference, essential to the **NUCRS**, which has a logophysical basis surmounting the Cartesian Cut. The extension to mitosis, in terms of the light torsion spacetime and cell tensegrity, and the **KB**, will appear elsewhere.

Acknowledgements: My deep gratitude to the Organizers of CASYS'11, especially Prof. Dr. Daniel M.Dubois and Dr. Salvatore Santoli, for their invitation to contribute to the pioneering ¨Physics & Logic of Anticipation in Biosystems Session¨, Dr.Helmutt Loeckenhoff for his kind challenge to stand to the occasion; to Dr.Melanie Purcell for discussions on the **KB**, Dr. Istvan Diénes for encouragement and indicating to me reference [19] and Drs.V. Hill & P.Rowlands for allowing me to reproduce Fig. 4. To my wife Sonia and my children, Tania and Tsafrir, who gave me all that science and philosophy cannot provide, and them also.

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