Nature's code

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Nature's Code

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Abstract. We propose that the mathematical structures related to the 'universal rewrite system' define a universal process applicable to Nature, which we may describe as 'Nature's code'. We draw attention here to such concepts as 4 basic units, 64- and 20-unit structures, symmetry-breaking and 5-fold symmetry, chirality, double 3-dimensionality, the double helix, the Van der Waals force and the harmonic oscillator mechanism, and our explanation of how they necessarily lead to self-aggregation, complexity and emergence in higher-order systems. Biological concepts, such as translation, transcription, replication, the genetic code and the grouping of amino acids appear to be driven by fundamental processes of this kind, and it would seem that the Platonic solids, pentagonal symmetry and Fibonacci numbers have significant roles in organizing 'Nature's code'.

1. THE UNIVERSAL REWRITE SYSTEM IN NATURE

Biological systems, though operating at the edge of chaos, are extremely ordered, whereas the tendency for nature is to become more disordered. Biology is, in effect, a race between order and entropy with the odds stacked in favour of entropy. So biological systems must create order, i.e. process information, with as much efficiency as possible. Theoretical studies by Freeland and Hurst suggest that the genetic code known on Earth has an extraordinary efficiency; of a million possible codes studied, only one could conceivably have been more efficient.[1-2] The genetic code we have inherited does not seem to be the product of pure chance; and it would appear, in fact, that the efficient processing of information requires certain algebraic and geometric structures, which are also found in systems organized at other scales, in particular, physics.

There seems to be evidence that a universal rewrite system operates in nature at a fundamental level.[3-4] Essentially, this uses a create / conserve process to generate its own system of mathematical structure, based only on the permanent condition of zero totality, and not on any assumed pre-existing number system or algebra. A convenient, but not unique, representation of this mathematical structure is through an infinite Clifford algebra of nested quaternion systems ($i_1, j_1, k_1; i_2, j_2, k_2$, etc.), so that the successive units introduced at orders 2, 4, 8, 16, 32, 64 are scalar, pseudoscalar, quaternion, multivariate vector (or complexified quaternion), double quaternion, and multivariate vector quaternion, with respective multiplication factors of $(1, -1)$, $(1, i_1)$, $(1, j_1)$, $(1, i_2)$, $(1, j_2)$, $(1, i_3)$. Here, i_1, j_1 and i_1j_1 represent the quaternion operators i, j, k; the incomplete quaternion set i_3 represents the complex number i; while the products i_2i_2, i_2j_2 and i_2j_2 become the multivariate vector units $\mathbf{i}, \mathbf{j}, \mathbf{k}$.

Mathematically, the series continues to infinity, with $(1, j_3)$, $(1, i_4)$, etc., but, physically, we note the special significance of order 64, which introduces the algebra associated with the fundamental physical state, the fermion, that is the Dirac algebra or gamma matrices. This is the order needed to incorporate the component orders 2, 4, 8 and 16 as identifiable units, and, in physics, these orders are identifiable respectively with the fundamental physical parameters mass, time, charge and space. At this level, we observe, uniquely, an infinite number of *nilpotent* solutions, which, by squaring to zero, immediately produce the zero totality alphabet at this and all subsequent

levels, and are distinguishable from each other by their higher order algebraic coefficients. Essentially, the combination of

time	space	mass	charge
pseudoscalar	vector	scalar	quaternion
i	$\mathbf{i}$ $\mathbf{j}$ $\mathbf{k}$	1	i j k

requires an algebra of 64 units (including + and − signs), but in the nilpotent structure we compactify these into five composite units (equivalent to the gamma matrices)

$i\mathbf{k}$	$i\mathbf{i}$ $i\mathbf{j}$ $i\mathbf{k}$	1j

which are sufficient to generate the entire Dirac group, and associate these with new (composite) physical parameters, which we describe as energy (E), three components of momentum ($\mathbf{p}$), and rest mass (m). The nilpotent structure

$$\left(\pm ikE \pm i\mathbf{i}p_x \pm i\mathbf{j}p_y \pm i\mathbf{k}p_z + 1jm\right) = \left(\pm ikE \pm i\mathbf{p} + 1jm\right). \tag{1}$$

now represents the fundamental unit of physics, the fermionic state. In quantum mechanics, the expression ($\pm ikE \pm i\mathbf{p} + 1jm$) can represent either operator or amplitude and the nilpotent equation

$$\left(\pm ikE \pm i\mathbf{p} + 1jm\right)\left(\pm ikE \pm i\mathbf{p} + 1jm\right) = 0. \tag{2}$$

has multiple meanings, including Pauli exclusion. We can also take −($\pm ikE \pm i\mathbf{p} + 1jm$) as the total 'vacuum' state, left by extracting the fermion from zero totality, so that equation (2) also implies that the fermion can only be defined at the same time as its vacuum state, and that the combination means that each fermion defines its own zero totality universe.

The creation of the nilpotent algebra by the compactification process outlined in (1) has many important consequences. Apart from introducing discreteness to otherwise continuous quantities such as time and mass, the compactification creates symmetry-breaking (between the quaternion units), as an 8-fold structure becomes 5-fold, and chirality because of the loss of independent information due to the reduction in sign variation; and the most significant physical quantity now becomes angular momentum, which is the only one structured at the highest level of the algebra – multivariate vector quaternion.

A significant aspect of the creation of the nilpotent state is that one of the quaternion sets remains incomplete. This is the one that appears as the complex factor on the energy or time term, and, by analogy, on the weak component of charge. A fermion is, in one sense, always interacting to overcome this anomaly. Ultimately, its only complete way of doing this is by annihilation with the rest of the universe. However, a partial annihilation is produced by any of the processes of material aggregation which result in a bosonic-type state. The mechanism which results in the creation or destruction of (combined) bosonic from or into (uncombined) fermionic states is described as the harmonic oscillator. The harmonic oscillator is a classic indication of aggregation or complexity in a system. It is a statement that no system is ever 'closed'. All fermions interact with each other via discrete quantum transitions; E and $\mathbf{p}$ are never fixed. This lack of closure is an expression of the second law of thermodynamics, and is the driver for all processes.

A significant aspect of the quantum harmonic oscillator is the spin ½ which is intrinsic to the fermionic state. The reason why it is ½ rather than 1 is because the fermion can only be defined at the same time as its vacuum partner, and the combination can in this sense be imagined as 'double helical'. The fermion / vacuum duality and spin ½ also makes the weak interaction ultimately dipolar, with the classic inverse fourth-power force which is characteristic of aggregating systems, including the Van der Waals force of molecular cohesion, and the hydrogen bonding which connects together the double strands of DNA, which is distinct from the Van der Waals force which gives stability between each twist of the double helix.

2. THE UNIVERSAL REWRITE SYSTEM APPLIED TO BIOLOGY

It would appear that the fundamental rewrite system, with its 5-component nilpotent operator, displays in compactified form all the fundamental units of *natural process*. Summarising a large body of work, it is possible to show that, defining a nilpotent operator for physics simultaneously leads to the creation of point singularity and discreteness; compactification (from 8 units to 5) and chirality (as a result of the loss of some sign degrees of freedom in the compactification); symmetry-breaking (between the 5 units) and spontaneous symmetry-breaking (because of the chirality); (double) helicity and angular momentum (with its double 3-D nature); irreversibility

(because of the chirality of the time and energy operators); 5-fold symmetry (cubical → spiral) and hence the Fibonacci sequence; and a harmonic oscillator-based tendency to aggregation and complexity (because of the pseudoscalar nature of the time / energy term needed for nilpotency). These, in fact, would appear to be universal processes, originating in the fundamental algebras and geometries of the rewrite system, and there are many indications that they apply in biology as well as in physics, in particular to the genetic code and its translation / construction mechanism for proteins. Here, we see that the Dirac nilpotent fermion plus vacuum structure, with its four fundamental components (space, time, mass and charge), the 64 elements of its algebra, the double helical structure, chirality, and 5-fold broken symmetry (E, $\mathbf{p}$, m), corresponds closely to the structure of the DNA / RNA genetic code, with its four bases (A(denine), G(uanine), C(ytosine) and T(hymine)), 64 triplet codons, double helical structure, chirality, and 5-fold axial symmetry.
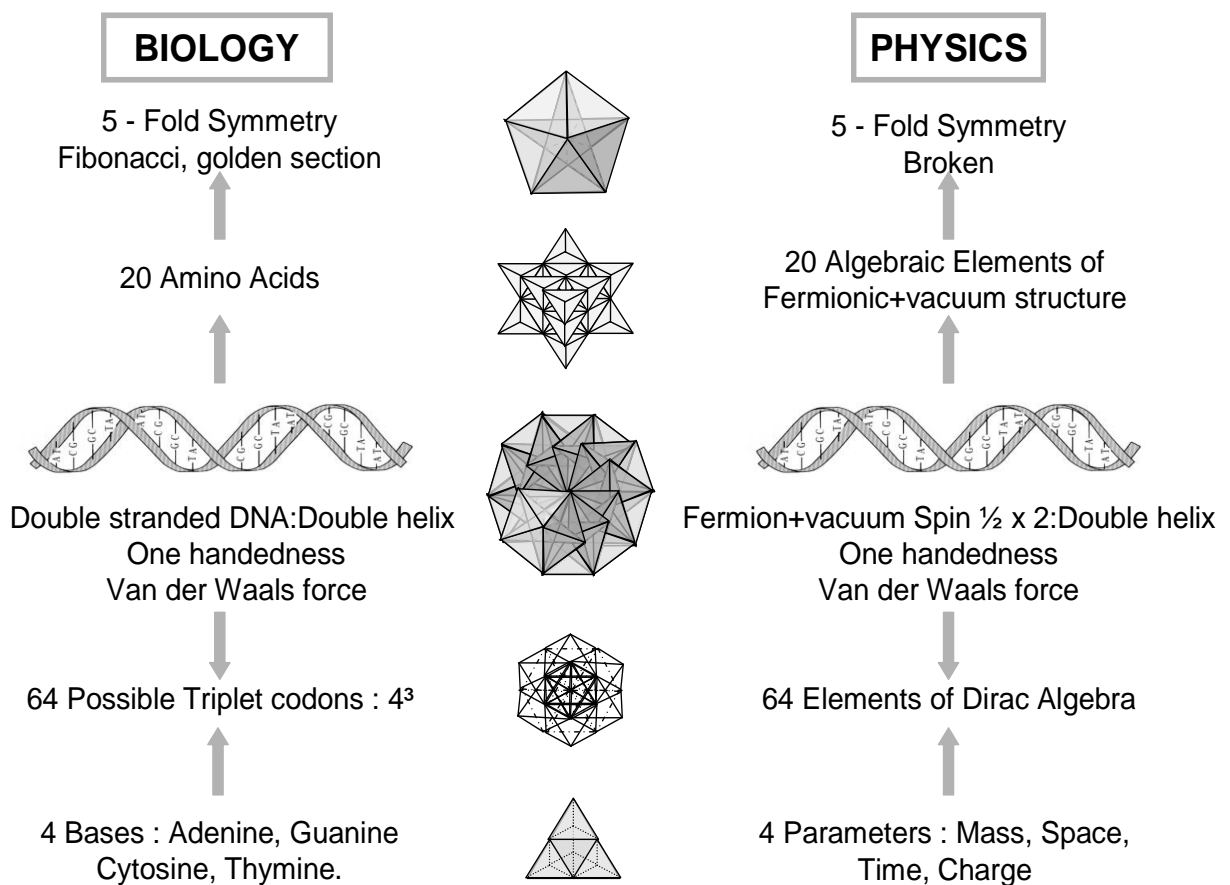
BIOLOGY

5 - Fold Symmetry
Fibonacci, golden section

↑

20 Amino Acids

↑

Double stranded DNA:Double helix
One handedness
Van der Waals force

↓

64 Possible Triplet codons : 4^3

↑

4 Bases : Adenine, Guanine
Cytosine, Thymine.

PHYSICS

5 - Fold Symmetry
Broken

↑

20 Algebraic Elements of
Fermionic+vacuum structure

↑

Fermion+vacuum Spin ½ x 2:Double helix
One handedness
Van der Waals force

↓

64 Elements of Dirac Algebra

↑

4 Parameters : Mass, Space,
Time, Charge

FIGURE 1. The unification of physics and biology

3. DNA, TRANSCRIPTION AND TRANSLATION

DNA is made up of 4 deoxyribonucleic acid bases (dNTPs): A, T, G and C. Two of these contain purines (A and G) and two pyrimidines (T and C). Within the double stranded helical structure of DNA, A pairs with T via a double bond and G pairs with C via a triple bond, i.e. the purines A and G pair respectively with the pyrimidines T and C. During the process of transcription the DNA unzips to expose the single strands and the enzyme RNA polymerase proceeds to make a reverse copy of one strand (the coding strand). This copy replaces all the deoxyribonucleic acids with the ribonucleic acid bases A, U(racil), G and C, with the Ts being replaced by Us, and the subsequent message

(the single-stranded mRNA) is decoded by the protein machinery composed of ribosomes (made up of 65% rRNA and 35% protein) and tRNAs during the process known as translation. The mRNA is translated into proteins by reading the RNA bases in groups of 3 known as triplet codons. The tRNAs each carry an anticodon that recognises a specific codon and each carries a specific amino acid. As the translation progresses a chain of amino acids is constructed that becomes a protein molecule. The number of triplet codons that can possibly arise from 4 bases is 4^3 or 64 but the number of amino acids nature uses is only 20. Here we recognize a parallel with the 64 units of the Dirac algebra and the 20 components of the fermion state (fermion plus vacuum).
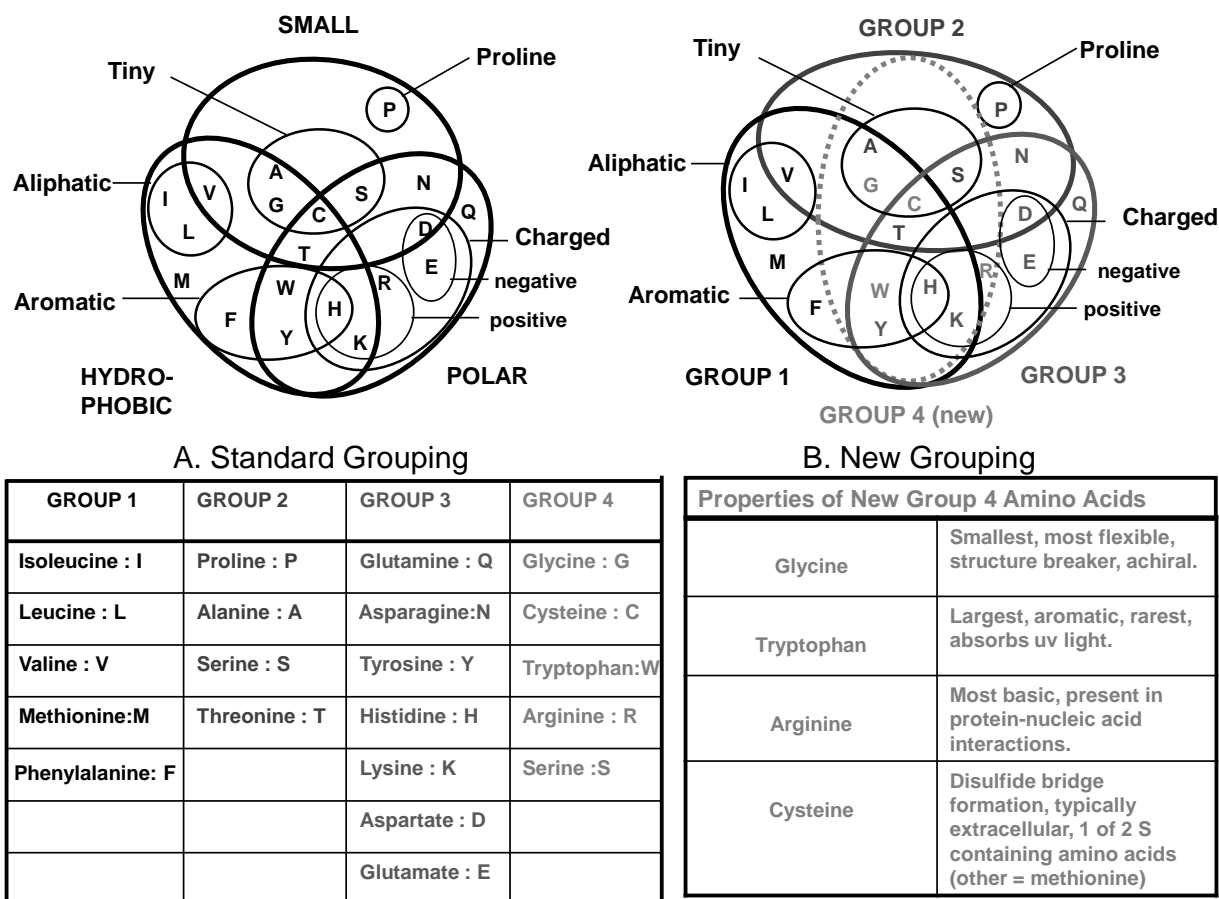

A. Standard Grouping

GROUP 1	GROUP 2	GROUP 3	GROUP 4
Isoleucine : I	Proline : P	Glutamine : Q	Glycine : G
Leucine : L	Alanine : A	Asparagine:N	Cysteine : C
Valine : V	Serine : S	Tyrosine : Y	Tryptophan:W
Methionine:M	Threonine : T	Histidine : H	Arginine : R
Phenylalanine: F		Lysine : K	Serine :S
		Aspartate : D	
		Glutamate : E	

B. New Grouping

Properties of New Group 4 Amino Acids	
Glycine	Smallest, most flexible, structure breaker, achiral.
Tryptophan	Largest, aromatic, rarest, absorbs uv light.
Arginine	Most basic, present in protein-nucleic acid interactions.
Cysteine	Disulfide bridge formation, typically extracellular, 1 of 2 S containing amino acids (other = methionine)

FIGURE 2. Grouping of the 20 amino acids. (a) Standard grouping according to chemical properties; (b) grouping dependent upon middle base of triplet codon; Tables show members of each group and the properties of the new group 4.

At order 64, the units of the rewrite algebra are composed of 32 + and 32 − parts, and DNA can also be considered to carry 32 + codons and 32 − ones. This can be achieved by considering the 2 strands as mirror images, where T, A, G and C are present on one strand; its opposite counterpart on the other strand would have the partners A, T, C and G. If the codons are now split into 2 groups, dependent upon the central base within the codon being either a purine or pyrimidine, we have 2 sets of 32 that are mirror images (order 32). Interestingly, this produces 2 distinct groupings: one contains codons that code for amino acids that are predominantly nonpolar and the other for those that are predominantly polar. These 2 groups can be split again to produce 4 groups dependent upon the central base within the triplet codon and reflect order 16 of the universal rewrite system (see section 6). The division results in 4 groups of amino acids, two of which are distinctly polar and nonpolar with the other two showing a degree of overlap. In Fig. 2 we can see a standard textbook diagram (A) showing the grouping of amino acids according to their chemical properties and, alongside, the resultant grouping obtained when the amino acids are grouped by the specific central base within the triplet codon (B). Remarkably, the two groupings are identical in the placement of each amino acid, dependent upon its specific chemical property, and now produce 4 distinct groups previously

unconsidered. The first group (distinctly nonpolar) contains all the 4 known start codons, the third group is distinctly polar (+vely and −vely charged) and the fourth group contains those amino acids with extremes in chemical behaviour. Similar grouping attempts made by placing emphasis upon the first or third codons yield an entirely random result. This is not unexpected for grouping dependent upon the third base, as this is known as the 'redundant' base.

4. THE FIVE PLATONIC SOLIDS

At an even more fundamental level, the structure of DNA and the genetic code are related to the more basic ideas of Platonic solids and the Fibonacci sequence. A significant aspect of 3-dimensional space is that there are exactly five Platonic solids, or convex polyhedra with equivalent faces constructed of congruent convex regular polygons. These are the tetrahedron, cube, octahedron, dodecahedron and icosahedron which are five recognised resonance states of the sphere. Significantly, the tetrahedron is a mathematical reciprocal of itself, the octahedron is a reciprocal of the cube and the dodecahedron is a reciprocal of the icosahedron and vice versa. These solids nest one within the other as shown in Fig. 3.
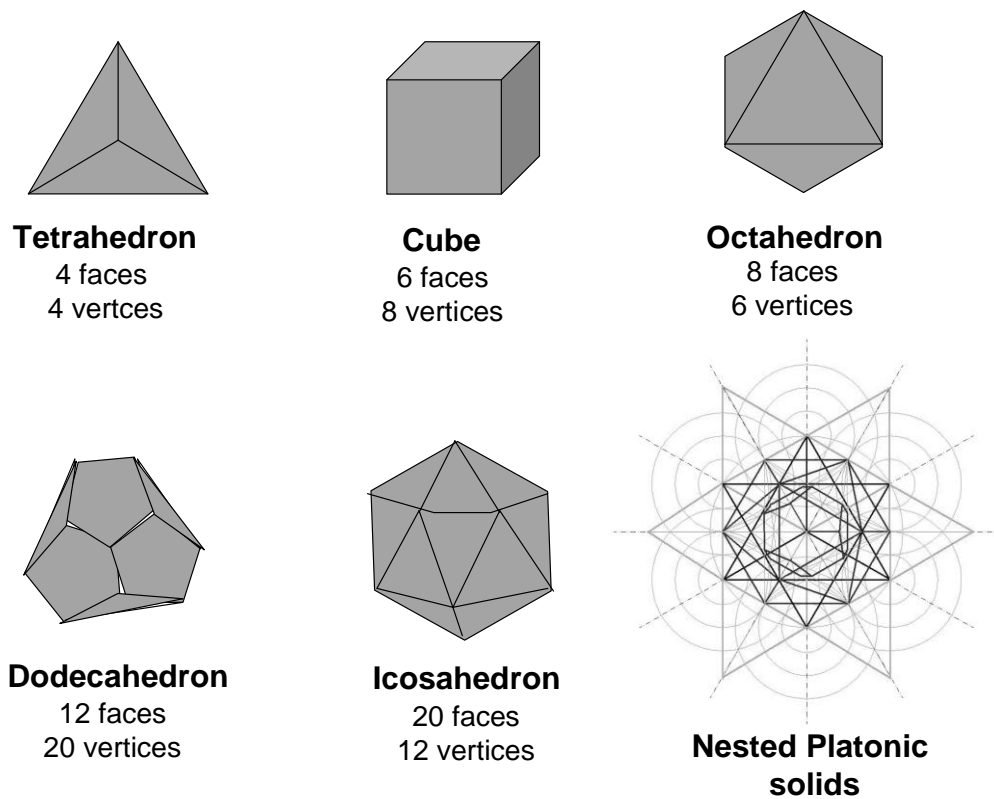
Tetrahedron
4 faces
4 vertces

Cube
6 faces
8 vertices

Octahedron
8 faces
6 vertices

Dodecahedron
12 faces
20 vertices

Icosahedron
20 faces
12 vertices

Nested Platonic solids

FIGURE 3. The five Platonic solids

The 4 fundamental parameters involved in the fermionic state (mass, time, charge and space), which appear at the first 4 stages in the rewrite system, can be easily represented by either a cube or tetrahedron, or, if we include the vacuum (or dual) state as well, a star tetrahedron. The rewrite system shows that 3-dimensionality forces the parameters into a 3-fold separation of dual properties / antiproperties: real / imaginary, conserved / nonconserved, discrete / continuous (= 3-dimensional / nondimensional). As the tetrahedron is the reciprocal of itself, we can also use a tetrahedral representation in which the faces / vertices represent fermion / vacuum states, and are totally reciprocal. We can also use a star tetrahedron to represent this, or relate it to the cubical structure. The cube or star tetrahedron can additionally be used to represent the 8 fundamental units of the algebra required by the fermionic state, as can the octahedron, the reciprocal of the cube.

In a Platonic solid, if m polygons meet at a vertex, and each polygon has n vertices, then the number of faces $f = 2 + e - v$, where the number of edges $e = nf / 2$ and the number of vertices $v = nf / m$, each of these being determined

uniquely. (Significantly *m* and *n* can only be 3, 4 or 5 in 3-D space. These are the obvious 'dimensionalities' to result from the group plus dual, and the 8 primitive algebraic units of space, time, mass, charge.) In general terms, the Platonic solids produce pentagonal (5-fold) symmetries which are intrinsic to them as a result of their structuring within a fermionic state whose algebra requires 2.5×3-D. The fermionic symmetry-breaking, which does exactly this, is clearly related to that of the geometry. And 5-fold tiling is not repeatable, exactly like fermionic nilpotents. Symmetry-breaking, in both cases, is related to the creation of a 5-fold structure. As we have seen, a significant aspect of the Dirac algebra is that it does not need 8 primitive units, and + and − signs, to generate the 64 parts. *It needs only 5 composite ones*. In effect, the most efficient structure is not the most primitive one, and is also not the most symmetrical. The 1 + 3 / 1 + 3 symmetry that can be observed in the 8 primitive units is completely broken, when we write down the 5 composite units that most efficiently produce the 64-component algebra.

5. GEOMETRICAL STRUCTURES

The four bases of DNA – A, T, G and C – can be placed upon the four vertices of a tetrahedron (Fig. 4) such that the tetrahedron can be considered to contain, upon an information level, all the possible 64 (4^3) triplets defined by single stranded (sense) DNA or mRNA (with U replacing T). Double stranded DNA can now be represented by interlocking a second tetrahedron to produce a star tetrahedron such that both the sense and antisense strands are combined with the correct base pairing of A to T and G to C that occur within the double helix. The corners of a cube would also serve equally well here.

As previously mentioned, there are 64 (4^3) different possible triplets that can be obtained from four bases. These, theoretically, could code for 64 different protein building blocks (amino acids) but generally Nature selects only 20 amino acids which can be coded for by 1 to 6 different triplets. If we now look at higher orders of tetrahedra (defined by the numbers of tetrahedral units stacked in each direction within a single overall tetrahedral structure) (Fig. 4) it can be seen that the second order is composed of 1 octahedron and 4 tetrahedra and the third order is composed of 4 octahedra and 10 tetrahedra. If each triangular octahedral face is considered to represent a single triplet then each octahedron would have 8 possible triplets and, if each tetrahedron is considered to represent one amino acid, we would have:-

    for a second order level tetrahedron : 8 triplet codons and 4 amino acids

    for a third order level tetrahedron : 32 triplet codons and 10 amino acids.

Introduction of a second interlocking tetrahedral form to produce a star tetrahedron would double these values to:-

    second order level star tetrahedron : 16 triplet codons and 8 amino acids

    third order level star tetrahedron : 64 triplet codons and 20 amino acids.

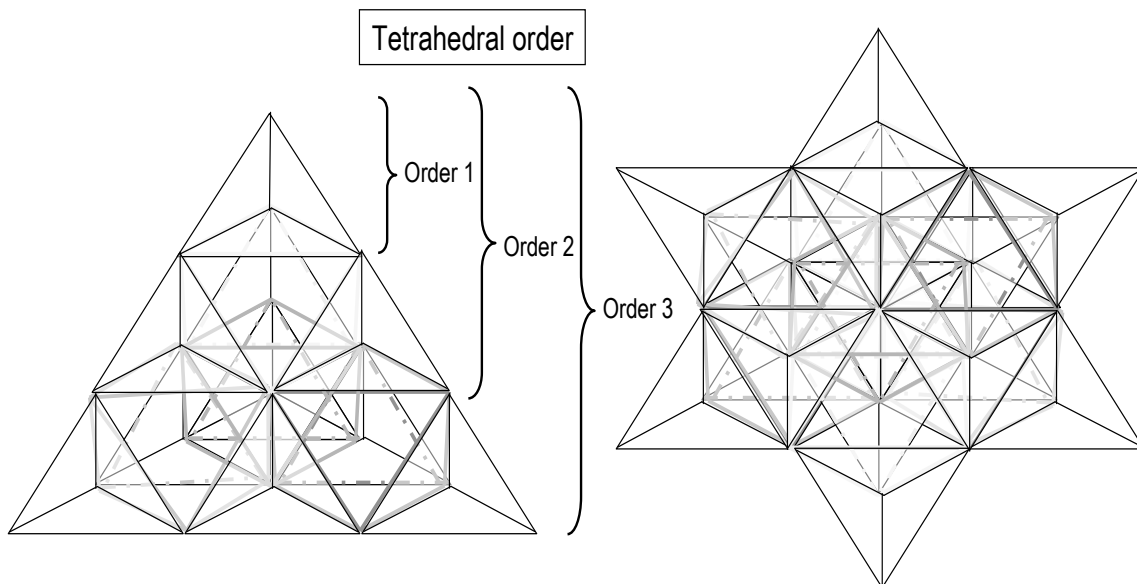The internal octahedra in 2 dimensions also highlight a form of cubic reiteration (Fig. 5).

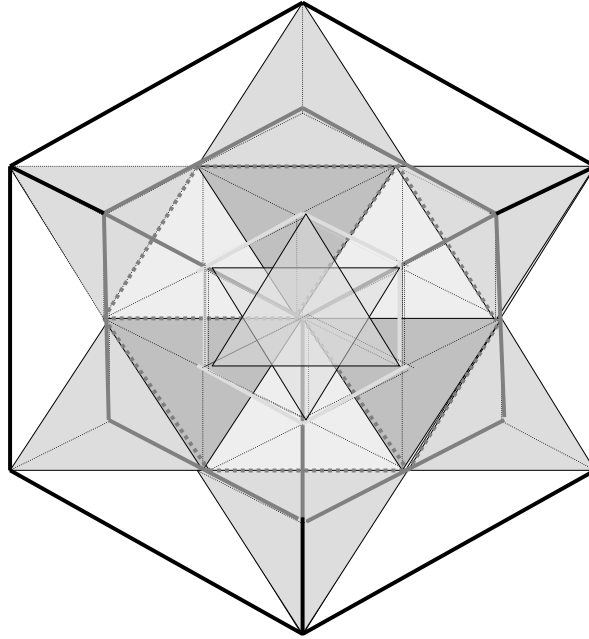**FIGURE 4.** Increasing orders of tetrahedra

FIGURE 5. Cube reiteration

6. THE REWRITE GEOMETRY

The direct connection of biology with the rewrite structure is now apparent, with the key information being the number of nested 3-D systems, as we progress from, say, 2 bases (purines, A and G, or pyrimidines T and C) and 4 bases (purines plus pyrimidines) (orders 2 and 4), to the formation of double stranded DNA (order 8) and then an unzipping of these strands to expose the –sense ssDNA to allow the production of a mRNA (+sense), when transcription takes place (order 16). In the translation process, the mRNA is transported to the ribosomes where it is held in place by the ribosomal RNA as are the tRNAs that correspond to the appropriate triplet codons within the message. Of course there are also the actual interactions between the mRNA and the tRNAs, and the tRNAs and their respective amino acids within the ribosome. Hence a four way interaction occurs to allow the translation process of all possible 64 codons to produce a protein molecule composed of the 20 amino acids (orders 32 and 64). Here the 8-fold symmetry breaks to produce the 5-fold symmetry relevant to the icosahedron and dodecahedron. In DNA replication, the double-strand DNA, composed of all 4 bases (order 64), can be represented by the third order level star tetrahedron which meets the requisite numbers of triplets possible from our 4 bases and also the number of amino acids used by Nature to construct proteins. The breaking of symmetry is observed in the alpha double helix itself which expresses a pentagonal-based chiral structure. The geometric sequence is shown in Fig. 6. The equivalent algebraic structures are given in Table 1.

TABLE 1. The Rewrite Algebra.

Group Order	Algebraic Units	3-Dimensionality
Order 2	$(1, -1)$	$0 \times 3\text{-D}$
Order 4	$(1, -1) \times (1, i_1)$	$0.5 \times 3\text{-D}$
Order 8	$(1, -1) \times (1, i_1) \times (1, j_1)$	$1 \times 3\text{-D}$
Order 16	$(1, -1) \times (1, i_1) \times (1, j_1) \times (1, i_2)$	$1.5 \times 3\text{-D}$
Order 32	$(1, -1) \times (1, i_1) \times (1, j_1) \times (1, i_2) \times (1, j_2)$	$2 \times 3\text{-D}$
Order 64	$(1, -1) \times (1, i_1) \times (1, j_1) \times (1, i_2) \times (1, j_2) \times (1, i_3)$	$2.5 \times 3\text{-D}$

Order 2: 2 base types
purine +pyrimidine
2
MASS

Order 4: 4 DNA bases
2 pur.,2 pyr.
4
TIME

+ sense ss DNA synth
A,T,G,C
+ 4

- sense ss DNA synth
T,A,C,G
- 4

Order 8: ds DNA
A T G C
. . . .
T A C G
8
CHARGE

RNA strand synthesis
+ sense mRNA (U,A,C,G)
(copy of - sense DNA)
+8

Unzipped DNA
-sense DNA exposed
and copied (mRNA)
-8

Order 16: Transcription
- sense DNA
+ sense mRNA
16
SPACE

+ sense mRNA
ribosomal
RNA positioning
+16

- sense tRNAs
ribosomal
RNA positioning
+16

Order 32:Translation
mRNA/ribosome, tRNA/
ribosome, tRNA/a.a.,
tRNA/mRNA
32

- sense tRNAs
+ sense mRNA
1 U/C 3 Pyrimidine
+ 32

SYMMETRY STARTS

- sense tRNAs
+ sense mRNA
1 A/G 3 Purine
- 32 **TO BREAK**

Order 64: Translation
all triplet codons
+ 64

**Harmonic osc.
Zitterwebegung**

Protein created
prodn. of protein chain
of amino acids (20)
BROKEN SYMMETRY

Helix formation
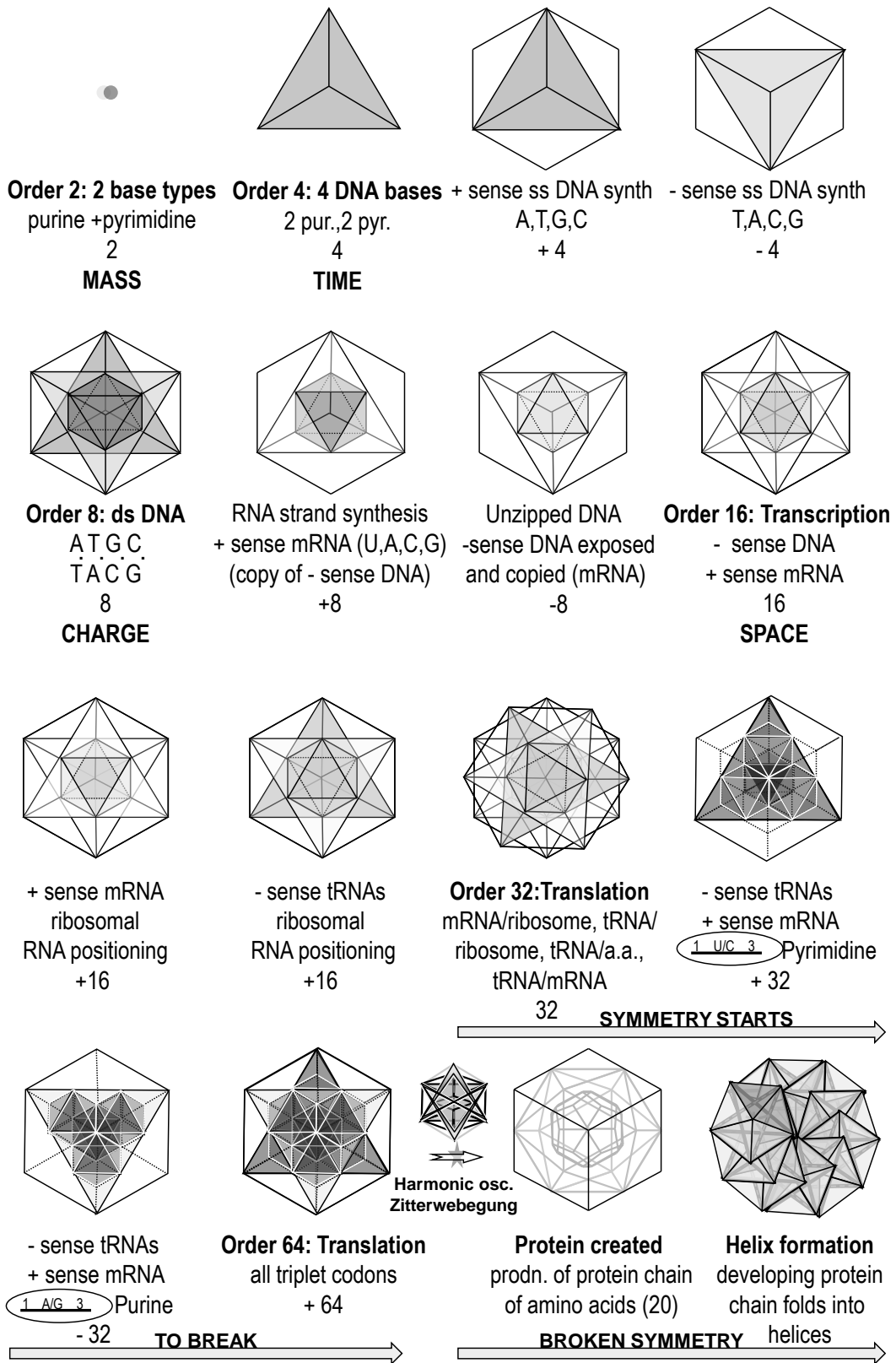developing protein
chain folds into
helices

FIGURE 6. The rewrite geometry applied to physics and DNA, transcription and translation
Order 8 here corresponds to the second order level tetrahedron with 8 triplet codons in an octahedron and 4

tetrahedral amino acids. Order 16 doubles this to a second order level star tetrahedron with 16 triplet codons in two octahedra and 8 tetrahedral amino acids. Order 32 produces a third order level tetrahedron with 32 triplet codons in 4 octahedra and 10 tetrahedral amino acids, while order 64 produces a third order level star tetrahedron with 64 triplet codons in 8 octahedra and 20 tetrahedral amino acids.

The stages at order 8 and order 32 are key 'phase transitions', producing, respectively the first octahedron and then the first 3-D (tetrahedral) arrangement of 4 octahedra. Orders 16 and 64 produce the direct doubling that is characteristic of timelike transition between spatial states characterized by the hidden time component in the multivariate vector system, due to the additional pseudoscalar 0.5×3-D. The cube reiteration in Figure 5 shows the exact parallel between the 1.5×3-D and 2.5×3-D structures when one complete 3-D system is mapped exactly onto another. Pentad (i.e. 5-fold) structures notably occur only at orders 32 and 64.

The rewrite system requires a double 3-D because an object is dual with the rest of the universe (or vacuum) in that the two combine to a zero totality. In particle physics, this means that a fermion has interactions with all other particles in the universe, and that these determine its final state. They also cause its changes. In a sense the vacuum is what the fermion will become, and we can picture it as like two spaces interpenetrating each other in a way that cannot be visualised in 3-D, but can be in higher dimensions. So we have 'static' dimensions and changing ones, just as we have conserved (mass and charge) and nonconserved ones (space and time), or, alternatively, amplitude and phase, or fermion and vacuum. Because the 'phase' part includes the idea of change, it is like the set of moving biological coordinates, assumed by Illert in his 2×3-D work on shells,[5] but we also need a rest frame of fixed coordinates which express what remains fixed, and as a reference. Significantly, the interaction with the rest of the universe in particle physics is through charge, which provides the second 3-D. Biology, with its self-replicating mechanisms, is even more obviously organised in this holistic way.

7. GEOMETRIC STRUCTURES APPLIED TO GENETICS AND CODING

The transcription and translation of the 64 codons of DNA into 20 amino acid building blocks of protein is analogous to the resolution of the 64 units of algebra into 20 in the fermionic nilpotent.[6] This 20 can be considered as a group of 4 pentads and we have just described the division of amino acids into 4 groups. It is also interesting here to note that there is a 'loss' of 4 units from the total of 64 (± 1, $\pm i$). In biology there are a series of 'stop codons' that do not translate into any amino acids but act as termination points in translation. These codons vary from one species to another but there are known to be 3 or 4 present within most genera. Perhaps the phase change observed at order 64, where we see the reiteration of the cube (in 2-D), is one that can be represented by the icosahedron. The icosahedron has 20 sides, where each can represent one amino acid, and each of the 20 component tetrahedra has 4 triangular faces that can represent a triplet codon, giving the full complement of 60 codons. Another method can be applied to give the same figures by placing a tetrahedron upon each icosahedral face to produce a star icosahedron. The breaking of symmetry from an 8-fold to a 5-fold structure within the algebra can be geometrically described by the formation of a pentagonal disc composed of 5 tetrahedra (with gaps totalling 7º 12'), and we are again reminded of the icosahedron where we can divide this structure into two such discs plus a ring of 10 tetrahedra which join them. What is remarkable is that 10 of these discs pack naturally to form one cycle of a double helical spiral, with the 10×7º 12' ratcheting the dNTP pair to the next twist in the spiral; we can now consider them as part of a string of icosahedra (albeit incomplete), and construct the internal reciprocal dodecahedra within them. The front two faces of the dodecahedra lie where the 10 dNTPs would be placed within a single cycle of the double helix of DNA. Amazingly, one disc even highlights 3 dNTPs, thus implicating one triplet codon. In fact DNA has a distinctive pentagonal symmetry within its structure as shown in Fig 7 D. The top down view of an icosahedron (two joined overlapping pentagonal discs) fits very well upon a computer generated scattergraph of DNA (Fig. 7 F) in the same way as the ring of 10 pentagonal discs, the outline of which constructs the outline of the icosahedron. Fig. 7 F also shows the 8-fold symmetry breaking into two overlapping pentagons in a way which recalls the symmetry-breaking which forms the fermionic nilpotent in (1).

The structure of amino acids that make up a protein can also be considered as having a tetrahedral format. When the string of amino acids fold they form two fundamental structures, namely helices and ß-pleated sheets (hexagonal lattices), and it is a combination of these that make up the proteins of all cells. The DNA helix is an alpha helix and is made up of bases that also exhibit selected chirality. Proteins, likewise, show a selected chirality in that the amino acids are L–forms and their D–form counterparts are often toxic to cells. The protein helices are generally alpha forms. Interestingly, when actual pentagonal / pentameric proteins are considered from a functional aspect within a

cell they appear to be involved in helix formation or moving motor type structures; e.g. the pentameric cap protein within bacteria drives the formation of flagellin helices. Hexameric proteins, by contrast, form membranes and cell walls, i.e. are more static in nature.
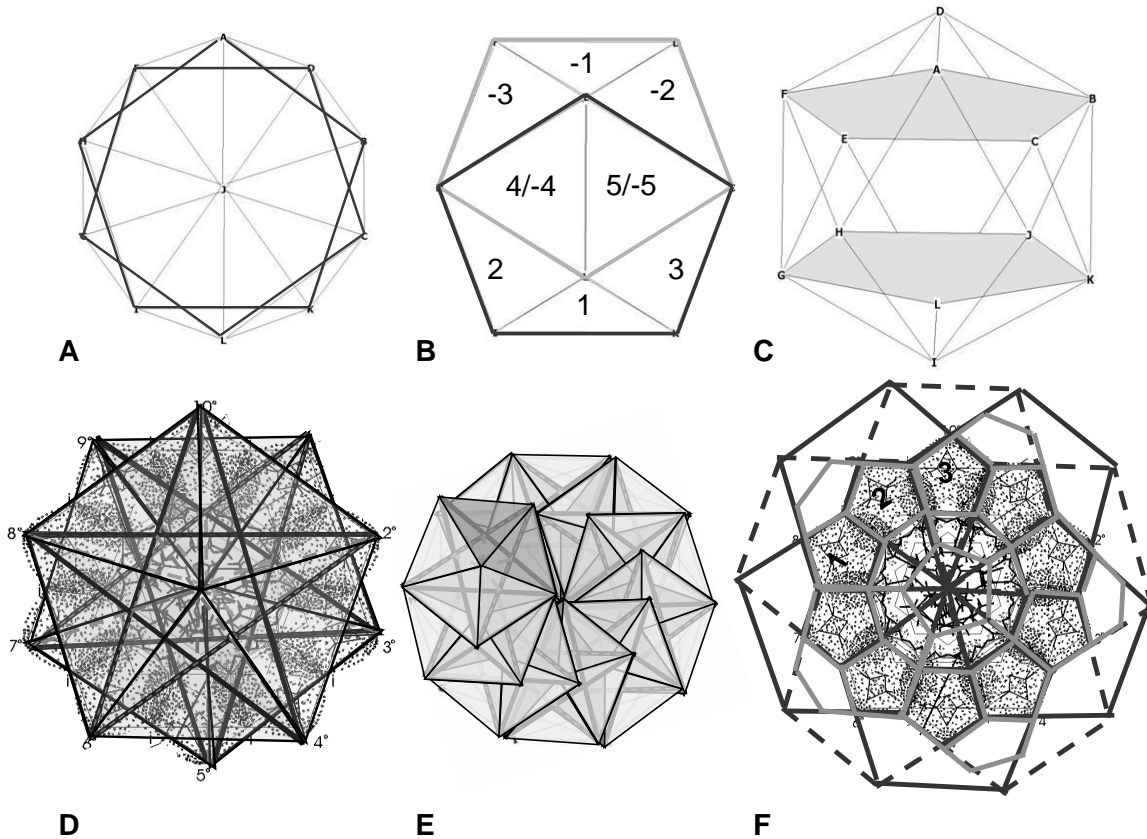

FIGURE 7. The icosahedron and the pentagonal geometry of DNA. A: top- down view; B: side view 1; C: side view 2; D: A overlaid onto scattergraph of DNA; E: Spiral of pentagonal disks overlaid (incomplete icosahedra), top-down view; F: E overlaid onto scattergraph of DNA (with internal dodecahedra – faces numbered identify dNTP positions).

8. CONCLUSION

Mathematical structures, both algebraic and geometric, related to the 'universal rewrite system', appear to define a universal process applicable to Nature, which operates in both physical and biological systems, and which may be described as 'Nature's code'.

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