Chapter 19

Nature's code

This chapter is coauthored with **VANESSA HILL**. Mathematical structures apparently underlying different aspects of physics and biology are examined in relation to their possible common origin in a universal system of process applicable to Nature, which we may describe as 'Nature's code'. We begin with a revision of mathematical and physical concepts essential to the rewrite procedure as developed in chapters 1 and 2. This is aimed at showing the significance to fundamental processes of 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, with an 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 are shown to be driven by fundamental processes of this kind. The role of the Platonic solids, pentagonal symmetry and Fibonacci numbers in organizing 'Nature's code' is explored in detail, with special reference to DNA, RNA and the genetic code.

19.1 The Dirac nilpotent as the origin of symmetry-breaking

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. The work in this chapter is aimed at showing 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 are some tantalizing hints that a few simple mathematical structures play a significant role in biology, as well as physics, when taken at the fundamental level. A key connecting idea is 3-dimensionality. Using the concept of a universal computer rewrite system and starting from the idea that zero totality is necessary at all time, we showed, in chapter 1, that we could devise an algebraic structure in which 3-dimensionality, through the linked property of anticommutativity, generates the entire system of discrete numbering on which mathematics is founded. At the same time, replicating biological systems seem to be generated in a way that conforms to similar mathematical processes, and to be constrained by the necessity of fitting into a context determined by the 3-dimensionality of space. It is, of course, one thing to hypothesize that this physics / biology link exists, another to prove it; but the link, if it exists, would be so significant that is worth examining a number of possible connections suggested by the underlying mathematics.

A significant question in the creation of all systems with large-scale order is how complexity can arise from simplicity. Related to this is the question of how asymmetry can arise from symmetry. The universal rewrite system suggests how this can occur in physics, and it will be interesting to see if the same applies in biology. In the rewrite system, anticommutativity is seen as the only true source of discreteness in nature. If **a** and **b** are anticommutative with each other, then neither can be anticommutative with anything else, except **ab**. So **a**, **b** and **ab**, or ***i***, ***j*** and ***ij***, form a closed or discrete set. The rewrite process generates an infinite succession of otherwise identical closed sets of this kind, which thereby generates a system of numbering. It also generates a series of Clifford-type algebras:

real scalar	units	± 1
complex (real + imaginary) scalar	units	$\pm 1, \pm i$
quaternion	units	$\pm \boldsymbol{i}, \pm \boldsymbol{j}, \pm \boldsymbol{k}$
multivariate vector (complex quaternion)	units	$\pm \mathbf{i}, \pm \mathbf{j}, \pm \mathbf{k}$, etc.

Remarkably, the algebras required for these four orders are respectively those required for the four fundamental physical parameters: mass (real scalar), time (pseudoscalar = imaginary scalar), charge (quaternion) and space (multivariate vector).

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

The combination of these requires an algebra of 64 units (including + and – signs). This is made up of

4 complex scalars	$(\pm 1, \pm i)$
12 complex vectors	$(\pm 1, \pm i) \times (\mathbf{i}, \mathbf{j}, \mathbf{k})$
12 complex quaternions	$(\pm 1, \pm i) \times (\boldsymbol{i}, \boldsymbol{j}, \boldsymbol{k})$
36 complex vector quaternions	$(\pm 1, \pm i) \times (\mathbf{i}, \mathbf{j}, \mathbf{k}) \times (\boldsymbol{i}, \boldsymbol{j}, \boldsymbol{k})$

This is, of course, also known as the Dirac algebra because it is the algebra which occurs the Dirac equation for the electron, although there it is often, more conventionally, expressed in terms of the five γ matrices. The significant thing here is that the algebra does not need 8 primitive units, and + and – signs, to generate these 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, because this can only be done by taking one of the 3-dimensional quantities (space or charge) and superimposing its units on the others. If we take charge (the conserved quantity), we obtain:

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

and, as we have seen, these five combined or composite units also acquire a composite physical character, derived from their components, respectively, energy (E), three components of momentum ($\mathbf{p}$), and rest mass (m):

$$E \qquad \mathbf{i}p_x\ \mathbf{j}p_y\ \mathbf{k}p_z \qquad m$$
$$= \mathbf{p} \text{ (when components combined)}$$

That is, the charges produce new quantities that are quantized and conserved (like themselves) but also retain the respective pseudoscalar, vector and scalar aspects of time, space and mass. In complete form, we have:

$$i\boldsymbol{k}E \qquad \mathbf{i}\boldsymbol{i}p_x\ \mathbf{j}\boldsymbol{i}p_y\ \mathbf{k}\boldsymbol{i}p_z \qquad 1\boldsymbol{j}m$$

As we have already established in chapter 3, a system made of these components is the most efficient packaging of the information concerning the four fundamental parameters, space, time, mass and charge, that can exist in

nature. In fact, no other type of physical system exists. We describe it as a fermion (or antifermion, depending on the sign of $i\mathbf{k}E$), and it turns out that the fermion / antifermion described by the combination ($\pm i\mathbf{k}E \pm \mathbf{i}\mathbf{p} + 1\mathbf{j}m$) is the fundamental unit of physics. The space, time, mass and charge components become compactified into a single unit. Very significantly, every packaging of this kind is a nilpotent or square root of zero. This means that it squares to zero with the 'vacuum state' $-(\pm i\mathbf{k}E \pm \mathbf{i}\mathbf{p} + 1\mathbf{j}m)$ created simultaneously when we extract it from a zero totality superposition. Another way of expressing this (which is derivable from certain mathematical properties of the nilpotent) is to say that it has a 'spin' describable in half-integer values, which becomes 'single valued' (full integer) when combined with its vacuum state or equivalent. (Significantly, no new information would be gained by allowing a sign variation in $1m$ in a fermion state, as opposed to vacuum.)

While the symmetry-breaking creation of the concepts of energy (E), momentum ($\mathbf{p}$) and rest mass (m) is the immediate result of the fermionic packaging, the process, as we have seen, also works simultaneously in the opposite direction by breaking the symmetry between the three charges ($\mathbf{i}, \mathbf{j}, \mathbf{k}$) as they take on the respective pseudoscalar, vector and scalar aspects of time, space and mass. So we now have, for charge:

weak	strong	electric
w	$s_R\, s_G\, s_B$	e
	(3 colours)	
$i\mathbf{k}$	$\mathbf{i}i\ \ \mathbf{j}i\ \ \mathbf{k}i$	$1\mathbf{j}$
pseudoscalar	vector	scalar

19.2 The significance of the pseudoscalar term

Two very significant facts are associated with defining ($\pm i\mathbf{k}E \pm \mathbf{i}\mathbf{p} + 1\mathbf{j}m$) as a nilpotent. The first is that, to ensure nilpotency, one term at least must be pseudoscalar, that is, contain the factor i. Otherwise the squared terms will not add up to zero. The pseudoscalar is the term that becomes the 'book-keeper' (energy, weak charge), the creator and destroyer, the aggregator and disperser of matter in all its forms. In the universal rewrite system, this factor occurs as part of an incomplete quaternion set – there are no intrinsic pseudoscalars – and it is in removing this incompleteness that all physical interactions are ultimately situated. Here, the pseudoscalar i occurs in the position occupied by the

parameters time, energy and weak charge, and the incompleteness manifests itself in the properties of all these quantities. The second significant fact is that a pseudoscalar quantity is, by definition, mathematically ambiguous. We cannot distinguish between + and – signs, *but both must be present*. This is what allows us to generate antifermions (–*E*) or (–*w*) and time reversal symmetry (–*t*). The conditions are, of course, connected: antifermions do not have negative energy in ordinary time; they only have negative energy in reversed time. The result of the sign ambiguity in the pseudoscalar term is that the fermion and vacuum are always a dual combination.

As previously stated, though the Dirac nilpotent is structured as (± *i***k***E* ± ***i*****p** + ***j****m*), it is also often convenient to multiply throughout by *i* and write it as (± ***k****E* ± *i****i*****p** + *i****j****m*). The bracketed expressions are really column (or row) vectors whose four components take up the four sign variations of ± *i***k***E* ± ***i*****p**. The four components represent the fermion state itself and three vacuum 'reflections' representing the effects of the three charges. In other words, the nilpotent, when structured in the column vector form (± *i***k***E* ± ***i*****p** + ***j****m*), incorporates both energy and charge information. Information about charge 'occupancy' is determined by relative phases. The three vacuum 'reflections' are structured as ***k*** (± *i***k***E* ± ***i*****p** + ***j****m*), ***i*** (± *i***k***E* ± ***i*****p** + ***j****m*), ***j*** (± *i***k***E* ± ***i*****p** + ***j****m*), which represent respective the weak, strong and electric vacua. If we multiply (± *i***k***E* ± ***i*****p** + ***j****m*) by any of these any number of times it has no effect. We can consider the three things as 'partitions' of a total, or gravitational, vacuum, which would be 1 (± *i***k***E* ± ***i*****p** + ***j****m*). Multiplying (± *i***k***E* ± ***i*****p** + ***j****m*) by this would make it disappear (Pauli exclusion). (The reason why there is no independent *m* sign change, of course, is that there are only three charges. This has very important consequences in ensuring that there are only positive values for mass and ultimately energy, as also for proper time.)

The whole meaning of nilpotency is that the object squares itself to zero, and, from the rewrite mechanism which generates it, it would appear that the reason is that a fermion can have no existence outside of the total vacuum or 'rest of the universe'. In this sense, the total vacuum is a continuum (not partitioned), whereas the three 'partitions' are discrete. We create a fermion only with its other half. The total effect remains zero. A fermion always acts in such a way as it is trying to find this other half. However, the only perfect partner for a fermion is the completely delocalised vacuum – or rest of the universe. Fermions can be pictured as incomplete systems which are forever seeking the ideal partners needed to reduce them immediately to zero. This is the reason why we have

aggregated matter. We can consider this by analogy with Newton's third law of motion, where body A does not act on body B but on the rest of the universe, and the same applies for body B supposedly acting on body A. However, body B can become, *in effect*, the rest of the universe if it is, say, very close to body A. (Thermodynamics, as we have previously implied, is relevant here, and the distinction between closed and open systems; the nilpotent fermionic state is unique in being an open system, but defined to conserve energy.)

In the same way, we can create local aggregates of fermionic matter by a fermion, say $(\pm i\mathbf{k}E_1 \pm \mathbf{i}\mathbf{p}_1 + \mathbf{j}m_1)$, effectively finding its other half in another fermion, say $(\pm i\mathbf{k}E_2 \pm \mathbf{i}\mathbf{p}_2 + \mathbf{j}m_2)$. (Of course, 'fermion' is a generic term here: either or both of these states could be antifermionic.) The equivalent of the squaring operation here is the 'vertex' $(\pm i\mathbf{k}E_1 \pm \mathbf{i}\mathbf{p}_1 + \mathbf{j}m_1)(\pm i\mathbf{k}E_2 \pm \mathbf{i}\mathbf{p}_2 + \mathbf{j}m_2)$, which eliminates all quaternionic components when all four product terms are combined; and, if we make the specification that all products of fermions are non-quaternionic, then we only need to specify the lead term in an expression such as $(\pm i\mathbf{k}E_1 \pm \mathbf{i}\mathbf{p}_1 + \mathbf{j}m_1)$, say $(i\mathbf{k}E_1 + \mathbf{i}\mathbf{p}_1 + \mathbf{j}m_1)$; the other three terms become automatic.

An interaction occurs where the creation of a vertex leads to changes in the E and / or $\mathbf{p}$ terms of the components; and, where the E and / or $\mathbf{p}$ become equalized, the vertex becomes a new combined, bosonic, state, with a purely scalar value. Such a state can only exist at all, however, if the two halves have different signs for either $i\mathbf{k}E$ or $\mathbf{i}\mathbf{p}$, or both, which the combining force (the weak interaction) will not recognize. The three possibilities create spin 1 bosons (reverse E in the second fermion), spin 0 bosons (reverse E and $\mathbf{p}$ in the second fermion), and 'Bose-Einstein condensates' (reverse $\mathbf{p}$ in the second fermion). Bose-Einstein condensation is, of course, a particular case of the very general physical concept called the Berry phase, with many distinct manifestations – other examples are the Aharonov-Bohm effect, the quantum Hall effect and the Jahn-Teller effect. Fermions, like electrons, self-aggregate, for example, with something like a nucleus or a magnetic field line to create a system with single-valued spin (not multiples of ½). It is probable that nonzero Berry phase is manifested in some way with all fermions – we just don't see it in most cases, because the system with which it is connected in this way is too dispersed. It is through this kind of phenomenon that matter self-aggregates over long distances.

Ultimately, quantum mechanics is about relating the packaged and conserved energy and momentum terms in the nilpotent expression $(i\mathbf{k}E + \mathbf{i}\mathbf{p} + \mathbf{j}m)$ to the nonconserved parameters time and space, from which they were originally

derived; and to do this we make ($i\mathbf{k}E + \mathbf{i}\mathbf{p} + \mathbf{j}m$) into a differential operator in which E and $\mathbf{p}$ represent the quantum operators $\partial / \partial t$ and ∇, expressing the variation in time and space. In the case of the system not being free or isolated (which is, of course, always true in reality), we also add on respective scalar and vector potential energy terms to these operators, which reflect the particular fields (i.e. other fermionic states) to which the fermion is subject. (Again, in reality, this will be an infinite number, though in practice one or a few may be dominant.) What happens now is that the operator requires a *unique* phase term on which to operate – or unique within the symmetry constraints of the fields involved. The result of the operation will then be an amplitude, which will always square to zero. So, in the case of a free particle, the operator ($-i\mathbf{k}\partial / \partial t + \mathbf{i}\nabla + \mathbf{j}m$) generates the uniquely defined phase term $\exp -i(Et - \mathbf{p}.\mathbf{r})$, which, when differentiated by the operator, produces ($i\mathbf{k}E + \mathbf{i}\mathbf{p} + \mathbf{j}m$), which squares to zero.

In more complicated cases, where the operator iE is not simply $\partial / \partial t$, we get a completely different phase term. A standard example is the hydrogen atom, where the inverse quadratic force (Coulomb, $\propto 1/ r^2$) requires $iE \rightarrow \partial / \partial t + A / r$, and the phase term has a real, not imaginary, exponential. For a discrete point particle, with spherical symmetry in space, it can be shown that there will be no solution unless there is a Coulomb term in iE. We can also show that there are only three solutions with spherical symmetry: inverse quadratic force (Coulomb); inverse quadratic plus constant force; and inverse quadratic plus anything else. The first gives the characteristic electric force solution; the second produces confinement, with the characteristics of the strong interaction; the third is a harmonic oscillator, irrespective of the actual nature of the force law. This is a creator and destroyer, with the characteristics of the weak interaction and the van der Waals forces responsible for aggregated matter. It is exactly what we would expect for dipolar and multipolar forces of any kind.

Ultimately, ($i\mathbf{k}E + \mathbf{i}\mathbf{p} + \mathbf{j}m$), in whatever form it is, uniquely determines the phase to be associated with it, and also the amplitude. The phase can be seen as corresponding in many ways to what we call ‘vacuum’, while the amplitude corresponds to the particle. In a sense, the phase is the connection of the particle to the rest of the universe, the carrier of nonlocality, the origin of the idea of phase conjugation (which determines locality) and the holographic principle (see chapter 20). It is like a signal sent out by a fermion asking other fermions, etc., to organize themselves with respect to it, and to aggregate. It is also a fundamental part of the intrinsic duality of the nilpotent fermion. We have amplitude on the one hand, and operator plus phase on the other, and they must be identical.

19.3 Spin and aggregation of matter

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. No process is reversible. Time is unidirectional.

To arrive at the standard quantum mechanical harmonic oscillator, means realising that spin ½ is intimately connected with the weak interaction, and results from a particular aspect of it (its incompleteness). Spin ½ in physics comes from a fermion only being created simultaneously with its vacuum, and the spin is defined with respect to vacuum. A fermion cannot be defined otherwise. As we have already stated, it is like an interaction in the case of Newton's third law – not body A on body B, but body A on the rest of the universe (which is mostly B), and body B on the rest of the universe (which is mostly body A). Vacuum is the rest of the universe. It is a manifestation of the nonlocal aspect of quantum mechanics (and is probably the same thing as 'gravity' – again relating to Newton's third law). Now we can imagine the spin of the whole system as a kind of 'helical' motion. Interestingly, it is *double helical*, because the vacuum 'spins' ½ at the same time as the fermion. The total is spin 1 (or 0), so the combination produces an ordinary 2π rotation, though each half rotates through 4π. It may be significant, from the point of view of the universal applicability of the nilpotent rewrite system that a double helical 'DNA-type' nebula, about 80 light years long, and indicative of 'a high degree of order', has now been detected about 300 light-years from the centre of the Milky Way.[1] Here, the requirement of a strong magnetic field acting on the rotating body suggests that the best analogy is with a fermion acting in a boson-like manner in a magnetic field.

Another interesting aspect of spin is that it is generated from the vacuum via the weak interaction. The weak interaction is dipolar (a dual ± source), because of the sign ambiguity in the pseudoscalar parent quantity, and the basic force law for dipole-dipole is inverse quartic ($\propto r^{-4}$), just as the basic unipole-unipole law is Coulomb or inverse quadratic ($\propto r^{-2}$). In physics, *any* third body (or 'pole') introduced into a system where two bodies (or 'poles') have a $1 / r^2$ attraction /

repulsion, will produce an additional $1 / r^4$ dependence. In other words, the $1 / r^4$ dependence is a natural result / expression of aggregation.

The most famous example of inverse quadratic plus inverse quartic in physics is the analogous perihelion precession of the planets produced by gravity. That is, while the inverse quadratic term produces the orbit, the inverse quartic term makes the orbit spin. So, we can consider the weak term as generating the spin. In effect, the ½-integral 'spin' can be seen as the weak interaction operating a continual switching between the $+E$ and $-E$ or $+t$ and $-t$ states (*zitterbewegung*), or fermion and vacuum. In the planetary case, the main reason for the inverse quartic term is the disturbing effect of other planets. That is, the orbit of Mercury round the Sun is disturbed by all the other planets in the solar system. Another way of expressing this is to say that the tendency to aggregation within the Sun-Mercury combination is supplemented by the tendency to aggregation between this combination and other aggregated bodies of matter. Any tendency to such aggregation creates a dipolarity.

The weak term is indeed the crucial one for the collective behaviour of matter. Matter becomes collective only when it overcomes the weak Pauli exclusion (the uniqueness of each fermionic state) by creating *physical* dipoles, rather than matter-vacuum dipoles. This can be seen as a kind of localization. It has been suggested in chapter 10 that spin is a manifestation of a weak dipole moment. That is, it shows a bias to one sign over the other. This does not happen with strong and electric interactions. Particle physicists attribute the left-handedness of the weak interaction for fermions and right-handedness for antifermions to the idea that there is a filled weak vacuum. It is notable that the weak charge and energy are located in the same place in the Dirac nilpotent. We note here also that collective matter has a left-handed bias in the same way as the weak interaction: All proteins are composed of L-amino acids, all sugars are the D form and all nucleic acids in RNA and DNA are D form and it is tempting to conclude that this must have the same origin.

Continuous vacuum energy, such as we would expect from a 'filled' vacuum, is what we mean by nonlocality. It is the continuing connectedness, through the vacuum, of apparently discrete fermionic states, and it is required to maintain Pauli exclusion. Rest mass is a localization and therefore discretization of the continuous total vacuum energy. The continuity of vacuum energy is the reason for the left-handed bias of fermionic states, but, in discretizing it as rest mass, we also allow an element of right-handedness to emerge (as also E and $\mathbf{p}$).

19.4 Self-organization of matter

All processes in the entire universe can be considered as corresponding to the elimination of those aspects of the structure of the fermion which keep it separate from the rest of the universe: weak charge; ½-integral spin; a single energy state. In the first instance, fermions aggregate to become bosons or boson-like states, but this then proceeds to higher levels. In general, physical systems self-aggregate through the dipole-dipole van der Waals force, a classic expression of the action of vacuum, and, as we have seen, the concept of aggregation – in effect, complexity – originates, in physics, in the harmonic oscillator. Physically, the 'oscillator' aspect is seen in the behaviour of the molecules responsible for the various physical states of matter – gases, liquids and solids – which also represent different manifestations of the van der Waals force.

We think of this force as being electric or electromagnetic, because the components of matter are electrically charged, and so there are significant electrical forces involved; but the reason for the aggregation in the first place concerns the weak force. Any tendency for matter to aggregate is all about overcoming the weak force of Pauli exclusion or ½-valued spin. Any spin ½ object, or any object with spin ½ components, has a tendency to try to effect a physical realization of the 'rest of the universe'. In terms of weak charges, this is like trying to cancel them. So $+w$ cancels $-w$, or, since the sign of the weak charge is ambiguous, $+w$ cancels $+w$. But this is only a tendency – it can never be satisfied, because a 'real' partner can never cancel out a state completely.

Hydrogen bonding is one of the classic dipole-dipole forces (sometimes described as 'van der Waals' though some authors restrict this term to the intermolecular attraction), and, of course, it is precisely this which keeps the bases together in the two strands of DNA. The strands of DNA can be thought of as like the fermion and its partner (and they are equally subject to harmonic oscillation, as the links continually break and reform). All phase transitions necessarily involve a van der Waals-type force, because what is happening in a phase transition is that seemingly 'independent' systems are being more closely connected, apparently isolated systems are being realised as being connected with other apparently isolated systems. Anything which disturbs an apparently isolated (canonical, energy-conserving system) manifests itself as dipolarity, leading to a van der Waals-type force, and a physical manifestation of helicity.

The formation of a nucleus is a classic phase transition. Even though the nucleus is held together by a van der Waals-type version of the strong force (a

multipolar remnant of the quark-quark forces within the individual protons and neutrons), the real thing which makes it possible is the cancelling out of the fermionic nature of its components, or their weak charges. A phase transition occurs when there is a significant change in the number of independent states of energy and momentum in a system. Ultimately, phase transitions which decrease the number of independent states of energy and momentum (e.g. the formation of real bosons by the equalization of energies of fermion and antifermion) increase the amount of order in the system and decrease the entropy (and complexity); those which increase the number of independent states of energy and momentum decrease the order and increase the entropy. Natural processes will always favour the latter because the tendency is to multiply connections. We might suppose also that the emergence of higher structures at this stage follows a fundamental mathematical pattern guaranteeing maximum efficiency. A Bose-Einstein condensation is another classic example of a phase transition. Here the number of independent states of energy and momentum is decreased by the fact that many 'bosonic' states can be aggregated into a single state of energy and momentum because bosonic wavefunctions are scalar and so are not subject to Pauli exclusion.

DNA and RNA appear to behave in a way pre-determined by the mathematical structure required for nilpotency, and for a totality which always remains zero. The nilpotent fermion replicates itself in the vacuum, effectively through its phase, and it may be that a similar thing is involved in DNA. There is no reason to believe that the chemistry is unique (and, of course, T in DNA is replaced by U in RNA), but it may well be the case that, as soon as nature hit on a mode of replication, it took off and replicated. So aggregations happened until a particular replicating one developed. A universal phase effect must certainly have been involved.

It is even possible that some biological form of the Pauli exclusion principle may operate in these circumstances. It is a widely known fact that the enzymes responsible for DNA replication and repair within bacteria (the DNA polymerases) all have an error rate generally between 1×10^3 and 1×10^7. However, these error rates are values given for *in vitro* situations and cannot be directly applied *in vivo*. Different bacterial species have differing numbers of these polymerases each responsible for slightly different processes and each has an error rate that will be cumulative as a whole. These error rates increase when the system is under stress or within suboptimal conditions, and it may be that this error rate is part of a system for adaptive evolution. When the actual error rates

are considered as a whole it is unlikely that any one bacterial cell is in fact a true identical clone of another – a situation that may remind us of the Pauli exclusion principle.

19.5 The filled weak vacuum and the one-handed bias in nature

It is important to recognize that the force responsible for the emergence of higher-level structures in Nature is a strictly nonlocal or vacuum one. In fact, the organizing factor in all aggregation of matter is the weak force between fermion and vacuum. The fermion effectively has an unpaired weak charge which can always interact weakly with vacuum, because the weak vacuum is *filled*. In principle, this is precisely what weak filled vacuum means: there is always something with which the fermion interacts, and it is nonlocal. It is the filled vacuum that is responsible for spin ½, chirality, *zitterbewegung* (vacuum fluctuation), van der Waals dipolarity and rest mass. Its manifestations very likely include the prevalence of matter over antimatter, thermodynamics, and the arrow of time, and its origin comes from the fact that mass-energy and time are both continuous concepts, even in the discrete fermionic state.

As we have seen, the fermion's whole objective is to cease to exist, but this cannot happen because it would require the delocalised whole of the rest of the universe to become localised at the same point. However, the thing that makes it want to do this – the unpaired weak charge – can do this by combining with a fermionic / antifermionic partner in the bosonic state. However, many bosonic states are not a true union, and the structure remains open; for example, in the hydrogen atom – the parts are still distinct and try to combine with other fermions / bosons – e.g. the H atom becomes H_2 molecule, etc. The van der Waals force which drives the process originates in the fermion's weak interaction with vacuum. Though the ordinary weak interaction between two real particles or weak charges is very short range, the interaction with vacuum has unlimited range because the weak vacuum is continuous, and we normally describe the van der Waals force as arising out of the fluctuations in vacuum (which are a result of the weak charge / vacuum dipolarity), and calculate it via the Casimir effect, which is an expression of a continuous vacuum. So this is a real link between aggregated structures at all levels. In a sense, this is the 'physical' side of 'process', and there should be a set of fundamental symmetries associated with this which operate at all levels.

An example of this may be the chirality or 'one-handedness' in both physics

and biology, already mentioned, where many people have long sought a link. Thus, the spin term which emerges from nilpotent fermionic structure has an inherent bias towards left-handedness in its weak interactions. This is an intrinsic property of the nilpotent fermion operator, and it automatically implies a filled vacuum (or bias towards $+E$ and $+t$). The computer version of the rewrite system suggests that it is an aspect of defining the concept of 'negative' (see 6.11 and Appendix B). Biology also has the same one-handed bias. Thus, amino acids can chemically exist as Dextro or Laevo (light) rotatory forms. However, biological systems only use L-forms, D-forms being toxic in many cases. (Glycine is an exception being a symmetrical molecule.) In addition, it would seem that D-forms of sugars take precedence within Nature, and D-form nucleic acids in RNA and DNA. Perhaps, this also has a mathematical origin.

19.6 The idea of 3-dimensionality

Studies of the universal rewrite system, etc., have shown that there are two ways of looking at 3-dimensionality: nonconserved and conserved. In the nonconserved version, as in ordinary space, the dimensions are indistinguishable. But the conserved case is a higher-order, more composite, concept, in which the 3 dimensions are different. This is what happens with the Dirac nilpotent. The $\boldsymbol{k}$, $\boldsymbol{i}$, $\boldsymbol{j}$ are different, and always in the same specific way. Always one dimension represents scale (say m), another dimensionality itself (say $\mathbf{p}$), and the remaining one the book-keeping (e.g. handedness) (say E). The weak interaction is the classic book-keeper. This is its only function. Biology may be using conserved 3-dimensionality and mapping it onto the nonconserved 3-dimensionality of space; and this is why, we will suggest, the *tetrahedron* can reproduce not only the other Platonic solids but also biological structures, at least approximately.

Biology, in fact, seems to require a double 3-dimensionality in the same way as physics does for quantum mechanics and the structure of particles. Illert, for example, has proved that the minimum correct representation of the growth of a sea-shell requires a doubling of conventional 3-D space, and Santilli has applied his mathematical formalisms to accommodate this.[2] It seems to be required to describe development *in time*, which, in biology, is also connected with spirals and handedness. This would make sense if we need the 3-D of $\boldsymbol{k}$, $\boldsymbol{i}$ and $\boldsymbol{j}$ to relate space and time in $(\pm i\boldsymbol{k}t \pm \boldsymbol{i}\mathbf{r} + 1\boldsymbol{j}\tau)$, or momentum and energy in its Fourier transform, $(\pm i\boldsymbol{k}E \pm \boldsymbol{i}\mathbf{p} + 1\boldsymbol{j}m)$.

However, the structure of this object suggests that we need an additional

pseudoscalar term, which according to the rewrite system is really the manifestation of an incomplete additional 3-D system. This provides the classic pattern of the 'conserved 3-dimensionality' associated with the creation of ($\pm i\boldsymbol{k}E \pm \boldsymbol{i}\mathbf{p} + 1\boldsymbol{j}m$) and ($\pm i\boldsymbol{k}t \pm \boldsymbol{i}\mathbf{r} + 1\boldsymbol{j}\tau$). In addition to the ordinary space-like 3-D of **p** or **r**, there is also the 3-D 'charge space' or 'angular momentum space' of $\boldsymbol{k}$, $\boldsymbol{i}$ and $\boldsymbol{j}$, and the incomplete 3-D of iE and it. From a fundamental point of view, we see that the development of increasing complexity is related to the existence of the fifth, symmetry-breaking, term in the fermionic state, or, more fundamentally, in the rewrite process as applied to natural phenomena.[3] Though the mathematical structures go on to infinity, only 2.5 quaternion series appear to be needed for infinite replication in a 'physical' universe. At the same time, replicating biological systems seem to be generated in a way that conforms to similar mathematical processes, and to be constrained by the necessity of fitting into a context determined by the 3-dimensionality of space. There appear to be similarities in that the 3-dimensionality has to be applied, strictly, 2.5 times.

19.7 Application to biology: DNA and RNA structure

Several important aspects seem to relate fundamental physical structures to those of biology, as though the process was somehow universal and independent of level:

The concept of double helix
The significance of 64 units
The significance of 20 units
Chirality
The relevance of Platonic solids (tetrahedra, cubes, etc.)
The 5-fold broken symmetry (Fibonacci numbers)

We have already made some mention of the double helix and chirality, but all of these relationships are particularly relevant to DNA, RNA, and their action in coding to produce amino acids for proteins. Both DNA and RNA are macromolecules and they are polymers, the monomers of which are called nucleotides. A single nucleotide consists of a 5-carbon sugar, either deoxyribose (DNA) or ribose (RNA), one or more phosphate groups, and a nitrogen containing base. Four different nucleotides are found in DNA differing only in the nitrogenous base. The nucleotides are given one letter abbreviations as shorthand for the four bases; adenine (A) guanine (G) cytosine (C) and thymine

(T). RNA is also comprised of 4 different bases and the same convention is followed for nomenclature, however in RNA the base thymine (T) is replaced by the base uracil and a single letter U is employed as shorthand.

Within a cell DNA is present as a supercoiled double-stranded macromolecule; two polynucleotide chains held together by weak thermodynamic forces (hydrogen bonds) to form a double stranded right-handed helical spiral. The two polynucleotide chains 'run' in opposite directions with A always pairing with T and G with C. For a given protein one of the two strands is referred to as the sense (coding) strand and the second the antisense (non-coding) strand. Some idea of the complexity of this system may be reached by reflecting upon the fact that the total amount of DNA in a single human cell is approximately 1.8 m long and 4 nm wide.

Proteins are made up of amino acids. The precise number, and sequence, of amino acids makes up the primary structure of a polypeptide chain. A functional protein may consist of a single, or several polypeptide chains. DNA must therefore carry genetic information that determines not only the number and types of amino acids that appear in a polypeptide, but also their exact sequence in the chain. The code for this primary structure cannot be carried within the sugar-phosphate 'backbone' of DNA since this part of the structure is identical in all DNA, variation only occurs in the base sequence. Therefore the sequence of bases in DNA determines the sequence of amino acids in a polypeptide chain. However it is apparent that, if DNA is to use the sequence of 4 different bases to code for 20 different amino acids, the code cannot be as simple as 1 base coding for 1 amino acid. In fact each amino acid is coded for by a sequence of 3 nucleotide bases, this allows 64 variants. A triplet of bases is called a codon.

19.8 Transcription

To access the genetic information incorporated in DNA it must be converted into a usable molecular 'format'. This is the so-called messenger RNA (mRNA). The process by which this achieved is called *Transcription.* During transcription a single strand of mRNA is synthesised using a double stranded DNA molecule as a template. The two strands of the DNA molecule are separated from one another, exposing the nitrogenous bases. Only one strand is actively used as a template in the transcription process. The RNA sequence that is made is a direct copy of the nitrogenous bases in the DNA sense strand *but* it is the complementary sequence. If a guanine (G) base is part of the sequence on the

sense DNA strand, then the RNA molecule has a cytosine (C) base added to its sequence at that point In the RNA molecule uracil (U) substitutes for thymine (T). In this way the process of transcription constructs a small (relatively), mobile mRNA molecule comprised of a nucleotide sequence which is complementary to a coding sequence in the DNA molecule.

19.9 Translation and triplet codons

Translation is the process by which the genetic information in mRNA directs the synthesis of a polypeptide by controlling the order of insertion of amino acids into the growing polypeptide. This is achieved by means of a second much smaller form of RNA namely transfer RNA (tRNA). A cell contains about 60 different types of tRNA. It is mainly single stranded, 70-90 nucleotides long, and some portions of the molecule are double stranded giving the whole molecule a cloverleaf shape. Each tRNA molecule possesses two important features:

1. An anti codon site, which consists of a triplet of unpaired bases. The sequence of bases in this site varies from molecule to molecule and there is an anti codon sequence that is complementary to each codon sequence found on mRNA.

2. An amino acid binding site at the free end of the molecule that can bind a specific amino acid.

The particular amino acid that binds to each tRNA molecule is determined by the anti codon sequence. The actual amino acid is that which would be specified by the nucleotide sequence complementary to the anti codon, i.e. the codon on mRNA. For example the mRNA codon UCU specifies the amino acid serine. Thus the tRNA molecule that could recognise and bind serine would carry the anticodon AGA. Consider the whole process:- The DNA triplet codon for the amino acid serine is AGA; this is transcribed into the complementary mRNA triplet codon UCU. This codon is recognised by a tRNA molecule carrying the codon AGA and this tRNA is attached to the amino acid serine.

There are 64 (4^3) different possible triplets that can be obtained from the four DNA bases A, T, G and C which theoretically could code for 64 different protein building blocks or amino acids, but Nature (generally) selects only 20 amino acids which can be coded for by 1-4 triplets as shown in Table 19.1.

2nd Position

1st Position 5'end	U		C		A		G		3rd Position 3'end
U	UUU	Phe	UCU	Ser	UAU	Tyr	UGU	Cys	U
	UUC	Phe	UCC	Ser	UAC	Tyr	UGC	Cys	
	UUA	Leu	UCA	Ser	UAA	STOP	UGA	STOP	
	UUG	Leu*	UCG	Ser	UAG	STOP	UGG	Trp	
C	CUU	Leu	CCU	Pro	CAU	His	CGU	Arg	C
	CUC	Leu	CCC	Pro	CAC	His	CGC	Arg	
	CUA	Leu	CCA	Pro	CAA	Gln	CGA	Arg	
	CUG	Leu*	CCG	Pro	CAG	Gln	CGG	Arg	
A	AUU	Ile	ACU	Thr	AAU	Asn	AGU	Ser	A
	AUC	Ile	ACC	Thr	AAC	Asn	AGC	Ser	
	AUA	Ile*	ACA	Thr	AAA	Lys	AGA	Arg	
	AUG	Met*	ACG	Thr	AAG	Lys	AGG	Arg	
G	GUU	Val	GCU	Ala	GAU	Asp	GGU	Gly	G
	GUC	Val	GCC	Ala	GAC	Asp	GGC	Gly	
	GUA	Val	GCA	Ala	GAA	Glu	GGA	Gly	
	GUG	Val*	GCG	Ala	GAG	Glu	GGG	Gly	

Table 1. The 64 Triplets, 20 Amino Acids and Stop/Start* Codons of The Genetic Code.

19.10 Triplet codons and the Dirac algebra

Is there a link between the 64 amino acid triplets and the 64 units of the Dirac algebra? Are the biological structures determined by the same kind of algebra as the physical ones? In principle, the physical structure is an example of 'conserved 3-dimensionality'. This means that it follows the pattern of a quantity such as angular momentum, with 3 non-symmetric 'dimensions' representing, say, magnitude, dimensionality itself, and handedness; or scale, dimensionality and 'book-keeping'. In the Dirac nilpotent, these concepts are represented by the respective terms ***jm***, ***ip*** and ***ikE***. The structure always requires the interlocking of two complete quaternionic sets and an incomplete one (which manifests itself as the pseudoscalar term); and it seems to occur in every case in which a 3-dimensional quantity becomes a conserved one.

Such an algebraic structure always requires 64 terms, and it is worth examining the structure of the units of the genetic code to see if they can be related to the known algebraic structure of the Dirac fermionic state. In the case of the amino acid triplets, the actual structure in physical space may be

considered the conserved object, and the 3-dimensionality is that of space itself. Classifying the codons, we find that there are

$$4 = 4 \times 1 \text{ with 3 letters the same}$$
$$24 = 4 \times 3 \times 2 \text{ with 3 letters different}$$
$$36 = 4 \times 3 \times 3 \text{ with 2 letters the same}$$

The last is made up of 4 possible letters to be duplicated, 3 letters other than the first chosen, and 3 possible ways of arranging the 3 letters (that is 3 positions for the nonduplicated one). Parallel to this, the Dirac algebra has

(A) 4 complex numbers (+ / –) (1, i)
(B) 24 = 12 + 12 complex 3-D objects (+ / –) (1, i) × (***i***, ***j***, ***k***) quaternions
+ (+ / –) (1, i) × (**i**, **j**, **k**) vector (single 3-D)
(C) 36 complex 3-D × 3-D numbers (complex vector quaternions)
(+ / –) (1, i) × (***i***, ***j***, ***k***) × (**i**, **j**, **k**) (double 3-D)

To apply this to the genetic structures we could take the (+ / –) (1, i) to represent the 4 options for bases (or stop codons). A and U or T could be say +1 and –1; and G and C +i and –i. In each case above, this is where the 4 comes from. The groups of 3, etc., would then be to do with the amount of variation allowed. They are certainly connected with dimensionality. It is interesting to see if the 20 that produce the amino acids can be written out to fit into this pattern. Any given representation of the Dirac nilpotent really only uses 20 units of the 64-part algebra, say:

i***k***	***i*i**	***i*j**	***i*k**	***j***
k	i***i*i**	i***i*j**	i***i*k**	i***j***
–***k***	–i***i*i**	–i***i*j**	–i***i*k**	–i***j***
–i***k***	–***i*i**	–***i*j**	–***i*k**	–***j***

That is, it uses: none of (A)
8 of (B) (+ / –) (1, i) × (***j***, ***k***)
12 of (C) (+ / –) (1, i) × (***i***) × (**i**, **j**, **k**)

So, in a nilpotent fermionic structure such as (± i***k***E ± ***i*i**p_x ± ***i*j**p_y ± ***i*k**p_z + ***j***m), there will be just 20 algebraic terms from the 64 that are important, if we want to represent particle and antiparticle, and also vacuum. (Here, we need to take into account multiplying by –1 and or ± i.) We could guess that these match up to the

amino acid-producing codons using:

8 with 3 letters different	± ***k***	± ***ij***
	± ***ik***	± ***j***
12 with 2 letters the same	± ***ii***	± ***ii***
	± ***ij***	± ***ij***
	± ***ik***	± ***ik***

(We note here that, in the biological case, there is a preference in each species for specific codons for each amino acid, i.e. there is a greater percentage of one type of tRNA for each set.)

We require a third of all possible codons with 3 letters different (8 out of 24), e.g. those in which a codon has its own + / – partner only on the outside.

A G U	A C U
U G A	U C A
G A C	G U C
C A G	C U G

Again, we only want one third of the 36 codons with two letters the same (12 out of 36), e.g. those again with their own + / – partners. Effectively, after we have excluded those with three identical letters (equivalent to (+ / –) (1, *i*)), we want a symmetrical third of the remaining codons. Of course, biological molecules will not be as precise as single physical particles, so we will have variation (and perhaps 'mimicry'). But we might expect an outline pattern of some kind to emerge which reflects this algebraic patterning, and preliminary analysis of the codons producing the amino acids in various species suggests that the 12 / 8 split has at least approximate validity.

For a codon with three identical bases, we should imagine a version of the 20 significant Dirac units as multiplied throughout by quaternion ***j***. This still produces the same quaternionic units for the top four pairs in each of the two columns set out above, but the last two pairs would become + / – *i* and + / 1, which are the four terms that correspond with the four codons with three bases the same. The strong showing of these codons is particularly interesting because it goes against absolute randomness over the whole 64 being the reason for the 12 / 8 split. The randomness, such as it is, is only between the quaternion elements. We could imagine that, at the most primitive level, the variation is not random,

but has a highly structured pattern, though higher species might diverge increasingly from the original blueprint, and such an analysis might prove to be a way of measuring evolution. What seems most likely to be the case is that the initial life-forming process follows the mathematical rule because of the demands of conserved 3-dimensionality, and those of self-assembly related to fermionic structures, but, of course, in very complicated life forms the pattern provides only a very general constraint.

Even the breakdown of the two sets of 64 show very similar mathematical patterns, along with the 20 units in each case, which are required:

AUG 1***k****i*; AUA 1**i*****i***; ACA 1**j*****i***; AAA 1**k*****i***; AAC 1***j***;
UGG –1***k****i*; UGC –1**i*****i***; UAC –1**j*****i***; UCC –1**k*****i***; UUU –1***j***;
GAC *i****k***1; GAA *i****i****i*; GUA *i****j****i*; GCA *i****k****i*; GGG *i****j***;
CAC – *i****k***1; CAA – *i****i****i*; CGA – *i****j****i*; CUA – *i****k****i*; CCG – *i****j***.

Here, the codons are grouped into four pentads, with the first base determining whether the first coefficient is 1, as –1, *i* or –*i*. The second base in the three central codons of each pentad is represented by a vector term, corresponding to a different base in each; while the quaternion labels correspond to the final bases, which are different for the pseudoscalar, vector and scalar terms. In this representation, we might imagine the stop codons taking algebraic forms such as –1, *i* and –*i*, though a more systematic representation of the 20 units might privilege vectors rather than complexified quaternions in the third and fourth pentads (as in the table in 15.4):

AUG 1***k****i*; AUA 1**i*****i***; ACA 1**j*****i***; AAA 1**k*****i***; AAC 1***j***;
UGG –1***k****i*; UGC –1**i*****i***; UAC –1**j*****i***; UCC –1**k*****i***; UUU –1***j***;
GAC **k**1; GAA *i***ii**; GUA *i***ji**; GCA *i***ki**; GGG **j**;
CAC – **k**1; CAA – *i***ii**; CGA – *i***ji**; CUA – *i***ki**; CCG – **j**.

By comparison, the 4 × 3 pentads of particle physics are the fermionic states of the Standard Model, which can be imagined as being divided into fermions and antifermions (corresponding to, say, 1, –1), isospin up and isospin down (1, *i*, or quaternion, vector) and 3 generations (successively privileging ***i***, ***j*** and ***k*** or **i**, **j** and **k**), each of which repeats the characteristics of the others.

For many amino acids, the third ba1e in the codon is partially redundant. Nearly all amino acids are predominantly coded by the first two bases, which remain the same as well as unique to that acid – only serine, leucine and arginine,

with 6 triplet codons each, are exceptions. In all these cases, one alternative has the complete range of options for the third base, while the other has a choice of two. In serine, the alternatives are UC and AG; in leucine they are UU and CU; and, in arginine, CG and AG. In all cases, where the first two bases make six bonds (in the conventional arrangement), the third base is entirely redundant, with all four options for the third base (A, U, G, C) being available. This is true also in three of the cases where they make five bonds; in nine other cases, there is a choice between two options for the third base, and in one case, there is just a single option. Where the first two bases make only four bonds, there are three options for the third base in one case, two options in five cases, and a single option in one case. There is a general tendency, therefore, for a decreasing number of options for the third base, where there are more bonds made by the first two bases, as we might expect. In those (seven) cases where two different amino acids share the same two first bases, the third base divides into U / C or A / G in nearly every case; only isoleucine (U / C / A) and methionine (G) provide a slight exception to the pattern. In the case of bacterial start codons, it is not at all unreasonable that the most significant bases are the *last* two, which are invariably UG, with the first base entirely redundant (A / U / G / C); while stop codons correspondingly *begin* with the same base (U) with limited options for the final two (AA, GA and AG).

An analysis of grouping of amino acids according to their specific triplet codons also yields interesting relationships. A standard method of grouping is shown in Fig. 19.1 and is dependent upon such factors / properties as size, polarity, charge, hydrophobicity, etc. However, if we attempt to group the amino acids according to the positioning of the nucleotide type within the triplet codon a different picture arises. When we attempt amino acid grouping using the A, T / U, G, C in the first position of the triplet codon, a completely random result is obtained and a similar lack of grouping is given by the position of the base within the third position – usually termed as the ‘redundant base’. This is not surprising, in that this third position placement allows for variation in coding for the same amino acid. However, when the group is defined by the middle base (i.e. as in the columns in Table 19.1) we find there is a definite pattern (Fig. 19.2) which gives a similar group profile to the standard system of grouping by chemical properties and yet because there are four bases a fourth group is defined. Table 19.2 lists the amino acids of each new group.

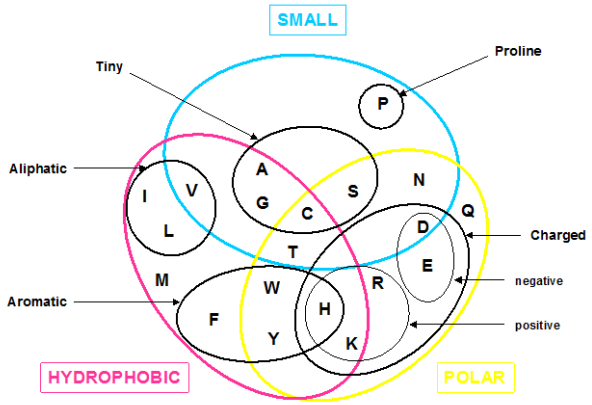


Fig 1. Standard 'Properties' Grouping of Amino Acids

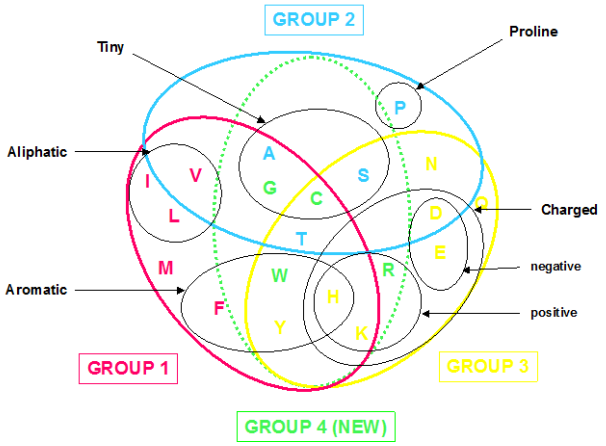


Fig 2. Grouping of Amino Acids Using The Second Base of Triplet: Group 1: T/U; Group 2: C; Group 3: A; Group 4: G.

When the properties of these four groups (Table 19.2) are looked at closer we see that group 1 now carries all the recognised bacterial start codons; ATG, TTG, CTG, GTG and group 4 contains the amino acids which display the 'extremes' of a certain property (Table 19.3); e.g. glycine is the smallest most flexible amino acid that acts as 'structure breaker' within proteins; tryptophan is the least used amino acid within proteins, it is the largest, is aromatic and absorbs UV light; arginine is the most basic with the most extensive delocalised charge, generally

present in protein-nucleic acid interactions; cysteine is involved in disulphide bridge formation and is one of only two sulphur containing amino acids, the other being methionine with its triplet codon acting as the start codon.

GROUP 1	**GROUP 2**	**GROUP 3**	**GROUP 4**
Isoleucine: I	Proline: P	Glutamine: E	Glycine: G
Leucine: L	Alanine: A	Asparagine: A	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: Q	

Table 2. The 4 New Amino Acid Groups

Glycine	Smallest, most flexible, structure breaker, achiral.
Tryptophan	Largest, aromatic, rarest, absorbs uv light.
Arginine	Most basic, extensive delocalised charge, present in protein-nucleic acid interactions.
Cysteine	Disulfide bridge formation, typically extracellular, 1 of 2 S containing amino acids (other = methionine, the start codon).

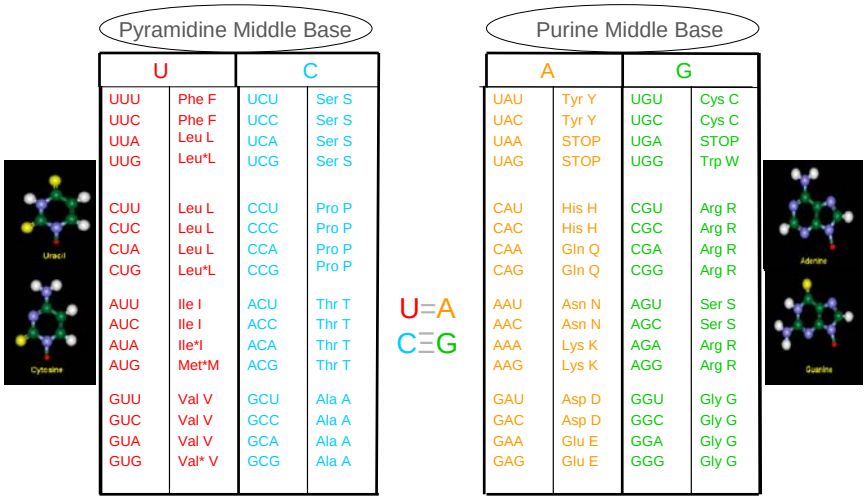
Table 3. Properties of Group 4 Amino Acids
Extremes : smallest, largest, most basic, S containing.

The algebraic structure can be considered as composed of 32 + terms and 32 – terms. It is interesting to see if such a split can be seen within the triplet codon

set, and also to see if the full set of algebraic terms can be allocated to the 64 codons, in addition to the allocation of the 20 algebraic units to the corresponding 20 amino acids.

The system that revealed the previously described group structure within the chemical properties of the amino acids was by division into groups depending upon the bases A, T, G and C as the middle base of each triplet codon. The codon table (Table 19.1) can also be split into two groups dependent upon the type of middle base (pyrimidine or purine) within the triplet. The purines and pyrimidines hydrogen bond to each other upon opposite strands of the DNA helix and can be considered as opposites upon the + and – ve sense DNA strands. Splitting the triplet codons into these two groups dependent upon the middle base of the triplets does indeed reveal another level of order. The group with a pyrimidine base (U / T, C) as the middle codon (Group A) reveals a trend for triplet codons that code for amino acids of predominantly nonpolar / hydrophobic nature and those with a purine (A, G) as the middle base (Group B) as those coding for amino acids of a polar / hydrophilic nature (Fig. 19 3).

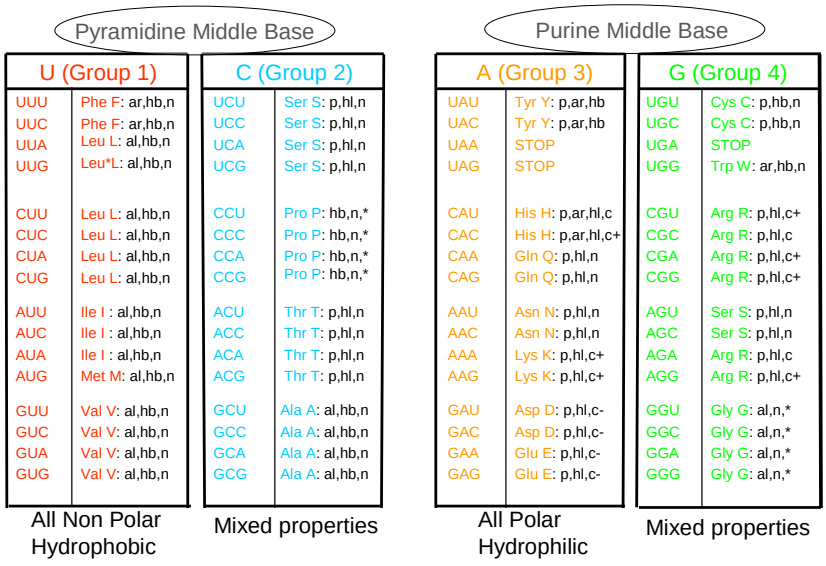
If we divide each of these two groups of 32, further into 16 codons with their respective middle bases A, U / T, G and C (Fig. 19.4), we see that the Group 1, containing U / T as the middle base code for amino acids that are all distinctly hydrophobic, nonpolar and neutral; Group 2, containing C as the middle base, code for amino acids that are all neutral and have two amino acids that are hydrophilic and two that are hydrophobic. Group 3, containing A as the middle base, are all polar and 6 out of 7 are hydrophilic, 4 are charged (2 + and 2 –) and 2 neutral. Group 4, with G as the middle base of the triplet codons, gives the most mixed group of amino acids with 3 out of 5 being polar, 1 charged +ve and 4 neutral, 2 hydrophilic and 2 hydrophobic. It appears that Groups 1 and 3 have the most distinctive clustering of amino acid properties based upon nonpolarity / polarity, and Groups 2 and 4 those of less well defined grouped properties. It may be that, for the less well defined groups, there are other properties not yet considered that have greater applicability.



U		C	
UUU	Phe F	UCU	Ser S
UUC	Phe F	UCC	Ser S
UUA	Leu L	UCA	Ser S
UUG	Leu*L	UCG	Ser S
CUU	Leu L	CCU	Pro P
CUC	Leu L	CCC	Pro P
CUA	Leu L	CCA	Pro P
CUG	Leu*L	CCG	Pro P
AUU	Ile I	ACU	Thr T
AUC	Ile I	ACC	Thr T
AUA	Ile*I	ACA	Thr T
AUG	Met*M	ACG	Thr T
GUU	Val V	GCU	Ala A
GUC	Val V	GCC	Ala A
GUA	Val V	GCA	Ala A
GUG	Val* V	GCG	Ala A

A		G	
UAU	Tyr Y	UGU	Cys C
UAC	Tyr Y	UGC	Cys C
UAA	STOP	UGA	STOP
UAG	STOP	UGG	Trp W
CAU	His H	CGU	Arg R
CAC	His H	CGC	Arg R
CAA	Gln Q	CGA	Arg R
CAG	Gln Q	CGG	Arg R
AAU	Asn N	AGU	Ser S
AAC	Asn N	AGC	Ser S
AAA	Lys K	AGA	Arg R
AAG	Lys K	AGG	Arg R
GAU	Asp D	GGU	Gly G
GAC	Asp D	GGC	Gly G
GAA	Glu E	GGA	Gly G
GAG	Glu E	GGG	Gly G

Fig 3. The 32+ and 32- Split of the 64 triplet Codons



U (Group 1)		C (Group 2)	
UUU	Phe F: ar,hb,n	UCU	Ser S: p,hl,n
UUC	Phe F: ar,hb,n	UCC	Ser S: p,hl,n
UUA	Leu L: al,hb,n	UCA	Ser S: p,hl,n
UUG	Leu*L: al,hb,n	UCG	Ser S: p,hl,n
CUU	Leu L: al,hb,n	CCU	Pro P: hb,n,*
CUC	Leu L: al,hb,n	CCC	Pro P: hb,n,*
CUA	Leu L: al,hb,n	CCA	Pro P: hb,n,*
CUG	Leu L: al,hb,n	CCG	Pro P: hb,n,*
AUU	Ile I : al,hb,n	ACU	Thr T: p,hl,n
AUC	Ile I : al,hb,n	ACC	Thr T: p,hl,n
AUA	Ile I : al,hb,n	ACA	Thr T: p,hl,n
AUG	Met M: al,hb,n	ACG	Thr T: p,hl,n
GUU	Val V: al,hb,n	GCU	Ala A: al,hb,n
GUC	Val V: al,hb,n	GCC	Ala A: al,hb,n
GUA	Val V: al,hb,n	GCA	Ala A: al,hb,n
GUG	Val V: al,hb,n	GCG	Ala A: al,hb,n

A (Group 3)		G (Group 4)	
UAU	Tyr Y: p,ar,hb	UGU	Cys C: p,hb,n
UAC	Tyr Y: p,ar,hb	UGC	Cys C: p,hb,n
UAA	STOP	UGA	STOP
UAG	STOP	UGG	Trp W: ar,hb,n
CAU	His H: p,ar,hl,c	CGU	Arg R: p,hl,c+
CAC	His H: p,ar,hl,c+	CGC	Arg R: p,hl,c
CAA	Gln Q: p,hl,n	CGA	Arg R: p,hl,c+
CAG	Gln Q: p,hl,n	CGG	Arg R: p,hl,c+
AAU	Asn N: p,hl,n	AGU	Ser S: p,hl,n
AAC	Asn N: p,hl,n	AGC	Ser S: p,hl,n
AAA	Lys K: p,hl,c+	AGA	Arg R: p,hl,c
AAG	Lys K: p,hl,c+	AGG	Arg R: p,hl,c+
GAU	Asp D: p,hl,c-	GGU	Gly G: al,n,*
GAC	Asp D: p,hl,c-	GGC	Gly G: al,n,*
GAA	Glu E: p,hl,c-	GGA	Gly G: al,n,*
GAG	Glu E: p,hl,c-	GGG	Gly G: al,n,*

Key:- ar = aromatic al = aliphatic p = polar hb = hydrophobic hl = hydrophilic
n = neutral charge c+ = positively charged c- = negatively charged

Fig 4. The Chemical properties of the 20 Amino Acids

19.11 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 cube, dodecahedron, icosahedron, octahedron and tetrahedron (Fig. 19.5) which are five recognised resonance states of the sphere.

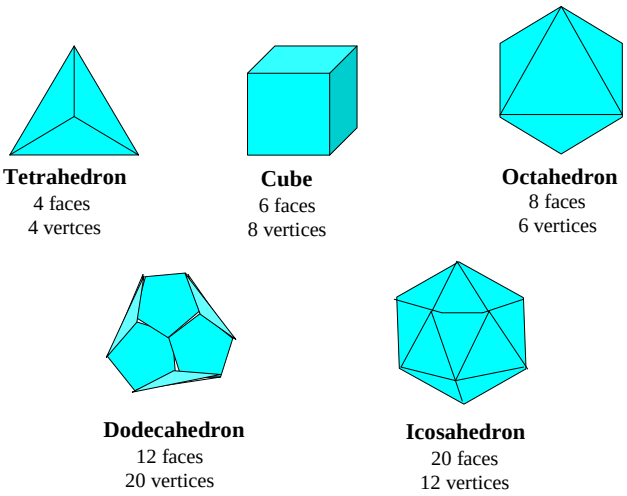


Fig 5. The 5 Platonic Solids

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. 19.6.

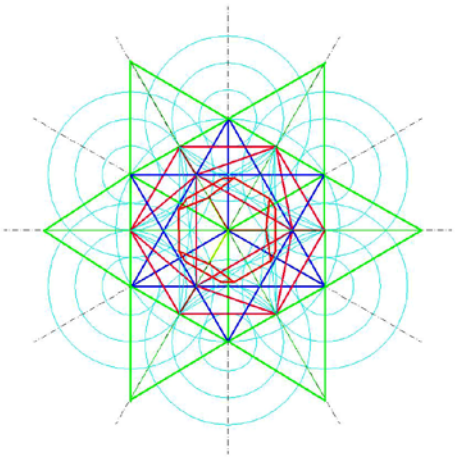


Fig 6. Nesting of The Five Platonic Solids.

The 4 fundamental parameters involved in the fermionic state, which are fundamental components of 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 (see chapter 4). The rewrite system shows that 3-D 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 (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 $e = mf / 2$ 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.) The tetrahedron shows the set and the dual set, using the six edges coloured to represent the properties and antiproperties; and the vertices or faces to show *either* the set or the dual set. The next tetrahedron filling space would be opposite, like fermion / vacuum (which is what the set / dual set is really all about). If we flatten the tetrahedral representation onto a plane we obtain the kites / darts needed for 5-fold Penrose

tiling.

In general terms, the Platonic solids produce pentagonal symmetries which are intrinsic to them as a result of their structuring within a conserved 3-dimensionality (2.5 × 3-D). The fermionic symmetry-breaking, which does exactly this, is clearly related to that of the geometry. And Penrose 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.

19.12 Fibonacci numbers

5-fold structures, such as Penrose tiling, also introduce the Fibonacci series and the Golden Section, which is so important in biological growth, the sunflower being a characteristic expression of its operation. Fibonacci numbers are an integer sequence in which each new term is defined simply as the sum of the two previous integers: 0 1 1 2 3 5 8 13 21 34 …; the ratios of successive integers: 3/2, 5/3, 8/5, 13/8, 21/13, 34/21 … converge towards the Golden Section value, $\Phi = (1 + \sqrt{5}) / 2 = 1.618 \ldots$, while the inverse ratios tend towards $\Phi' = (1 - \sqrt{5}) / 2 = -0.618 \ldots$, so that $\Phi + \Phi' = 1$ and $\Phi\Phi' = -1$, where the two numbers are the roots of the equation $x^2 - x - 1 = 0$. The Golden Section is the ratio into which any line segment will be cut if the whole segment has the same ratio to the larger part as the larger part has to the smaller; it is also the one that the relative numbers of the 2 different tile types in Penrose tiling (kites / darts – flattened tetrahedral) tends towards. It occurs, in the Platonic solids, with the pentagonal symmetry of the icosahedron (3 golden rectangles transect) and its reciprocal, the dodecahedron (which has pentagonal faces). In addition, the 4-D image of a tetrahedron projected onto a 2-D plane gives a star pentagon which can be constructed within the dodecahedron.

The 20 of the reciprocal icosahedron is clearly visible in physics in the structure of the nilpotent operator which has 4 groups of 5, and contains the dualities of mass-energy / charge, fermion / vacuum, space / phase space, localised / nonlocalised, etc. The 4 × 3 pentads of 19.10 can also be represented

by the 12 pentagonal faces of a dodecahedron which connect at vertices in groups of 3, or by the 20 triangular faces of an icosahedron, which connect at vertices in groups of 5. In each case, there are a total number of 4 groups of 5 × 3 or 3 × 5, that is 60, faces connecting at the vertices but the spherical 3-D symmetry (equivalent to privileging one of ***i***, ***j***, ***k*** or **i**, **j**, **k**) reduces this to only 20 that are independent.

The icosahedral structure may also be applicable to the 20 amino acids in that the work described in 19.10 shows there is some indication of amino acid grouping into 4 groups, dependent upon the middle base of the associated triplet codon. If a tetrahedron is placed upon each face of the icosahedron to give a tessellated form, with a total of 60 triangular faces, we can then allocate triplet codons to each tetrahedral, triangular face, that relate (directionally) to the appropriate amino acid. It is interesting that here we have to lose 4 triplet codons of the 64 to give us the required 60 and we do have 3 known stop codons. Evolution may well have resulted in the loss of one stop codon and it is already known that there are variations of which codons code for specific amino acids in the process of 'codon capture'.[4] There are also known stop codon variations; for example, the codons that normally code for arginine, AGA and AGG, code for stops in vertebrate mitochondria,[5] while the stop codon UGA, has been replaced by tryptophan in Mycoplasma species[6] and UGA by selenocysteine and UAG by pyrrolysine in Archaea (recently found rare amino acids) in some archaebacter.[7] In physics, the 64 fundamental algebraic units are made up of 12 (= 3 × 4) sets of 5 generators for the entire group (each with an in-built 3-D property) and the 4 units of ordinary complex algebra (± 1, ± i), with no dimensionality.

The use of the Fibonacci series as a means to explain all information processing in nature has been discussed by Stein Johansen, partly in connection with the universal rewrite system.[8] His description of the generating process as '1 step back and take it with you' relates to the dual conserve / create of universal rewrite. His algorithm for information processing also splits the numbers into 5s and 3s, with a bifurcation at 8 (8 + 3 = 11; 8 + 5 = 13). The 5-fold symmetry additionally seems to be responsible for introducing the fractal aspect in which the same patterns repeat themselves at different levels in Nature. Here, we observe that the rewrite system produces, in addition to the repetitive Clifford algebra sequence, in which the 2^n algebraic units are the basic ones, a new type of non-repeating 'unit of uniqueness' which, for the first time, combines the properties of recursive and iterative systems through its symmetry-breaking 5-fold symmetric structure.

A classic case of the Fibonacci sequence is the growth of a spiral shell ending in a point-singularity. D'Arcy Thompson observed that a shell grows in size without changing its shape, leading to growth in a logarithmic or equiangular spiral, with radius $r = a \exp(b\theta)$ from the point source.[9] This shape can be observed, typically, when the long side of a Golden Triangle, an isosceles triangle from within a star pentagon, with apex angle = $180^o / 5 = 36^o$ (the Golden Attractor), is continually used as a base for a new Golden Triangle. Here, the successive bases have the ratios 1Φ, $1\Phi + 1$, $2\Phi + 1$, $3\Phi + 2$, $5\Phi + 3$, $8\Phi + 5$ … . Illert, whose two 3-D systems are constituted from a fixed reference system (ordinary 3-D space) and a set of moving 3-D coordinates representing growth, has used the analogy of the spiral watchspring acting as a classical harmonic oscillator, obeying Hooke's Law ($F = kx$). Significantly, quasicrystals with icosahedral symmetry show no periodicity in ordinary 3-D space, but become periodic, and lose their Fibonacci character when structured within a 6-D cube, constructed from a parallel real 3-D space, and a perpendicular imaginary 3-D space. It may be that the significant distinction between organic and inorganic forms, in this context, is brought about by the extra half-3-dimensionality representing variation with time (and leading to helicity). In physics, this is the role of the weak interaction, which ordered crystalline structure is designed to suppress.[10]

In fact, in the fundamental rewrite system with its 5-component nilpotent operator, we may see, at once, all the fundamental units of *natural process* that apply to biology as well as physics. Defining the operator 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 $\rightarrow$ spiral) and 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).

In physics, the act of 'creation' is that of the fermionic state (and requires the simultaneous creation of relativity and quantum mechanics); but the structure can repeat at higher levels because it is a recurring pattern. An example from chemistry is the phenomenon of spontaneous chiral symmetry breaking in chiral autocatalytic systems in which continuous stirring of a solution of a salt such as

$NaClO_3$ (a nonequilibirum system in thermodynamic terms) can cause it to go through a symmetry-breaking transition in which it crystallizes almost entirely into either laevo- or dextrorotatory forms.[11] The significance of the creation of a dominant angular momentum state (through stirring) is apparent.

If universal rewrite is valid in the domain represented by Illert's work on the sea-shell, then the 5-fold Fibonacci aspect will require an additional incomplete 3-D (for time). The doubling of space is the creation of a *conserved* 3-D (angular momentum), while time and energy become the sources of chirality. If a tetrahedral arrangement is, say, the most efficient packing of 3-dimensional space, then this structure retains its identity when it is aggregated within a larger one, itself requiring 3-D spiral packing, and double helicity for stability.

19.13 Application of geometrical structures to DNA and genetic coding

The four bases of DNA – A, T, G and C – can be placed upon the four vertices of a tetrahedron (Fig. 19.7) such that the tetrahedron can now be considered to contain, upon an information level, all the possible 64 (4^3) triplets defined by single stranded (sense) DNA or mRNA (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 (Fig. 19.8). The corners of a cube would also serve well here.

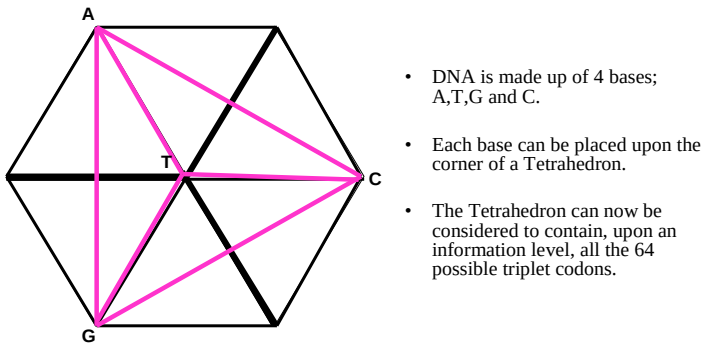


Fig 7. Single Stranded DNA : Tetrahedron

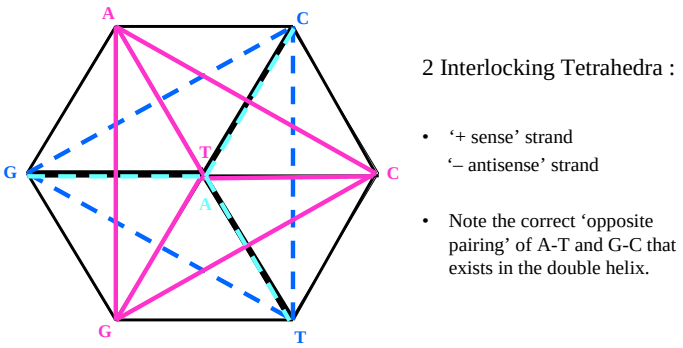


Fig 8. Double Stranded DNA : The Star Tetrahedron Within The Cube

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 as shown in Table 19.1. If we now look at different higher order levels of tetrahedra (Fig. 19.9) it can be seen that the second order is composed of one octahedron and four tetrahedra and the third order is composed of four octahedra and ten tetrahedra. If each triangular octahedral face is considered to represent a single triplet then each octahedron would have eight 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 (Fig. 19.10 and 19.11) to produce a star tetrahedron would now 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 third order level star tetrahedron now meets the requisite numbers of triplets possible from our 4 bases and also the number of amino acid used by Nature to construct proteins.

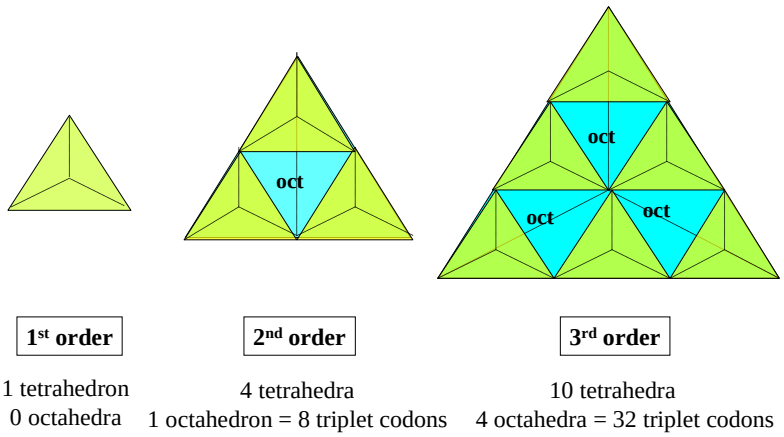


Fig 9. Higher Order Level Tetrahedra

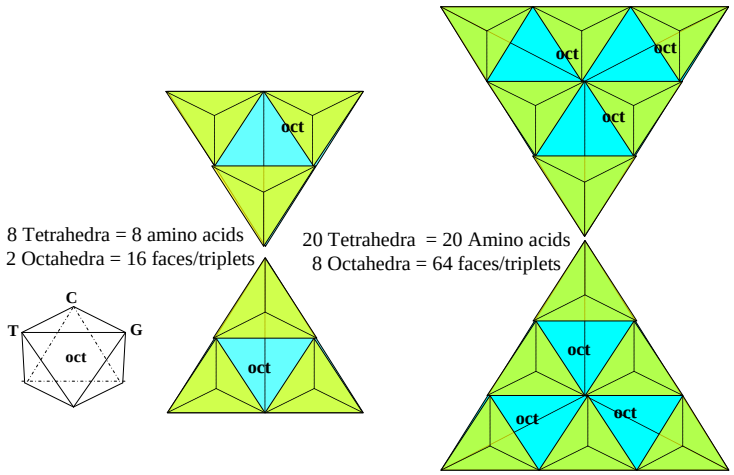
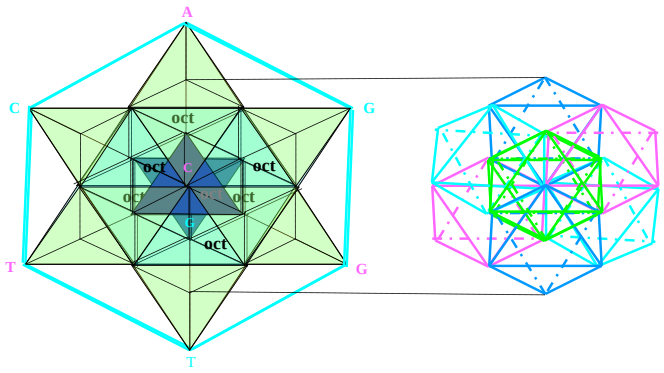


Fig 10. The Star Tetrahedron

Figures 19.11-14 give a deeper insight into how the tetrahedra and octahedra pack within this star. Interestingly, there is a fractal nature to these diagrams, highlighting the reiteration of the star / octahedron / cube. A fractal nature was

also previously observed within the higher order tetrahedra where one is reminded of the Sierpinsky fractal triangle.



Double stranded DNA enclosing info. of 8 octahedra giving :- 8x8 = 64 triplets and 20 tetrahedra/20 amino acids

The 8 octahedra/ 64 triplet codons

Fig 11. Interlocking the Two 3rd Order Level Tetrahedra

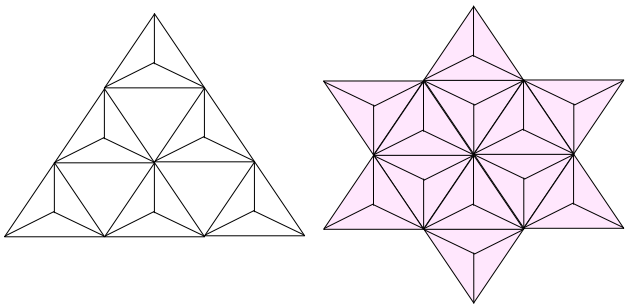


Fig 12. Packing of the 20 Tetrahedra within the Star Tetrahedron

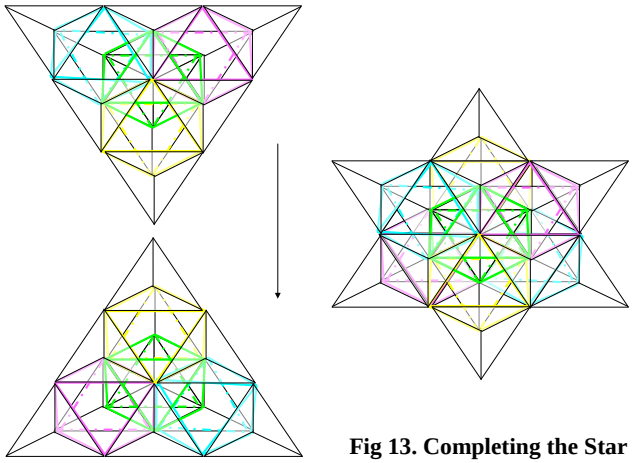


Fig 13. Completing the Star in full 3D

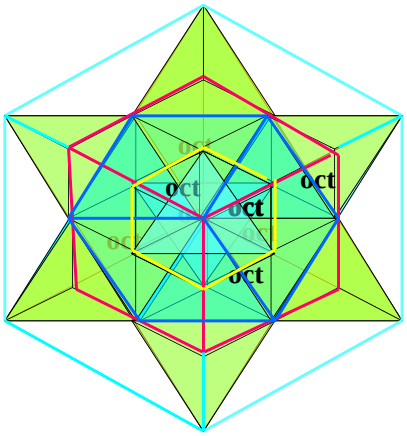


Fig 14. Cube Reiteration

The direct connection 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 and 4 bases (orders 2 and 4), to a base pairing (order 8) and a pairing bonding in strand formation (order 16), before ending at single-strand RNA / DNA (order 32) and double-strand DNA (order 64):

order 2	$(1, -1)$	$0 \times$ 3-D
order 4	$(1, -1) \times (1, \boldsymbol{i}_1)$	$0.5 \times$ 3-D
order 8	$(1, -1) \times (1, \boldsymbol{i}_1) \times (1, \boldsymbol{j}_1)$	3-D
order 16	$(1, -1) \times (1, \boldsymbol{i}_1) \times (1, \boldsymbol{j}_1) \times (1, \boldsymbol{i}_2)$	$1.5 \times$ 3-D
order 32	$(1, -1) \times (1, \boldsymbol{i}_1) \times (1, \boldsymbol{j}_1) \times (1, \boldsymbol{i}_2) \times (1, \boldsymbol{j}_2)$	$2 \times$ 3-D
order 64	$(1, -1) \times (1, \boldsymbol{i}_1) \times (1, \boldsymbol{j}_1) \times (1, \boldsymbol{i}_2) \times (1, \boldsymbol{j}_2) \times (1, \boldsymbol{i}_3)$	$2.5 \times$ 3-D

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 $0.5 \times$ 3-D. The cube reiteration in Figure 19.14 shows the exact parallel between the $1.5 \times$ 3-D and $2.5 \times$ 3-D structures when one complete 3-D system is mapped exactly onto another. Pentad 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 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 Illert's set of moving biological coordinates, 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.

In a sense, all our perceptions require the connection between the isolated part and the whole but, through the nilpotent algebra and the universal rewrite system, we know that this is a zeroing. We can picture this in any 3-D structure as the point at which the new shape is realised at any stage in the process – the fixed point – with the moving 3-D system giving us the new point of becoming. The point of preception is the point at which these coincide and at that point we observe only one 3-D. But the fact that we will then go onto a new perception is what justifies us using two lots of 3-D. Our perceptions, however, simply mirror the structure which is inherent in all natural systems. They operate, like everything else in the universe, according to Nature's code.

The task now is to assign the correct placement of the triplets to give the appropriate amino acid represented by each tetrahedron. Figure 19.15 shows the beginnings of this procedure.

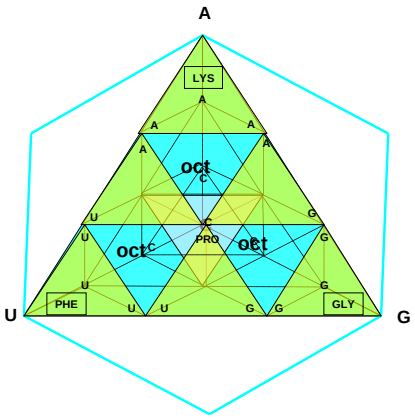


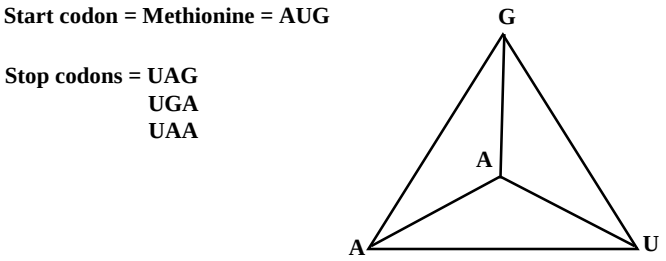
Fig 15. Beginnings of Placement of the Triplets and Amino Acids

Here, the corner tetrahedra can be nominated as the amino acid that relates to the triplet codon mirrored from the triangular face of an octahedron, e.g.

UUU = phenylalanine (PHE)	GGG = glycine (GLY)
AAA = lysine (LYS)	CCC = proline (PRO)

The predominant start codon AUG, that codes for the amino acid methionine and the three common stop codons (UAG, UGA and UAA) which do not

translate into any amino acids, can now all be defined by one tetrahedron as shown in Fig. 19.16. If we consider that each face rests upon that of an octahedral 'codon' face then this tetrahedron is likely to be the one in the very centre of the third order level tetrahedron which is completely surrounded by octahedra.



All 4 triplets can be defined by one tetrahedron -
perhaps the one in the very middle of the 3rd order tetrahedron.

Fig 16. The Start and Stop Codons

19.14 Pentagonal symmetry within DNA

In the previous section we have been mainly concerned with the 3 Platonic solids of 4-fold symmetry and all these can be defined by constructing a cube with a saltire cross (X) drawn across each cuboidal face as shown in Figure 19.17a. Five-fold symmetry is brought in by the icosahedron and its reciprocal the dodecahedron and hence the golden section proportion Phi ($\Phi = 1.618$) comes into play.

Nature expresses herself using the golden section: Phi and 5 now becomes important. Humans find beauty in both hearing and seeing this relationship and for this reason Phi was used in sacred wall paintings in ancient Egypt and vigorously applied in Renaissance art. The first 3 Platonic solids do not reveal this relationship but the icosahedron and dodecahedron do. Whereas the octahedron is transected by 3 squares the icosahedron has 3 golden rectangles in each of the 3 planes and the dodecahedron interestingly reveals another level of

order in that in reality this shape is constructed of 5 interlocking cubes. The icosahedron is often used by viruses and bacteriophages as it gives the greatest volume with stability, e.g. the polio virus, hepatitis A virus and T phages. Phi is very prevalent within Nature and numerous examples of its use exist, but the plant that displays this proportion in every way possible is the sunflower.

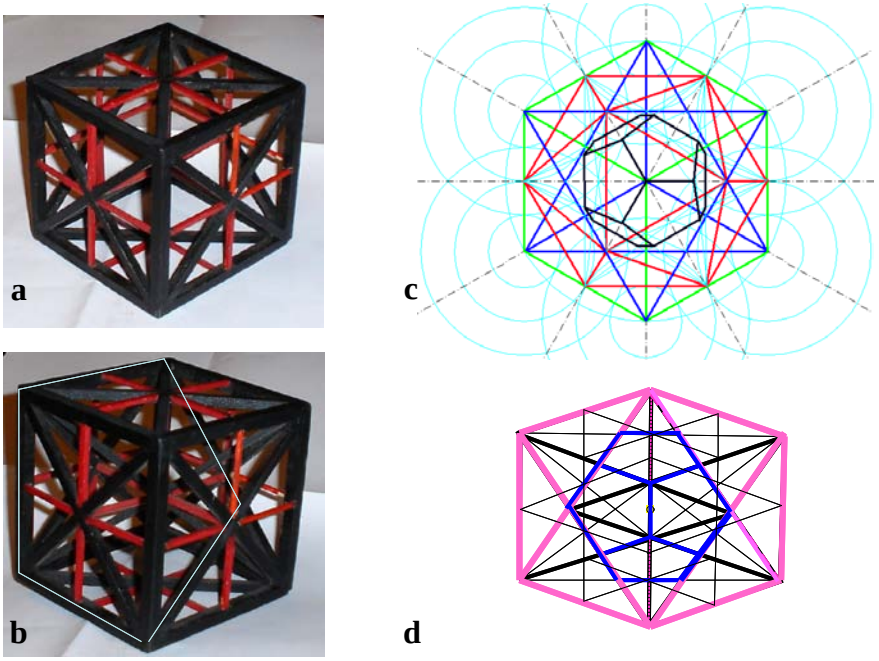


Fig 17. The Cube : Introducing Phi by Perspective Change.

Phi can be seen within our cube by drawing the second set of cross (+) lines on each cuboidal face and allowing a change in the cube's orientation such that the front corner appears to sit over a newly constructed cross point of two lines as shown in Fig. 19.17b. This can be difficult to visualise but Fig. 19.17c is a 2-D representation of the cube in the first orientation and Fig. 19.17d and Fig. 19.18 shows the 2-D outline of the cube in the second perspective. The latter now also gives a 2-D outline of the icosahedron using exactly the same outline of this new perspective of the cube.

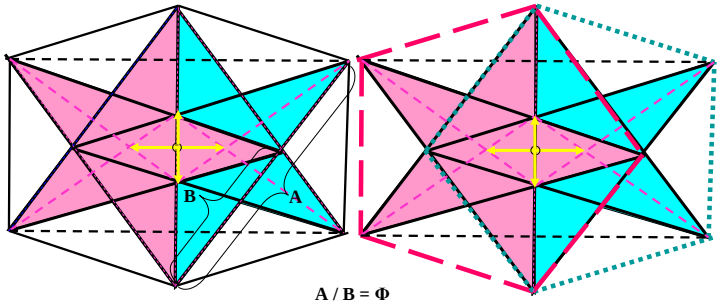


Fig 18. Perspective 2 : Showing Pentagons Within the Cube Polarity is Introduced and Φ

This change in cuboidal perspective appears to introduce polarity where the central point of the first perspective now opens up from a single point and expands north-south and east-west into a plane. Two overlapping pentagons with inscribed 5 pointed stars can now be defined (Fig. 19.18). This whole figure is governed by Phi and this image is also a correct 2-D, 'see-through' image of an icosahedron with its reciprocal dodecahedron inside (Fig. 19.19).

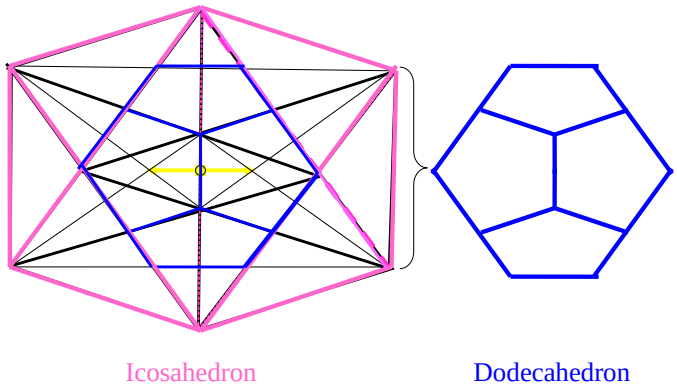


Fig 19. Icosahedron with Internal Reciprocal Dodecahedron

Within the algebra of symmetry breaking there is the reduction from the 8 to the 5-fold symmetry which we can represent by packing 5 tetrahedra into a disk (Fig. 20). There is a discrepancy here of 7º 21´, but this may also have relevance

as will be described later on. The structure revealed in Figure 19.20 can also be generated by a projection onto 3-space of the self-dual pentatope, which is the 4-dimensional analogue of the tetrahedron. The pentatope, with 5 vertices, 10 edges and 10 faces, is the simplest regular figure in 4-D.[12] The connection may well be an expression of the fact that space, though fundamentally 3-dimensional, is part of a larger structure of nested 3-dimensionalities, which, in the universal rewrite system, is created after the scalar mass, pseudoscalar time, and 3-D conserved quaternion charge; and some of the profoundest insights into physical space's 3-D structure may come from the properties of the larger structure within which it is embedded. In this sense, physical space can only exist as the 3-D spatial projection of the higher dimensionality incorporated in the nilpotent structure, but, in view of the fact that the 'fifth' dimension of the nilpotent structure (the proper time) is an invariant, and therefore essentially redundant, it is significant that the regular Platonic-type figures reach their maximal extent (6) in 4-D; at higher dimensionalities they reduce to 3. The manifestation of the extra dimensionality in biology may then be related to a chaotic variation with respect to time.

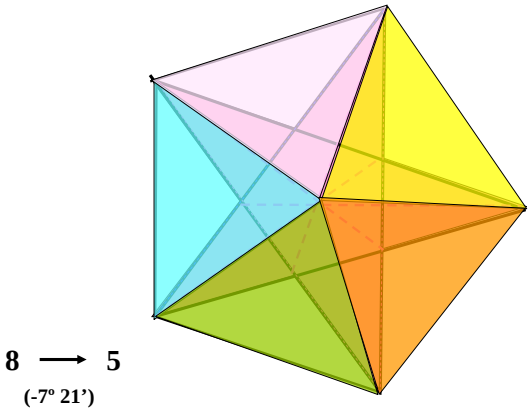
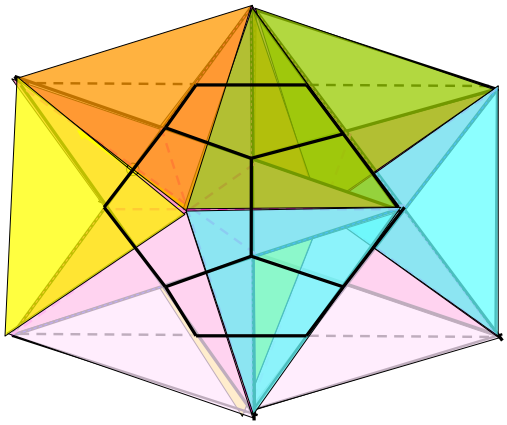


Fig 20. Breaking Symmetry: 5 Tetrahedrons Make One Pentagonal Disk



2 Pentagonal discs overlaid to produce an icosahedron (2D) plus internal dodecahedron.

Fig 21. Icosahedron Plus Reciprocal Dodecahedron Inside

If we now overlay two pentagonal disks a 3-D representation of the icosahedron can again be visualised in 2-D as shown in Fig. 19.21. Here the reciprocal internal dodecahedron has been highlighted which, as we shall see, has certain interesting consequences.

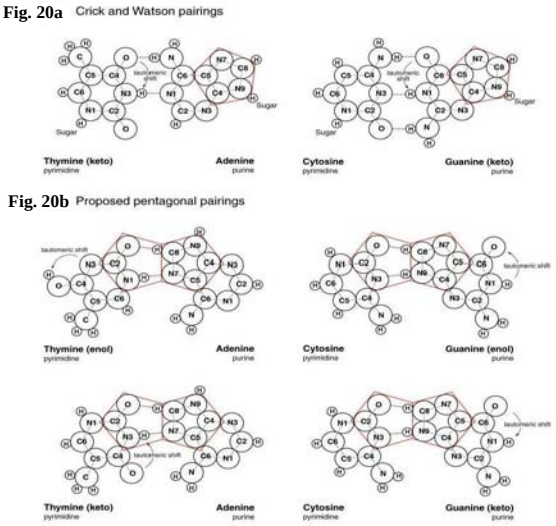


Fig 22. Nucleotide Pairing Within DNA.

Fig 20a.Watson and Crick pairings; Fig 20b.Curtis pairings (without placement of ribose sugar groups)

The Watson and Crick model for DNA structure[13] is well known but in May 1998 a second possible model was proposed by the artist Mark Curtis who designed one of the stamps for the millennium.[14] Curtis wanted an in depth understanding of this structure and believed that something was amiss when he attempted to build models according to the Watson and Crick theory.

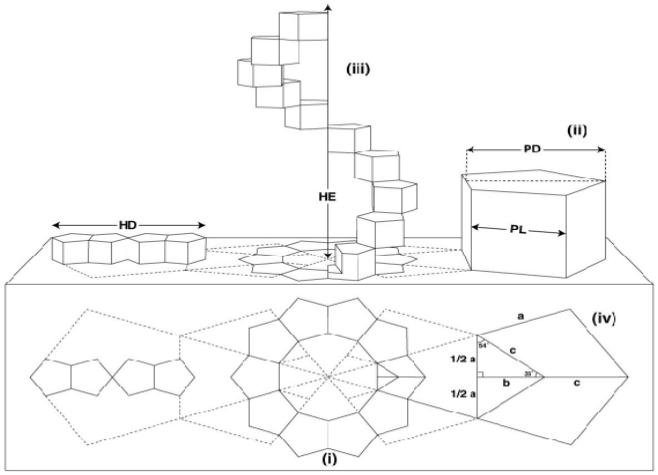


Fig 23. Curtis DNA model 1998.

After studying the original X-ray crystallography data and conferring with a chemist, it became apparent that there may be a different way to pair the nucleotides within the double stranded DNA that would give the same data. Hoogsteen[15] also proposed different base pairings which have subsequently been implicated to be involved in base pairing within tRNA and triple DNA helices. The Curtis model allows for the inclusion of both possible forms of the dNTPs (or units of base, sugar and phosphate) namely the keto and enol molecular forms of thymine and guanine whereas the Watson and Crick model only allowed for one, the keto form (Fig. 19.22a). However, the Curtis model does not indicate where the ribose plus phosphate group that makes up the backbone of the helix but like Hoogsteen pairings there may be examples within nature for these pairings (Fig. 19.22b). Fig. 19.23 shows Curtis's resultant helix as a stack of 10 pentagonal blocks representing the 10 nucleotides predicted by the X-ray crystallography data and below a view looking down the spiral of a ring of 10 pentagonal blocks / nucleotides. The stamp design Curtis finally produced was

available to the public in 1998.

It can be seen that by overlaying the icosahedral 2-D outlines or the pentagonal disks over Curtis's drawings of the paired nucleotides, two of the pentagonal faces of the internal dodecahedron align with these paired nucleotides (Fig. 19.24). If we continue this procedure further we build the same ring of pentagons displayed by Curtis for viewing the double stranded DNA spiral head on (Fig. 19.25). The pentagons of the inner dodecahedron in Fig. 19.25 have been highlighted with pentangles and can be seen to match the Curtis's ring which he represented by pentagonal blocks.

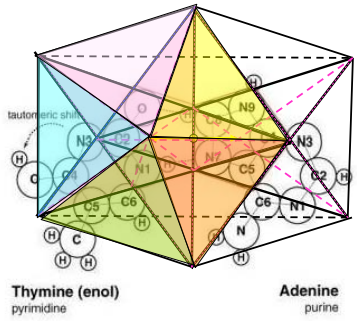


Fig 25. Enlargement of Curtis DNA Pairings Overlaid with Cube (perspective 2) and Pentagonal Disk.

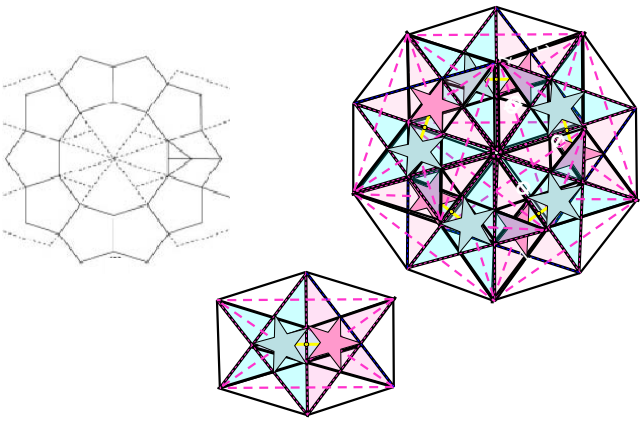


Fig 26. Adding the Icosahedra with Internal Dodecahedron To the Curtis Model.

We can of course overlay single pentagonal disks (of 5 tetrahedra) to give the same result (Fig. 19.26). It is interesting to note that one pentagonal disk now contains 3 nucleotides of one strand of DNA. This could represent an analogy to the triplet codons of 3 nucleotides that are then translated into one amino acid protein building block when 'in frame', i.e. the information of the 3 is contained within the pentagonal disk of 5 tetrahedra. This is reminiscent of the algebra where the 8 is resolved into 5 when the 3 is 'overlaid onto 5', i.e.:

time	space	mass	charge
pseudoscalar	vector	scalar	quaternion
i	**i j k**	1	***i j k***

being reduced from eight simple to five combined or composite units, i.e.:

ik **ii ji ki** 1***j***

Considering the original eight, the octahedron would serve as a good candidate for this analogy or the 2 × 4 corner tetrahedra within the second order star tetrahedron. The octahedron is also the reciprocal of the cube which is here the 2-D outline of our icosahedron.

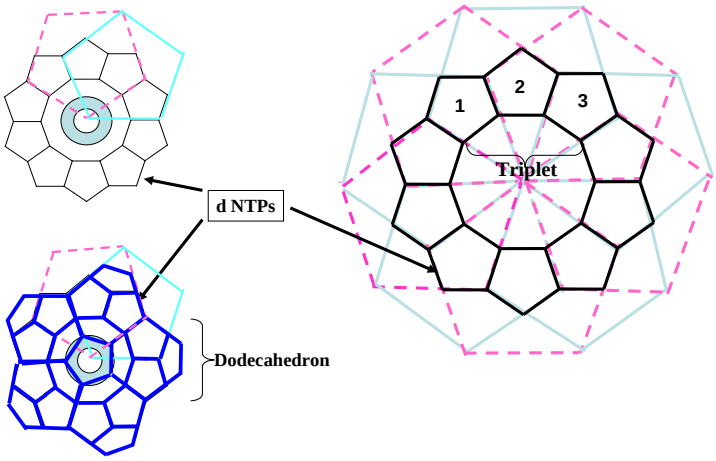
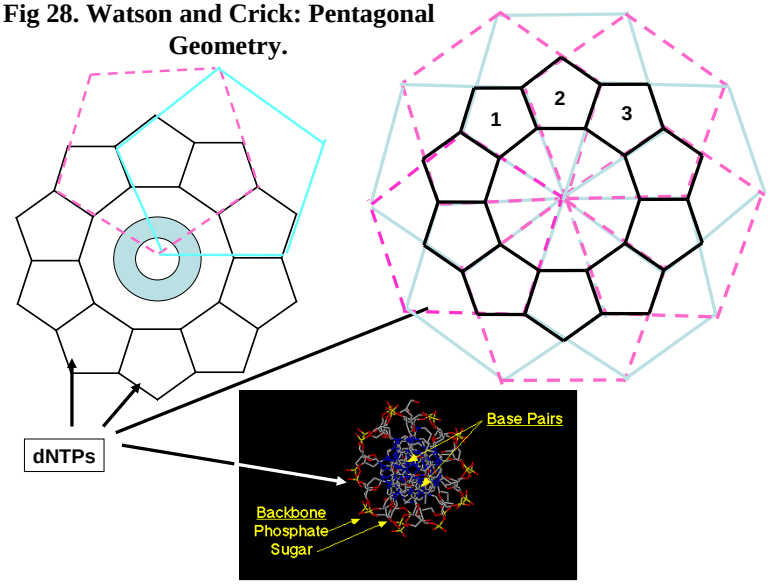


Fig 27. Highlighting The Nucleotides –One Triplet per Pentagon

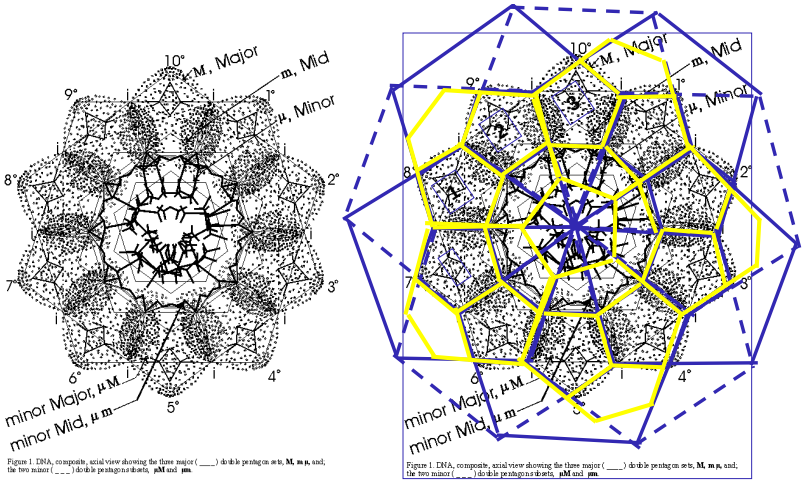
When this pentagonal scheme is applied to the Watson and Crick model of

DNA we find that it also fits well as shown in Fig. 19.27. The insert shows a stick model of the helix looking down the top of the spiral and it can be seen that it is the pentose sugar rings of the dNTPs that now relate to the pentagonal faces of the internal dodecahedra.

Fig 28. Watson and Crick: Pentagonal Geometry.



A computer generated scattergraph of DNA generated by Robert Langridge was analysed by Reginald Brookes[16] who suggested a different pentagonal geometry composed of concentric double pentagons as shown in Fig. 19.28 but our proposed geometry also fits well upon this scattergraph (Fig. 19.28). Again, the scattergraph shows a remarkable similarity to a 3-D projection of a regular solid in 4-D. This time it is the 120-cell or hyperdodecahedron,[17] and again this seems to make sense with relation to the higher dimensionality when the rewrite structure's most fundamental unit – incorporating a time-varying, even chaotic, sequence, which is not present in more ordered structures, such as those of inorganic crystalline materials – is projected onto a 3-dimensionality. Significantly, the dodecahedron and icosahedron, with their pentagonal symmetries, are represented only in 3-D and 4-D – other dimensionalities only have cubes, tetrahedra and octahedra as Platonic solids.

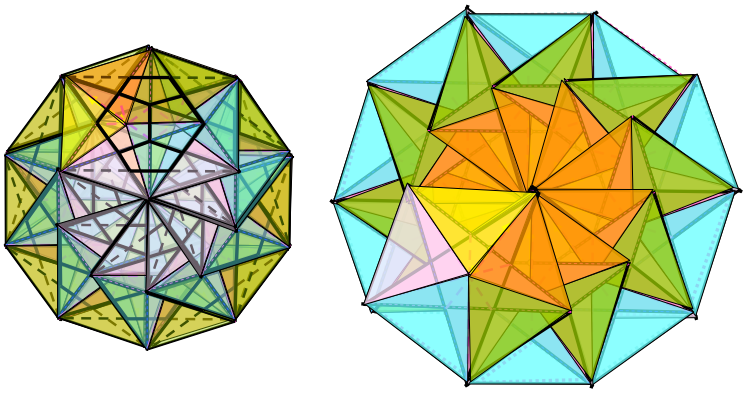


A. R.Brookes pentagonal geometry overlaid upon R.Langridge's scattergraph of DNA

B. New pentagonal geometry overlaid upon R.Langridge's scattergraph of DNA

Fig 29. Computer Generated Scattergraph of DNA: Pentagonal Geometry

The stacking of the pentagonal disks defining the DNA helix is shown in Figs. 19.29 and 19.30. Figs. 19.29 and 19.30 are pictures of models of these diagrams made from tetrahedral dice. The model building process clarifies that 2 spirals of 5 stacked pentagonal disks carry the 10 nucleotides and that 2 strands of these fit together to produce the double stranded helix. It is interesting to note that there is a groove running around the molecule that implies space for a third strand of disks – could this be for the RNA or the stabilising water molecules? Double stranded DNA is known to unzip to allow a copy of RNA to be made which is then sent elsewhere to be translated into proteins. After the RNA copy has been completed it needs to unzip itself to release the RNA and the DNA strands are then rezipped together. Perhaps the missing 7º 21´ causes the necessary instability for this zip / unzip process by giving a spring effect and fulfils the *zitterbewegung* effect that we see in physics.

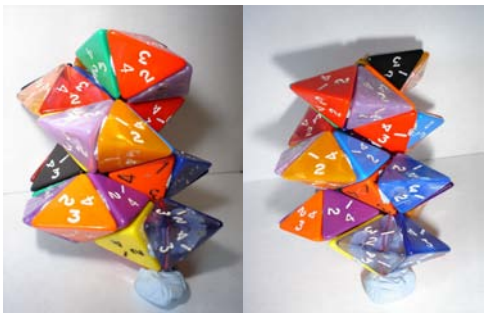


A. Overlaying icosahedra plus reciprocal dodecahedra

B. Overlaying pentagonal disks

Fig 30. The DNA Helix Defined by Stacked Pentagonal Discs.

Single Stranded DNA:
Two Spiral Strands of Pentagonal Disks : 5 per Turn



Double Stranded DNA:
2 Spiral Strands of Pentagonal Disks with a Total of 10 Disks per Turn.

Fig 31. 3D models of DNA with Pentagonal Disks of Tetrahedra

The need for 2 × 5 dNTPs for every twist of DNA is interesting. Each twist of a single strand contains 1 codon and 2 other dNTPs (cf 1 × 3-D + 2 others in the nilpotent). You can only guarantee a codon if there are 5 dNTPs. Now, if we start with a codon in the twist, it takes 3 sets of 5 dNTPs, i.e. 3 twists, to complete a 'cycle' and start with a codon again. Here, we may think of the Fibonacci series in the way that Johansen does. Also, the twisting in DNA is continuous – it doesn't begin and end anywhere – which is reflected in the fact that the coded part of the sequence is entirely coded, with no gaps.

Two further aspects of the double helix may be mentioned here, in connection with its appearance in both biological and physical contexts. One is the first observation of the structure on the large scale (80 light years = 7.6×10^{17} m) in the nebula near the centre of the Milky Way, already referred to. The other is the phenomenon of spectrin repeats, found in several proteins involved in cytoskeletal structure, for example, spectrin, alpha-actinin and dystrophin. These repeats create a triple helical bundle, which we may liken to the DNA / RNA connection or to vacuum process of fermion becoming virtual boson and then virtual fermion again; or the real process by which all fermionic states absorb and emit gauge bosons (equivalent to a combination of fermion and antifermion) in all discrete interactions.

19.15 The cube and the harmonic oscillator

As previously discussed, the packing of pentagonal disks may have relevance to the spiral which is so important in both DNA and the spin of the fermion with its vacuum. However, as has been described, two disks can also be viewed in 2-D as a cube. The switching between the two perspectives of the cube (Fig. 19.17 and Fig. 19.31a, b) is interesting in that it can also be considered as a harmonic oscillator (Fig. 19.31d). One can visualize the cube spinning and the fermion and vacuum switching places (*zitterbewegung*) when the front flips to the back and the back face then holds precedence. The cycle can then complete when the front face flips forward again. A second element this relates to is the Klein-4 group and dual group (which can be seen as relating to particle and vacuum), where the complementary colours say red and cyan, used for the group / dual group, point to opposite corners of the cube and could be considered as switching. Rotation of the cube would, of course, produce the same effect.

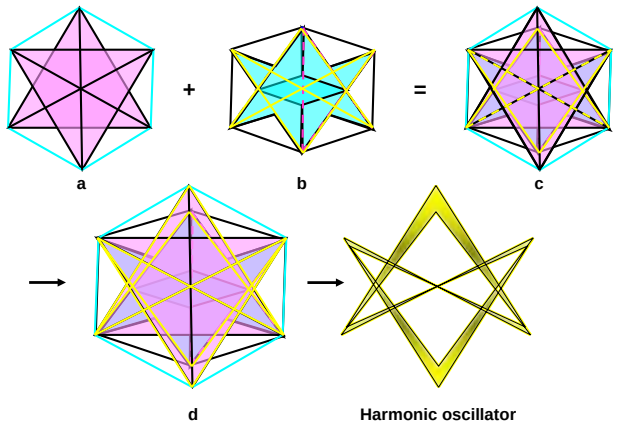


Fig 33. The Spinning Cube as The Harmonic Oscillator

Extending the dimensions, a 4-D cube with an internal star tetrahedron in rotation can be seen creating and annihilating two discs of five tetrahedra as if it were going through a phase-switching transition, exactly as in *zitterbewegung*, the fourth dimension being identified with ± *t*, ± *E* and ± *w*, and being the 'vacuum space' in which the real 3-D structures are created.[18]

A particular example of a cubical symmetry with a nilpotent physical, but not yet a biological, application (though it is likely that one is ready to be found), is provided by the Rubik cube structure, which is a regular cube, divided into 27 smaller cubes or cubelets, with each face of the large cube divided into 9 cubelet faces. The 54 cubelet faces are divided equally between 6 colours (or 3 colours and 3 anticolours), so that there are 9 of each colour, and each of the cubelets has the same relative ordering of colours on its faces. The structure, however, can be rotated internally, so that any colour shows on any of the cubelet faces of the larger cube. Corner cubelets have been viewed as giving the correct ± 1/3, ± 2/3 twists corresponding to the electric charge values observed for the quark components of mesons and baryons. The 3 colours (primary) and 3 anticolours (secondary), however, could also be seen as representing the three directions of the momentum operator in the nilpotent structure when the cube is in its most organized state ($i\mathbf{k}E + \mathbf{i}\mathbf{i}p_x + \mathbf{j}m$) ($i\mathbf{k}E + \mathbf{i}\mathbf{j}p_y + \mathbf{j}m$) ($i\mathbf{k}E + \mathbf{i}\mathbf{k}p_z + \mathbf{j}m$). The six faces then represent the six possible phases, i.e. when the whole momentum $\mathbf{p} = +\mathbf{i}p_x$, $-\mathbf{i}p_x$, $+\mathbf{j}p_y$, $-\mathbf{j}p_y$, $+\mathbf{k}p_z$, $-\mathbf{k}p_z$. Anything else then represents a degree of mixing between two or more phases. When each face has 3 colours and 3 anticolours, the mixing is perfect. Of course, the quantum mechanical picture of the proton requires perfect mixing between the 6 phases ($SU(3)$ symmetry). (This would

require a 6 × 6 × 6 cube with faces containing equal numbers of each coloured cubelet.) Another way of looking at it is to rotate the perfectly organized cube (each face one colour), allowing each face to be seen by the viewer for the same amount of time. The 8 agents that produce all possible colour changes (combinations of colour and anticolour) represent the 8 gluons. There are only 8, not 9, because only 2 combinations of red / antired, green / antigreen, blue / antiblue are considered to be independent. (The standard 3 × 3 × 3 becomes relevant if we consider colour / anticolour as occupying the same cube and we consider 3 colours alone. A 4 × 4 × 4 cube would give us the convenient total of 64 cubelets.)

19.16 The rewrite process as Nature's code

If the existence of four bases reflects the basic structure of a universal rewrite system, then we would expect to find a similar set of dualities to those observed for space, time, mass and charge, and we would expect to find some natural process in which they could emerge in a relatively uncomplicated way. If the rewrite process gives us Nature's code, it is not obvious that, apart from existing at the most fundamental level, it will also reappear in similar form in particular structures higher up the natural hierarchy. Such reproductions of features of small-scale systems in larger ones, however, certainly exist in nature, and generally reflect some concept of *coherence* between the small-scale elements, organized by some powerful driving mechanism. The double helical structure and five-fold symmetry of DNA would suggest an application of 'Nature's code' by such a mechanism even if there were no other indications in the number and characteristics of the base elements, and the fact that the component structures are based on the relatively basic chemistry of only a few light elements suggests that the organizing principle is more significant to the process than the specific characteristics of the chemistry.

The nitrogenous bases found in nucleotides are, in fact, relatively simple structures, with a common feature: a heterocyclic ring derived from the parent compounds pyrimidine and purine. The ring structure is composed of both nitrogen (position 1 and 3) and carbon (positions 2, 4, 5 and 6). The pyrimidines T and C, and the purines A and G, are relatively minor variations on this pattern; and purine can be considered as a derivative of pyrimidine as it consists of a pyrimidine ring with an imidazole ring (a five-component ring, again with two nitrogen atoms) fused together. Here, we have one duality. Significantly, also,

each of the purines has a pyrimidine *partner* (which makes it 'dual', in another sense), and the bonding atoms of these complementary atoms will line up oppositely on a single strand of DNA. So, we have O-N[-OH] and N-NH[-NH] bonds linking A-T reversing the order for the same bonds used in C-G. If we want a closer analogy with the physical case, we can say that the more structured A and G might be considered to correspond to the more structured physical parameters space and charge, which each have a specific partner in time and mass. Also, the A-T partnership might be considered the 'driver' or source of variation in the same way as the nonconserved space-time partnership is in physics. Thymine certainly initiates change with its replacement by uracil in RNA, while adenine triphosphate (ATP) is the main source of energy transfer in living systems. This suggests the approximate correspondence: A / space; T / time; C / mass; G / charge.

The question remains how such bases could emerge from some natural process which is not purely random (in the sense that, though the chemical structures may emerge randomly, they will be quickly 'selected' for their relevance to the overall scheme). Very possibly, special conditions (for example, high temperature, electricity, magnetism, liquid or gaseous environment) will be required to generate the structures in the right proportions – and so the generation of 'life' is not an *inevitable* result of chemical chaos; it is an inevitable consequence only of the conditions being available for the universal rewrite mechanism to operate on a scale higher than the most fundamental as a result of the creation of some necessary condition of coherence. Given the right conditions, however, positive feedback mechanisms might be expected to take place to enhance a process that would need to evolve only once. Fossil evidence from prokaryotes, which resemble present-day bacteria but may be as much as 3.3 billion years old, suggest that the genetic code developed at a single time at a relatively early date in the Earth's history. There was no multiple evolution.

Proteins are, of course, the essential basis of life, and include a number of enzymes which play a significant role in the transfer of genetic information; but proteins are made of twenty amino acids, selected only from those that follow the coded sequence presented by the four bases in DNA, and there is no other driving mechanism to link them in the seemingly random polypeptide chains, with their multiplicity of folded shapes. Though amino acids are relatively simple chemicals, which are easy to reproduce from basic elements under extreme conditions, there is no mechanism for linking them in protein structures which would then develop a coding system to reproduce them. It is virtually impossible

to believe that the more complicated system logically preceded the simpler one, though one could see DNA, RNA and protein structures evolving together through a process in which the evolution of one aided and was aided by the evolution of the others. There are some arguments for believing that RNA preceded DNA, but DNA, with its double helix, is much the more stable structure, and it is certainly difficult to believe that the bases A / T and C / G should form their pairings by accident, rather than as part of the molecule's original design. Although tRNAs also form double stranded conformations they involve the inclusion of over 30 rare bases, with up to 10% of the total number of bases. It is apparent from this, that these are more complicated molecules than DNA. An argument for the temporal precedence of RNA would have to conclude that the extra bases were discarded when the more 'perfect' base pairings of A, T, C and G made the creation of DNA possible.

The structure of the bases as variations on a single basic design almost suggests a modification process to produce the appropriate levels of 'duality', and the creation of DNA through a combination of single types of the elements with each of the valences 1 to 5 (namely, H, O, N, C, P, three of which are gaseous in the free state) suggests something like a minimalist approach. Carbon is, of course, the only basis for creating the molecules that we call 'organic', because its valence 4 gives it the perfect bonding for coherently structured large molecules; and the hexagonal benzene ring is one of the most stable (though dynamic), simple organic structures, easily formed.[19] The most efficient way of driving an evolving process involving small atoms or molecules to break the sterile uniformity produced by the benzene ring itself might be through interaction with a gaseous atmosphere or gas molecules dissolved in liquids (a kind of biochemical equivalent of the physical 'vacuum'); and, from the point of view of stability, bonding, and the kind of 'closure' produced by the base pairing, the two valence 3 nitrogen substitutions found on the rings in each of the bases would seem to provide definite advantages.

The significant role of ATP then suggests the potential importance of the combination of bases and triphosphate as a precursor of DNA. The pentavalence of the phosphorus atoms provides significant opportunities for bigger linkages. Here, we have to imagine the driving process as creating helical structure via a harmonic oscillator mechanism. To create an extended helical structure we need pentagonal symmetry. To create pentagonal symmetry, we need a combination of the two hexagonal structures produced by the A-T and C-G linkages (the hexagonal structure being a double tetrahedron in 2-D), and a pentose sugar

(another small 5 ring structure with a gaseous element substitution) interposing between the base and the phosphate. Significantly, proteins, deriving from DNA coding, show elements of helical structure, but much more disrupted than that of DNA itself.

19.17 The unification of physics and biology

We have explored several significant examples in which the mathematics of physics and biology seem to show similar underlying structures relating to more fundamental processes, and to the idea of 'process' itself (Fig. 19.32). In addition to this, we have shown that complexity arises from simplicity in all aspects of nature because the fundamental units of nature (fermions) are symmetrical only when taken in conjunction with the rest of the universe (vacuum). All types of aggregation in matter, at all levels, physical chemical, biological, and all phase transitions, are concerned with an attempt to overcome this asymmetry. The force involved in this process is the weak force (the fifth or asymmetric term) and it is ultimately through this force that we will find a deep link between physics and biology.

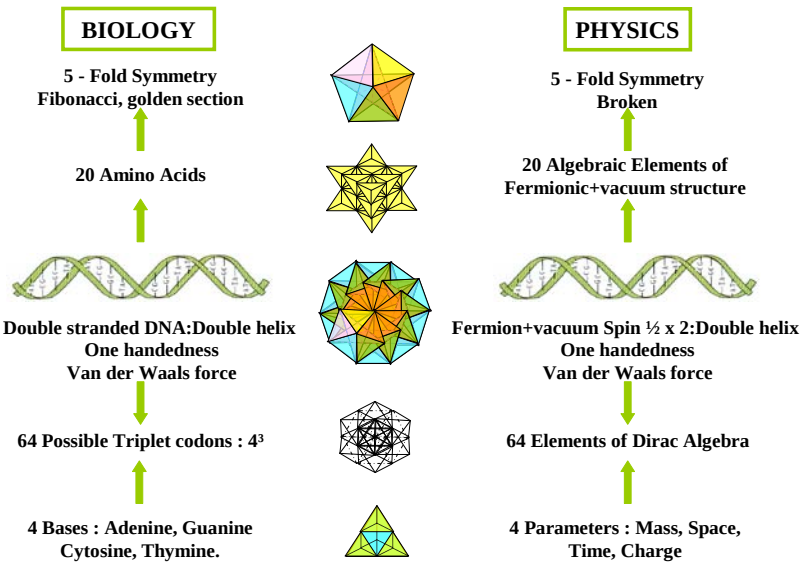


Fig 34. THE UNIVERSAL RE-WRITE SYSTEM
UNIFICATION OF PHYSICS AND BIOLOGY