The APL Theory of Human Vision

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Abstract

Vision is considered as a mechanism which deals with information processing by a living organism. The conjunction of several hypotheses led to a single theoretical model of quasi-automatic integration of information which processes compression and orthogonal transforming, without involving any classical calculation; the model, which was worked out completely with *APL* as the main research tool, will be exposed in *APL* also. It is based on special properties of matrices in modulo-2 integer algebra; the paper covers : considerations on information coding, explanations about the role of patterns formed by retina receptors, about the architecture of these receptors, (cylindrical rods "the shapes which see shapes"), about the behaviour of the electrons within the main information-processing molecule (retinal) and about the transmission of information in synapses as an annex.

0.0 Introduction

Although it will be difficult to verify a model in vivo, several simple remarks plead in favour of some plausibility :

a) perception and information transforming are processed by molecules (inter alia pigments such as rhodopsine the "processor" of which is retinene); so, vision, as a chemical-electrical process would involve many electron jumps; in fact, the whole of chemistry is a science of dynamical electronic binding and unbinding in which electronic states are - always - discrete states;

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b) the most efficient man-made information processors we know work with 0s and 1s; in fact, we are unable to process information efficiently with analogic devices : what we call "numeric" could also be named "binary";

c) Christian Huygens, the main founder of optics, already wrote in his "Traité de la Lumière", Paris, 1678 :

> "We only perceive differences."

d) reading and vision are coupled : we see, read - and understand - at the same time; **how** ?

0.1 A proof coming from darkness

A good way of studying how we can read (then the vision process at the same time), is to try to replace vision by "something else" which would allow people to read, nevertheless, in the absence of eyes : such a challenge was solved in an elegant manner more than 160 years ago (before Boole's algebra was known) by a blind man - aged 16 : Louis Braille, who had no notion either of advanced mathematics or of information theories; (we now may say that the the braille code is apparently connected to the structure of DNA, the code of our genetic patrimony, see the section devoted to the location of information in DNA).

What is the relation between vision, reading and *APL* ?

Sceneries we discover are scanned by our eyes; so are the lines of this text, from left to right, in English, but from right to left after translation into Arabic, Hebrew or *APL*; the direction of reading for hieroglyphs was the one of the animals' look in the ideograms (both ways were allowed). *APL* is a unique notation, among the ISO-standardised programming languages : it offers the "scan operator" (introduced with IBM's APL-SV, more than 15 years ago).

The following ISO-*APL* expression displays 10 binary 2-by-2 matrices, the heart of the braille code :

```
(40⍴2 0 1 0)⍕⍉(20⍴2)⊤719845 136955
 10 10 11 11 10 11 11 10 01 01
 00 10 00 01 01 10 11 11 10 11
```

Braille codes are 3D raised dots for 1s, and "nothings" for 0s. A third row of "nothings" completes the 2×2 matrices as 3×2 ones which code the first 10 letters of the Roman-French-English-ASCII alphabet. A space character between words, is a wide 3×2 or 3×3 matrix of "nothings", a space matrix. The correct interpretation of 0 is "zero" i.e. nothing, while 1 means "everything which is not nothing". Braille's 0s and 1s are not the logical "False" and "True" of logic, but integers 0 and 1 of MODULO-2 integer algebra, (in mathematics the one of **Z/2Z**).

Since the ten subsequent braille-codes in the alphabet reproduce the 10 first ones, with, this time, a third row below with a left dot raised, while the remaining useful letters were obtained raising both dots in the same 3rd row, "APL" would be spelled (there was no case-dependency in the original code which contained no "w", unused in French by that time, appended later for Dutch, German and English, as the last, fortunately still-free position), in correspondence with the following coherent display :

```
10 10 11 11 10 11 11 10 01 01
00 10 00 01 01 10 11 11 10 11
00 00 00 00 00 00 00 00 00 00
a  b  c  d  e  f  g  h  i  j

10 10 11 11 10 11 11 10 01 01
00 10 00 01 01 10 11 11 10 11
10 10 10 10 10 10 10 10 10 10
k  l  m  n  o  p  q  r  s  t

00 10 11 11 10 11 11 10 01 01
00 01 00 01 01 10 11 11 10 11
11 11 11 11 11 11 11 11 11 11
u  v  x  y  z  ç  é  à  è  ù

00 10 11 11 10 11 11 10 01 01
00 01 00 01 01 10 11 11 10 11
01 01 01 01 01 01 01 01 01 01
â  ê  î  ô  û  ë  ï  ü  œ  w
```

```
A   P   L
⊛   ⊛⊛  ⊛
    ⊛   ⊛
    ⊛   ⊛
```

An invisible third column of 0s fills the matrices as if they had a square 3×3 shape : there is no ambiguity at all, for a hump always appears in the first two rows of the leftmost column.

Nowadays, a 4th row may be added for cases (Shift, Ctrl, Alt keys), when blind people use specially-equipped PCs.

The finger, scanning, with its sensitive fingertip, the modulo-2 integer 3D matrix, from left to right, in parallel, along the three horizontal rows, perceives the relative differences in "altitude" of the humps (figured here as ⊛ characters), as a triple sequence of modulo-2 amplitudes or intensities (both are the <u>same</u> parameter, because 0 squared is 0, while 1 squared is 1 : non-linearities of number theory completely <u>vanish</u> in the marvelous modulo-2 integer algebra).

The iterative question states : "Does the current item differ, in level (EITHER raised OR unraised) from the preceding one ?" Relative information is <u>integrated</u> i.e. understood - in fact at the same speed as what WE are able to do when we read regular printed text, clearly by modulo-2 -integration (in *APL* 2|+\ω or 2|-\ω expressions which, when data are considered in the isomorphous binary algebra, indeed correspond to idiom ≠\ω). The braille code shows us the *intelligence* of ≠\ at work, directly under our eyes : What a pleasant paradox coming from absolute night, explained with *APL* more than 160 years after Braille's invention, proving that the mechanisms of vision (understanding and feeling as well) do not depend on the sense being active : touch *APL*, then understand and read-&-write better !

1.0 The retina-structure proof (<u>a</u>: Retina itself)

Our retina is arranged as a pattern which can be easily described in *APL*, though the necessary data structures do not exist. Cells - or, rather rods (cylinders which "see" the shapes, active at night especially) and cones (structures which "see" the colours, with three different maximum windows in the solar frequency spectrum) form a quasi-hexagonal pattern, i.e. what you obtain if you try to draw or plot, in a plane, as many tangent circles with the same radius as you can : such a hexagonal pattern (a regular hexagon contains 6 equal-sided triangles - cf. ref. **[LanS]** about von Koch's snowflake and the use of ≠\ in the construction of natural shapes with both symmetries and asymmetries) has, approximately, the following look (with, again, *APL* ⊛ symbols) :

```
⊛ ⊛ ⊛ ⊛ ⊛ ⊛ ⊛ ⊛ ⊛ ⊛ ⊛ ⊛          ⊛ ⊛
 ⊛ ⊛ ⊛ ⊛ ⊛ ⊛ ⊛ ⊛ ⊛ ⊛ ⊛          ⊛ ⊛ ⊛
  ⊛ ⊛ ⊛ ⊛ ⊛ ⊛ ⊛ ⊛ ⊛ ⊛            ⊛ ⊛
```

A natural hypothesis was the following : If light receptors ara assembled - even not as a perfect tiling, - so as to receive INFORMATION from the outer world, as *<u>hexagonal</u>* arrays, such arrays, containing information, SHOULD exhibit, as data structures, very interesting yet-unknown properties. So, it was decided to study such data structures, and to find, if any were possible, the connections with the ≠\ idiom again.

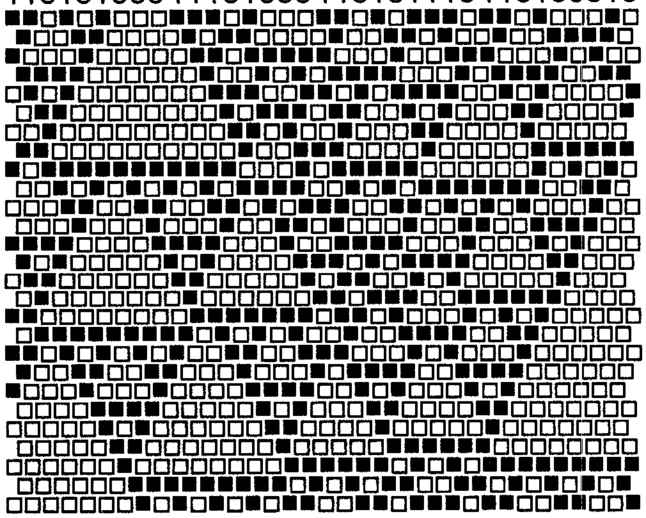
The result came immediately just like a mathematical bomb : the application of ≠\ to the elementary couple of opposed parities 1 0 produces 1 1; then, ≠\1 1 reproduces 1 0, so that the matrix of the only possible states for the smallest modulator one could imagine :

```
1 1  was isomorphous with both  ↑ ↑  and   XX
1 0                             ↑ ↓        XY
```

respectively the ***spin*** matrix (Pauli) and the ***sex*** matrix.

Fig. 1 A ternary network of neurobits

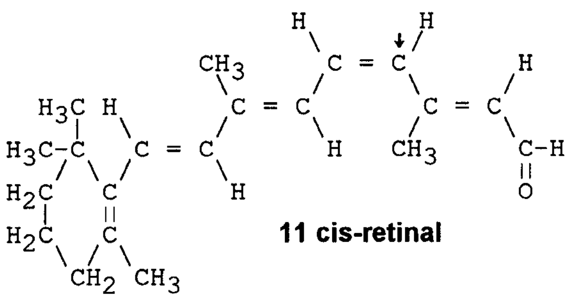
110101000111010001101011101110100010



00000001 01010101 1001101110110011001

Fig. 2 The basic chemistry of vision

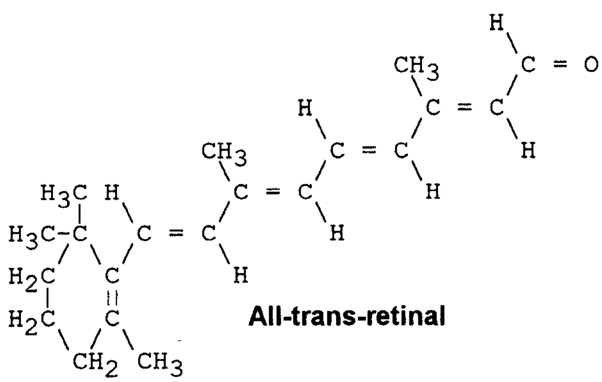
(a) the organic molecular computer at rest



11 cis-retinal

The small down-arrow ↓ points to the carbon atom (number 11) around which the carbon chain jumps when a photon activates the sleeping computer : symmetry changes from *cis* (bending on the same size) to *trans* (maximum linear extension) :

(b) the same computer, in extension, ready to operate



All-trans-retinal

Now, the symmetry of bonds is **ternary** around each node (carbon atom) in the chain of the pigment.

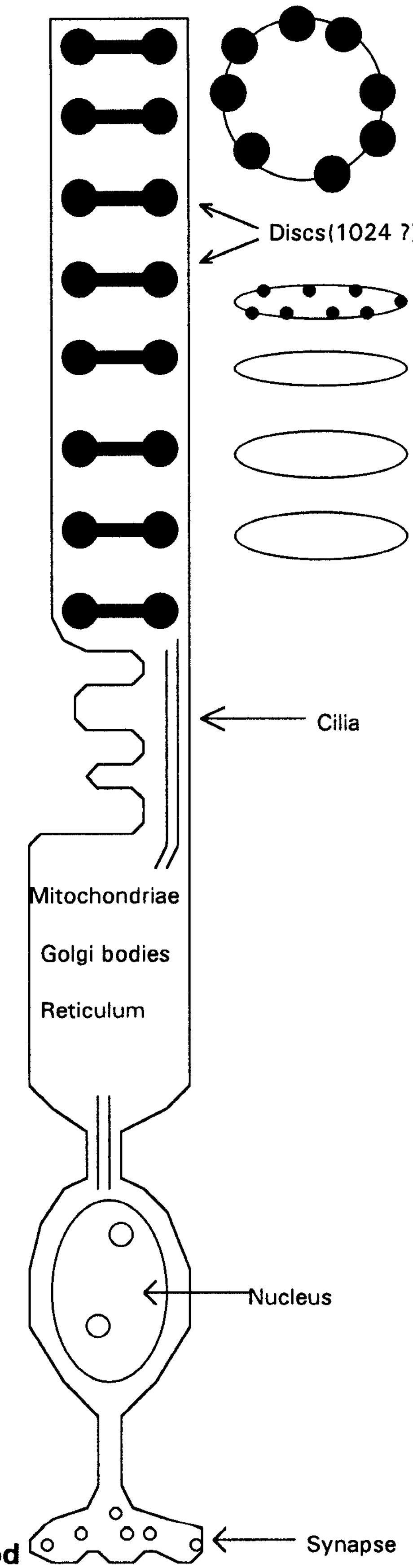


Fig. 3 A rod

And the same matrix, which corresponds to the 5th letter ("f" in the braille code), when squared modulo 2, is the 10th braille matrix ("j"). When cubed modulo 2, both these matrices givee the unit matrix (letter "e", the most frequent one, the pivot of French and English languages). In recent papers, matrices $\begin{matrix}1&1\\1&0\end{matrix}$ and $\begin{matrix}0&1\\1&1\end{matrix}$, as modulo-2 matrix inverses and squares of one another, which form a couple of conjugate complex cubic roots of 1, were named *biternions*, because they are made of **bits**, and are the **two** reciprocal operators of the **tern**ary symmetry of our *spacetime*. The modulo-2 sum of these matrices and of the unit matrix, is, like the sum of the N N^{th} roots of 1 in the complex plane (**j**, $\mathbf{j}^2$ and 1 in this case), a null matrix. Their modulo-2 determinant is 1. For the first time, we have an exact representation in a computer of the main constant of Nature, with only 4 bits, while the conventional Eulerian formulation of **j** as $e^{2\pi i \div 3}$ led to waste 128 bits in double-precision floating-point arithmetics, in *APL* as well as in FORTRAN, for an approximate representation, since the imaginary part is irrational. More details are available in ref. [**Lan**B], as well as a generalisation to a dense and exact representation of hypercomplex constants... just in bits, with no transcendental or other classical *musts* of number theory...

Ternary data structures in bits have indeed very special properties as far as information processing by cooperative "intelligent" structures may be concerned, as the *neurobit-network* of **Fig. 1** in the preceding page shows it :

In such an image - just a portion of an infinite plane of such neurobits - every pixel ("pel" in IBM terminology) which contains either a black square (1) or a light one (0), everywhere in the plane, is the finite difference in absolute value (or the finite sum modulo-2), of both pixels below, on the left and on the right. So, the first row is the equivalent of a derivative of the second row, a discrete derivative at the *quantum* level of information, the bit; so, the second row is the discrete integral of the first row (then, in *APL*, its "difference-scan"), slightly shifted by 1/2 pixel; when two neighbouring pixels are either black or light, the finite difference is 0 (light pixel); a black pixel means that both pixels below are **different**.

Any row is the (accurate) integral of the row above while it is also the derivative of the row below. But, if we rotate the figure by 1/3 turn (120°) either clockwise or counterclockwise, the same properties will be magically true everywhere for all pixels in all the now-horizontal rows after rotation.

Altogether, such a neural or retinian pattern is equivalent to a triple system of differential equations of very high-order : one in the successive horizontal rows, a second one in rows parallel to \ and a third one in rows parallel to / (altogether to the three sides of an upper-case *APL* or Greek symbol ∆).

A network of close-packed receptors in which information would be processed by ≠\ along **one** direction would exhibit this property automatically in the **three** directions, as soon as the pattern is hexagonal or approximately hexagonal; these properties exist in the usual Cartesian representation (a square lattice of receptors fills the plane in a less dense way), but it is much harder to detect them than in this topology with the 3-fold symmetry, the one induced by the **j** rotation operator (equivalent of a classical rotation matrix, but without trigonometric functions !); until now, rotation matrices were built with real numbers, because of the old habit of vector decomposition of complex numbers on Cartesian axes; the same habit of unmixing signals as sines and cosines by orthogonal projections led Fourier to set his orthogonal transformation (followed by Laplace and Gauss in the last century).

With the computer era, discrete Fourier transformation was investigated worldwide, giving birth to the FFT methods (with nice algorithms such as Cooley-Tukey's - available as *APL* workspaces in most popular implementations - or, more recently, Winograd's). Other orthogonal transforms are, e.g. the Patterson transform (widely used in crystallography), the Hadamard-Walsh transform (rather used for imaging and interferometry) and the discrete Stieltjes integral. Let us mention the more recent Morlet transform (alias the *wavelet* transform, which, already, gives much better results than the FFT when human signals such as voice ou music are analysed).

But it was unlikely that our brain and our small retina could compute exponentials, sines, cosines, square roots and analytically-*unsolvable* systems of differential equations, or NP-hard problems (the contour problem is a NP-hard problems, in other words a Travelling Salesman Problem, cf. [**Lan**TSP]) such as the ones found in any book about pattern recognition, acoustical imaging, fractal construction, complexity, graph theory et *tutti quanti*.

The ternary topology allows to revisit with a new eye (of course !) both vision theory and Fourier's concepts of a transformation which will become **trigonal** (with 120° angles) instead of **orthogonal** (with 90° angles), so that it can be processed directly in bits, as exposed in various papers (see the bibliography in [**Lan**B]), with, then, no other scalar operation than ≠ : even the ∧ primitive, still used in composition with ≠ in the modulo-2 matrix (inner) product (the *APL* idiom ≠.∧) will disappear. But, before, such matrix products will be still used as mathematical tools, in order to bring some proofs, which are easily checked using any *APL* implementation on any cheap microcomputer.

It took much time before strong proofs could be found so as to be exposed without difficult formulas; proofs are better expressed in one line of *APL* than with several pages of equations. Mathematics become simple, when they get simplified first, even if it takes years to do so.

In *APL* (especially with APL2 and TryAPL2 which have a "clean domino", i.e. a matrix inverter the result of which is coded in integers when all terms of the inverse are, mathematically, integers), one can check that matrix `P`, obtained as : `P←V∘.!V←⍳N` with - theoretically - any integer value for N, in 0 index-origin, has a matrix inverse that contains the same terms in the same positions, with alternating signs, acording to the parity of the sum of indices for rows and columns :

```
1  1  1  1  1  1  1  1 | 1 ¯1  1 ¯1  1  ¯1   1  ¯1
0  1  2  3  4  5  6  7 | 0  1 ¯2  3 ¯4   5  ¯6   7
0  0  1  3  6 10 15 21 | 0  0  1 ¯3  6 ¯10  15 ¯21
0  0  0  1  4 10 20 35 | 0  0  0  1 ¯4  10 ¯20  35
0  0  0  0  1  5 15 35 | 0  0  0  0  1  ¯5  15 ¯35
0  0  0  0  0  1  6 21 | 0  0  0  0  0   1  ¯6  21
0  0  0  0  0  0  1  7 | 0  0  0  0  0   0   1  ¯7
0  0  0  0  0  0  0  1 | 0  0  0  0  0   0   0   1
```

The property holds modulo 2 with the parities of these integers (1 as odd, 0 as even) : all such matrices M which contain 0s and 1s only, as well as their transposed matrices, will be self-inverse, modulo 2. These matrices have no known equivalents in other numeric algebras. *APL* is the most convenient tool to study them, at low (or even no) cost, on micro-computers.

Here is such a matrix `M` with `N←9` :

```
1 1 1 1 1 1 1 1 1
0 1 0 1 0 1 0 1 0
0 0 1 1 0 0 1 1 0
0 0 0 1 0 0 0 1 0
0 0 0 0 1 1 1 1 0
0 0 0 0 0 1 0 1 0
0 0 0 0 0 0 1 1 0
0 0 0 0 0 0 0 1 0
0 0 0 0 0 0 0 0 1
```

For Sierpinski matrices, refer to any book about fractals, ro ref. [**Lan**T] or to the bibliography in [**LanB**].

(These matrices are sub-matrices of a giant Sierpinski matrix with *infinite size*, which is a self-inverse matrix - it would be difficult to verify the inversibility for an infinite shape even with a powerful *APL* interpreter, but it is easy to prove it either by recurrence, or from the properties of the Pascal triangle and of the binomial coefficients it contains, cf [**Lan**N], and also [**Ivers**].) Then, every column is : the following column, difference-scanned : `M[;I-1] ≡ ≠\M[;I]`.

The nine bits or pixels, underlined below **Fig. 1** about the retina topology : `1 0 1 1 0 1 1 1` form an *APL* vector, which, right-matrix-multiplied by matrix M above, produce `1 1 1 0 0 1 1 0` i.e. the left side of the following finite-difference triangle, extracted from the same figure with black/light pixels :

```
        0
       1 1
      1 0 1
     0 1 1 0
    0 0 1 0 0
   0 0 0 1 1 1
  1 1 1 1 0 1 0
 1 0 1 0 1 1 0 0
1 0 0 1 1 0 1 1 1
```

(This would be true for any sub-triangle of the finite or infinite plane of neurobits, rotated or not, by ±120°.)

1. 1 Going down in the dimension scale Rods, Pigments, Electrons (b) (c) (d)

A human retina contains about one hundred million rods (which see shapes) and three million cones (which see colours); the active entity in all these special cells is *rhodopsine*, in which the light receptor, the essential pigment, is the *11-cis-retinal* (*retinene* for short). Since 1938 (Selig Hecht), it is known that a single photon excites a rod of the human retina; more details are available nowadays : a single photon will isomerise the bended pigment molecule into *all-trans-retinal*, cf. the pictures. This mechanical torsion induces the execution of "chemical computing"; the molecule has become linear : it is now a conjugate polyenic compound, i.e. with a sequence of 12 chemical bonds; 6 single bonds alternate with 6 double bonds (the structure is close to the one of vitamin A and provitamin A - alias carotene - which can make people orange-brown after exposition to UV light). See **Fig. 2** and **Fig. 3**.

After reviewing many papers which involve classical studies of a possible mechanism with two different points of view, coming either from theoretical-chemistry (based on quantum-mechanic computing) and from anatomo-physiology, the main clue, exactly as for the hexagonal pattern of the retina itself, came out after the establishment and the understanding of a precise relation between the shape - the anatomy, the observed structures of the main receptors and the (unknown) properties of isomorphous data structures of information with *APL* models : cylinders made of successive disks - something like the architecture of an old juke-box of the 1950's - which would be able to process information strictly in pure bits and not as macroscopic continuous numeric electric potentials (the only variable which can be measured *in vivo* - alas on quite a variety of mammals such as dogs, cats and monkeys... for which we hope this theory will lead to the end of their suffering because of electrodes going through their skulls).

The external segment of the rod cell is a cylindric stack of about 1000 disks (1 μm in diameter and about 30 μm for the length of the cylinder); every disk is about 15 nm thick (1 nanometer = 1E¯9 m ≡ 10 Å (Ångstrøms) ; an atomic distance in organic molecules is 1.33 Å for C=C bonds and 1.54 Å for C−C bonds). As a data processor, every rod would process a kilobit of information; the discotic structure corresponds to a "pariton" (cf. the references) in which successive bits (1 for one photon, 0 for no photon) could be introduced sequentially, coming from the outer world along a generating line of the cylinder : then, if information is difference-scanned along an adjacent generating line of the cylinder, if the new result is difference-scanned again along the following such line, etc..., the periphery of the cylinder will contain, on N generating lines - with N a power of 2 - all the different integrals (and differentials) of the original information : the Nth iteration of `ω←≠\ω` reproduces the original `ω`.

The discs and the generating lines are orthogonal; the circular sequence of bits, contained in the last disk is - automatically - the equivalent of an orthogonal transform of the original perceived sequence of bits (obtained with NO arithmetics); it was named the "cognitive transform" in previous papers. Serial information - the incoming succession : photons/no photons - has been converted to parallel information which can be transmitted - by cilia, to the more classical part of the rod cell, then to the terminal *synapse* (interconnection).

The most remarkable property of such an information-processing structure is its reversibility : if the circular cognitive transform is cut into a linear sequence, the cognitive transform of this new sequence will be EITHER one integral of the original sequence OR the original sequence itself as the Nth modulo-N integral). Then, if a sensitive disk receives, this time in parallel, photons from the outer world on its periphery, the generating lines of the whole stack of disks will contain each a different integral; thus, a single *cilium* may transmit - this time, sequential information - probably the integral which makes sense.

The SAME structure is able to work in two modes, assuming both serial to parallel and parallel to serial conversions !

The corresponding formulas may be written and experienced in *APL* :

For B a bit sequence with 1024 bits (a sentence or an *APL* program with 128 characters, with a 8-bit-per-character atomic vector), the 1024 successive bits of the cognitive transform C are obtained, iterating 1024 times :

```
⎕←¯1↑B←≠\B .
```

When C is known (here, the successive printed lines), the same algorithm, applied to P⌽C , reproduces B when P is either 0 or equals the size (shape) of C, but reproduces the P^{th} integral of B (i.e. the result of B←≠\B iterated P times) in the general case. This provides a fantastic way of computing directly any high-order integral (or derivative) for any information... once a fast algorithm has been written in order to compute to and fro the cognitive transform itself (see the helix-transform section, further on, in which the fast algorithm is detailed; then, a general theorem allows to deduce the fast algorithm for the cognitive transform, by symmetry).

On **Fig. 3**, the sketch of the rod has been simplified : the upper part of the rod-cell is shown with 8 discs only while there should be 1024. On the upper right, a disc is shown, seen from above, with 8 bit positions only, as black circles (again, instead of 1024). Below, a sketch in perspective allows to imagine the long tube as an information processor able to transmit by one cilium to the lower (more classical) part of the cell, the transform - and perhaps one integral (as a parity check), of the circular information induced above by received photons.

Intermission. An APL game for electrons

With what *APL* primitive(s) can electrons play, in molecules as well as in general (if one knows that electrons do not play dice) ? Electrons follow a fundamental rather qualitative law of Nature, which they share in common with many other entities (magnetic masses, sexes in the "regular" case) : entities with the same "sign" repel each other; entities with opposed "sign" attract each other; this property (which has been known from Antiquity for the "ελεκτρον" i.e. "amber" in old Greek - and minerals like magnetite, from Magnesia, a Greek colony) led to quantitative laws in electrostatics (namely Coulomb's law for charges, the same law as Newton's for gravitation as a function of inverse squared distances) which are expressed with numeric formulas, based on continuous functions; symbols + and − were proposed by Benjamin Franklin long before the existence of the responsible particle, a discrete entity, was thought of, then studied (by Thomson, not quite a century ago).

A real problem comes from the fact that electricity is not a continuous fluid but a propagation of jumping discrete entities, just like fishes or bitstreams of information; a chemical bond is also a discrete concept : **either** there is no bond **or** there is a bond : chemistry, the science of bond making and breaking, then biochemistry, then biology are sciences of discreteness, while a large part of physics still uses statistics (postulating that discrete states may be averaged); we know that between a 0-bit and a 1-bit, nothing exists; the same should be true for the electron : no averaging is possible between "no electron" and "one electron" (except with mathematical artefacts based on the postulates of quantum mechanics, which were necessary because no observation is fast enough to attain quantum time i.e. 5.10^{-44} s and Planck's quantum length).

Although the intimate structure of the electron remains a mystery (Mac Gregor wrote a whole book on this subject), its intrinsic behaviour - the qualitative law that everybody knows - can be expressed in *APL* with a simple formula, which is quantitative as far as information is concerned because pure information has no other quantitative needs than 0 and 1 for its accurate description; the same law is taught in mathematics for the product of algebraic constants; pupils learn by heart in every school :

+ by + is +
+ by − is − (attract)
− by + is − (attract)
− by − is + (repel)

This "sign rule" could be rather taught using integer modulo-2 notation, especially in physics, because, if, symbol "−" corresponds to the physical presence of an electron (with an elementary mass *m* and an electric negative charge *e*), on the contrary, symbol "+" DOES NOT refer to the physical presence of any positive charge, when only electrons play the game (no proton, no positon no ion), BUT means that one electron is just missing.

So, "+" is a charge-&-mass void, a no-electron.

Then "1" maps "−" as the "physical presence of one electron", "0" maps "+", as the "absence of one electron" or the "presence of zero electron".

Then, the elementary law of electrostatics and of electrodynamics becomes a PLUS (or MINUS) modulo-2 rule, which reduces to a XOR-rule then to α≠ω when presences and absences are expressed in information quanta i.e. bits. This elementary law of physics becomes a realistic quantum dynamic rule if the leftmost entity, α, either a no-electron (0) or an electron (1) is fixed within a tiny box of quantum space. It is possible to put either an existence or a non-existence into an empty box (to put a non-existence into an empty box is also a no-action); it is possible to put a non-existence into a full box; at last, it is impossible to put an existing entity into an already filled box. In other words, if α and ω are a couple of quantum boxes, with α fixed (as the origin of the system), the result of the electrodynamic action as the next state of the couple α,ω is given, in all cases, by... `≠\α,ω` in ISO-*APL* (ISO8485). Note that APL2 spares the comma because of strand notation.

A sequence S of "no electrons" will not evolve much : The identity `S ≡ ≠\S←N↑0` holds for any value of N. But as soon as there is a first 1 in the sequence, this 1 will not tolerate a second 1 as its closest neighbour on the right, and will force it to 0; on the contrary, a 1 with a 0 on its right, duplicates itself; then, the next iteration of `≠\` will swap the same 1 back to 0, etc... `≠\` is, for a long sequence of parities (electrons or excited neurons), a *chain-reaction* processor.

The law is more general than one thinks : If you buy a pair of shoes in a nice rectangular box, your shoes (like your feet) have "spins": a left shoe and a right shoe fit in the box upside down (↑↓). Neither two left shoes or one left shoe and one ⊖-mirrored right shoe (↑↑) do fit the box. Electrons have the same property (Pauli's exclusion principle) : A regular "covalent" chemical bond (single bond, noted by chemists as a single bar −) is a pair of electrons (named the σ-electrons) with opposed spins, shared by two atoms. In a double bond, stronger, then shorter, (noted by chemists as a double bar =), a second couple of electrons (named the π-electrons) is shared in addition. Some special molecules (in particular, the active pigment of vision) have alternating single and double bonds, noted e.g. C=C−C=C−C=C− etc... in a carbon chain, named *polyenic* by chemists.

Such molecules will be able to play the *APL* `≠\` game iterated, and to vibrate naturally. In fact, the second couple of electrons is distributed above and below the plane formed by the molecule with the other atoms to which C (carbon) is bound, mainly hydrogen atoms.

Coming back to the fractal game in the information processing molecules

If a chain of alternating bonds (also named a "conjugate" chain), is coded 1 for a double bond (more electrons than the single bond) and 0 for a single bond, a single photon (light), falling on an extremity of the chain may excite the first electron of the π layers, exactly as if a small ball had turned the right shoe up, which may be ejected from the box. Then an attempt of reorganisation of the whole chain starts. A succession of modulated photons (i.e. a binary string of photons (1s) and of no photons (0s), a signal) will make the chain play the `≠\` game, iteratively (it cannot and may not play any other game, once one has shown that the quantum law of electrodynamics reduces to the *APL* idiom in all cases). And, without any special computation, the other extremity of the chain will exhibit, automatically, a succession of excesses (1s) or lacks (0s) of charges which correspond to the equivalent of a Fourier transform of the incident photonic sequence, now seen as a direct signal in bits. The result is even better than what a Fourier transform would produce : it is much more like a discrete wavelet transform (see ref. **[Morlet]** inter alia), and exact (there cannot be a single bit lost, because `≠\` in a non-Gödelian *isentropic* algorithm, which never adds *noise* to the information it processes - cf ref. **[Lan**S].)

What `≠\`produces, iterated on sequences such as `S0←N↑1` or `S1←N⍴1` or `S2←N⍴1 0` is not very different, since `N⍴1 0` is the result of `≠\N⍴1` and since `N⍴1` is the result of `≠\N↑1` . The difference is a matter of *phase*; in all cases, we get a Sierpinski matrix, which is indeed the equivalent of a Pascal matrix for all binomials raised to all the necessary successive powers from 0 and up; the equivalent Pascal triangle, with integers, contains the sampling of Gaussian envelope curves at all scales ! (This is proved by the self-similarity of the infinite Sierpinski matrix, the infinite geniton G_∞, after the terminology we introduced in ref. **[Lan**T]) : The infinite geniton contains, both in its successive rows and columns the coefficients of $(\alpha+\omega)^V$. We shall not give the program in *APL* because V, in this case, is `⌽⍳∞` and computing could last for eternity. Of course, we have α and ω ∊ `0 1` and + is ± modulo 2 i.e. ≠ in logic.

The successive rows or columns B of the same matrix G_∞ are obtained after an infinite numbers of iterations of `B←≠\B` with, as initial *primordial* data, `B←∞↑1`. After having completed the job, one can check as an exercise, that G_∞ `≠.∧` G_∞ `≠.∧` G_∞ (i. e. G_∞ raised to the cube, modulo 2), is a unit matrix, i.e. that G_∞ is the matrix of the primordial symmetry operator *j* (i.e. $e^{2\pi i \div 3}$ after Euler) of an infinite spacetime containing all possible imaginable orthogonal parities (quark flavours, spins and sexes inter alia ! - theoretical physicists use the term **SU3** - Sophus Lie's notation for this symmetry).

The geniton contains many more symmetries than this one, namely the pentagonal one with Fibonacci effects : Fibonacci matrices are obtained as the successive matrix powers of the 2-geniton (sex and spin matrix) using, this time, conventional matrix product algebra :

Just try, in APL2 : `+.×\9⍴⊂2 2⍴1 1 1 0`

≠\ produces all the possible (formerly described as *chaotic*) integrals i.e.modulations, of any signal. I have spent over two years on the theory of human vision, consulting hundreds of books, and trying to explain what was known, observed or simply suspected, at all scales : photons, electrons, pigments, rod internal structure, retina network, synapses, how the blind read, how information could be coded within DNA i.e. within ourselves); this voluntary choice came from the fact that *APL* was the right tool with which it was possible to study the properties of bits seen no more as scalars, but as cooperative entities in chains (vectors), planes (matrices) or more strange topologies (such as cylinders and double helices, the best data structures for efficient programming).

Hypothesis for information in synapses

Transmission of information between cells (in synapses) uses a radically different chemical way, ions : the transit of smaller ions Na^+ and larger ions K^+ ; this transit of sodium/potassium ions through channelled membranes regulates a large number of parameters in the human body, inter alia blood pressure, which is best measured... in the retina. As animals coming from the sea, we have kept the salty taste of the ocean in many body liquids, especially in blood and tears. "Positive" cations Na^+ and K^+ are counter-balanced by anions Cl^-; sodium chloride NaCl and potassium chloride KCl dissociate into such ions when dissolved into aqueous media; K^+ and Cl^- ions have a nice property which would be useful for information transmission : the number of electrons around the atomic nucleus is the same, namely 18 electrons (2+8+8) in 3 layers (shells) for K^+ and Cl^-, while Na^+, smaller, has 10 electrons in 2 layers only : so, Na^+ can be recognised "in the darkness" as 0 (less electrons) from ions K^+ and Cl^- both counted 1 (more electrons, the same number, 18, as Argon, a stable rare gas).

The P matrix of the neutral system $\begin{matrix} Cl^- & K^+ \\ Cl^- & Na^+ \end{matrix}$

does match again the 2-geniton, the chromosomic sex matrix and the electronic spin matrix, etc... :

1 1	X X	↑ ↑	Can one escape a ≠\ rule ?
1 0	X Y	↑ ↓	Refer to the appendix which

establishes a new direct connection to the genetic code itself, with the presence of matrix $\begin{matrix} N & N \\ N & O \end{matrix}$ in DNA itself.

Nature cleverly used what was available in very large quantities, at the surface of our mother Earth, air (more N than O), and salt from the ocean, to make XX and XY i.e. ourselves). So many chemical coincidences, together with the fact that 1 1 is ≠\1 0 while 1 0 is ≠\ 1 1 , cannot be fortuitous; hence the hypotheses that the ballet of Na^+ and K^+ ions through membranes carry precise information, expressed in bits; the meaning of the messages would lie in the individual sequences of transiting ions through membranes in general, not in their average concentrations which just provide fuzzy indications - unfortunately all what we are able to measure, together with macroscopic electric potentials; to give an image, concentrations and potentials carry as much information and meaning as the average of word length for each paragraph of the present text, in comparison with the meaning of the text.

The study of information, arranged in new topologies, fits a good deal of our present knowledge about vision; it will perhaps also help to understand how our brain works; our eyes are a small pair (much more accessible anatomically than the mysterious cortex) of essential peripheral devices of the brain; this fantastic thinking machine has probably been running with all its accessories (e.g. fingertips, also able to scan braille parities) under a unique operating system (OS01 ?), for some million years. In order to improve its performances, may it scan itself - as recommended by Socrates - after having scanned all the differences in its environment, invented... gun powder and slide rules, fortunately as well as, hidden in ONE green or red fruit of the computer-science knowledge-tree, also the small ≠\ idiom.

What "difference-scan" physically means

In a physico-biological world, propagation (of sound, light, money, theories, jokes, viruses, fire, life, etc...) is the main dynamical concept; (propagation, "scan" or "scanning" are synonyms). Propagation of the elementary function (≠) will lead to build realistic and efficient models of the way electrons (and other entities) behave, not interacting as scalars only, but as co-operating populations.

Dynamically, "1≠1 is 0" means (as seen) : if one entity occupies a quantum box on the left, and if another filled quantum box is too close on the right, this latter quantum box will become empty (the entity has jumped, being repelled); the successive states are to be viewed with couples of entities, not with single entities : "≠\1 1 is 1 0" rather than "1≠1 is 0", because elementary interactions imply two scalars as players (arguments and, except in the case of fusion or annihilation, two scalars as results).

Action is possible coming from an existing entity (1), not from a non-existing one (0); then, one cannot fill what is full, but one can either fill or not fill what is empty (cf. in "APL2 at a Glance", the "no-coffee with or without cream" - empty-joke contest).

Newton's law, based on attraction and continuity, did not take *repulsion* into account; on the contrary, models built with ≠\ do include discrete repulsion, only at short range i.e. short distance : the interval between two adjacent bits is the "quantum gap" of the phenomenon being modelled directly at its own quantum level (scale in space as well as scale in time).

One may imagine a quasi-sphere of quantum entities, e.g. filled with small (but NOT infinitely small) quantum cubic boxes or small spheres, either empty (0) or full (1), the central box being full (1); then, a mechanism such as ≠\ acting from the center to the periphery in all directions, and iterated, will short-range swap to 0 the 1-entities which lie too close to the center, and will also empty all the quantum boxes which lie too close to other 1-entities which appeared somewhere in the quasi-sphere as a consequence of the preceding interactions; short-range repulsions alone are able to produce long-range attractions as an *optical illusion* when the model is observed dynamically in its globality, smoothed or averaged : the total number of 1s (macroscopic global density of mass or charge) will remain constant although it may considerably vary locally, when smaller volumes are considered.

When J repels K at short distance, if J and K do not form an isolated system (isolated systems only exist in school books, as ideal unrealistic models), but belong to a universe containing other entities of the same class, K comes slightly closer to some previously more distant neighbour e.g. L : so, K and L *seem* to have attracted each other, although the distances between both may be very large (of course, this appears to hold as the unique law if one ignores short-range repulsion). No mathematics are necessary to understand this qualitative law which may have quantitative consequences : when a newcoming (or just at-puberty) animal interferes with the territory of several congeners, with the idea of making its own territory at their expense, it is firmly repelled by the closest rival, necessarily towards the territory of a third party; in this sentence, one may replace the word "animal" by "businessman", "electron" or many other ones, without alteration of the meaning.

Over one century (cf. Verhulst's equation in ecology or the van der Pol oscillator in electricity), attempts of finding formulas such as : $X_{n+1} = \mu X_n (1-X_n)$ or sums of exponentials with adjustable constants, were "ad hoc" : the results are more or less correct as an average, between some limits, and must by no means to be considered as true laws of Nature.

When 1 1 1 1 is difference-scanned, one obtains 1 0 1 0 at the end. But there are two intermediate states : 1 0 1 1 (after the partial scan of the first 2 bits), 1 0 1 1 again (after the partial scan of the first 3 bits) before 1 0 1 0 is displayed; a second iteration of difference-scanning could start on intermediate sequences before the preceding difference-scanning is fully completed, etc...

Such a model is - for the moment - beyond the capacities of *APL*-programming; it shows, nevertheless, how a molecule with a conjugated chain of {rather dense in electrons} double bonds (coded 1) or {relatively poor in electrons} single bonds (coded 0), might behave as a powerful computer, integrating information - because ≠\ is the coherent equivalent in **Z/2Z** of +\ applied to numbers in **R** or **C**, i.e. the equivalent of an undefined integration in the domain of continuous functions.

While it is impossible to find how a molecule computes a square root, e.g. to evaluate a distance betweeen points - an essential question when points are drawn (as we were taught to do it) using Cartesian coordinates - we can suppose that human vision may be modelled using directly the algebra of information, with algorithms very close to the ones which are common in image-processing (e.g. the Gray-code of ≠\B is B), adapted to data which may be :

1) expressed in this algebra only (all data sets are expressed, in computers, with 0s and 1s, already - however with many different "standards");

2) set in topologies, i.e. data structures that may look strange for specialists of computer science, but are indeed present - in our own organs which process or keep information, (and look more familiar to the biologists than conventional rectangular arrays are for *APL*ers).

Combining both points, one discovers, studying more and more the properties of {0,1} data sets (thought of in integer modulo2 algebra, but processed directly in the isomorphous binary algebra), in topologies inter alia such as triangular/hexagonal plane structures, cylindrical structures (Corti organs in the inner ear are also rods), and double-helix structures, how Nature processes information in a fantastic way which relegates the "power" of our present-time computers to the one of a flint, the floating-point tool (another bit cruncher) of the Stone Age. In fact we needed more "natural" data structures... The same need appeared in *APL*, which progressed with the introduction of nested or enclosed arrays with which tree-like data structures can be easily built). *APL* provides facilities to model such strange topologies, cylinders as well as helices, using regular binary matrices; here is the example of matrix P, a *pariton* : (continuation after Fig. 4)

```
0 1 1 1 1 1 1 0 0 1 1 0 0 0 0 0
0 1 0 1 0 1 0 0 0 1 0 0 0 0 0 0
0 1 1 0 0 1 1 1 1 0 0 0 0 0 0 0
0 1 0 0 0 1 0 1 0 0 0 0 0 0 0 0
0 1 1 1 1 0 0 1 1 1 1 1 1 1 1 1
0 1 0 1 0 0 0 1 0 1 0 1 0 1 0 1
0 1 1 0 0 0 0 1 1 0 0 1 1 0 0 1
0 1 0 0 0 0 0 1 0 0 0 1 0 0 0 1
0 1 1 1 1 1 1 0 0 0 0 1 1 1 1 0
0 1 0 1 0 1 0 0 0 0 0 1 0 1 0 0
0 1 1 0 0 1 1 1 1 1 1 0 0 1 1 1
0 1 0 0 0 1 0 1 0 1 0 0 0 1 0 1
0 1 1 1 1 0 0 1 1 0 0 0 0 1 1 0
0 1 0 1 0 0 0 1 0 0 0 0 0 1 0 0
0 1 1 0 0 0 0 1 1 1 1 1 1 0 0 0
0 1 0 0 0 0 0 1 0 1 0 1 0 0 0 0
```

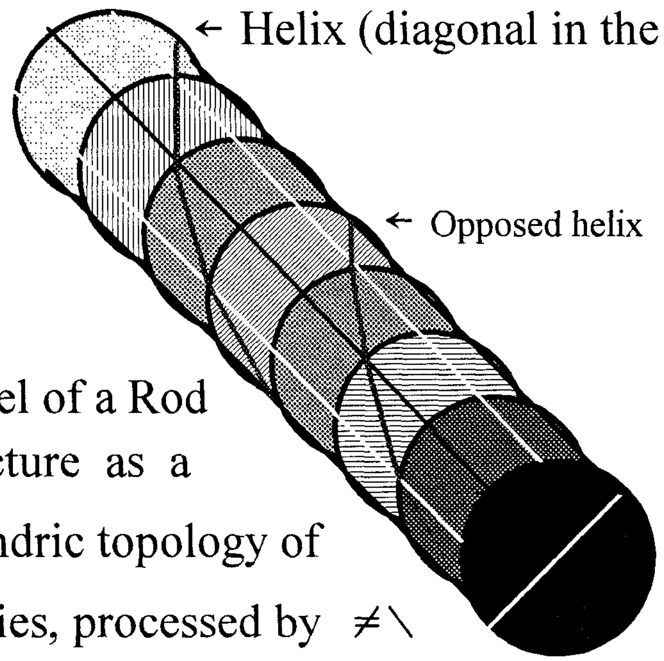


Fig . 4 Sampling the retina rods which may contain each 1024 such rings, not only 8 as on this sketch.

In rods (cf. **Fig. 3**) which see shapes; images are formed 55 times per second. A *rhodopsin* molecule the sensitive part of it is the 11-cis-retinal, may be activated, as measured in femtochemistry, in 0.2 nanosecond; cf. ref. [**Schoenlein** *et al.*], at the end of the page, [**Marr**], and [**Stryer**] (the most valuable book for discovering biochemistry in colour).

If *c* bits are either activated in parallel by some quanta of light (1) - photons, or not activated by no quantum of light (0), in the *receptive* ring above (*c* being a power of 2), if successive difference-scans are propagated from ring to ring, then a pariton structure is created in the rods : successive generating lines of the cylinder contain all the successive possible different linear quantum-integrals - and, the other way around the cylinder, the quantum-derivatives i.e. the Boolean logical successive differences, (a *linear* Gray code).

When the cognitive ring plays the role of a parallel input, then the generating lines are its serial transforms - and conversely.

The helices (2nd-diagonal parallel alignments in the flat pariton matrix) contain the transforms of the corresponding generating lines read backwards. The matrix operators of the orthogonal transformations in bits are the vertical and the horizontal mirror of the fractal **Sierpinski** matrix, which is the equivalent, in Z/2Z of a Hadamard (Walsh) transformer in Q or R, when one replaces both numeric addition and substraction by their equivalent which is ⊕ in Z/2Z or ≠ in *APL* : −1s of Hadamard's matrices are replaced by ~1s i.e. 0s.

All the properties (whole books exist on the subject!) which are known for the Hadamard-Walsh transform, still hold. ≠\ just brings to it fantastic simplifications ! Such a transform was used to compress and analyse information (images) coming from the Moon (1969) of from Mars (the Mariner project). Already, it allowed to process large amount of data without any product or division : only additions and substractions were necessary to compute the transform. With the APL-TOE theory, these operations now both reduce to a single one, their modulo-2 equivalent, the Exclusive Or. Images can be processed directly in bitmaps. Cf. ref. [**LanI**], which (although the text is in French), shows many examples of images which were, already 3 years ago, transformed directly in the memory of a slow computer (with fast algorithms) and hardcopied from the AtariST screen as bitmaps (up to 256,000 bits) on a cheap laser printer : just a few lines of APL.68000 Level I (the runtime of it being free...).

The analogy between Hadamard matrices and the genitons was explained in previous papers [**Lan**T], [**Lan**N] among others, plus a variety of papers in French which appeared in APL-CAM Journal thanks to J. de Kerf's courtesy.

[**Schoenlein**] R.W.Schoenlein, L.A.Peteanu, Q.W. Wang & C.V. Schank, R.A. Mathies, "*Investigation of the Primary Event in Vision Using 10 fs Blue-Green Optical Pulses*", Springer Series in Chemical Physics, Ultrafast Phenomena VIII, Springer, Berlin. ISBN 0-387-56475-6 (1993), pp. 53-7. The cis-trans isomerisation of rhodopsin is complete in 200 femtoseconds, suggesting that the photochemistry occurs from a vibrationally coherent (although still-unknown) system (p. 57).

The square matrix contains 16 rows which are the 16 successive iterates of `B←≠\B` with B the binary code of the two-character string `'AP'` (in a PC). The last row, i.e. the 16^{th} integral, reproduces `'AP'` in bits. After sticking this 16^{th} row to the first one, one will get a nice model of a rod structure, a cylinder with, now, 16 circular disks of information; the first disk on the left contains 0s; the second disk contains 1s; the third disk contains 1 0 repeated in alternance: this disk could be replaced by a smaller disk which could contain only 2 bits. The 4^{th} disk contains a 4-bit sequence 1 1 0 0, repeated 4 times; the 5^{th} disk contains the 4-bit sequence 1 0 0 1, repeated 4 times. The 6^{th} disk contains the 8-bit sequence 1 1 1 1 0 0 0 0, repeated twice; the 7^{th}, 8^{th} and 9^{th} disks also contain 8-bit sequences repeated twice. Disks 10 to 16 contain 16-bit sequences with no repetition.

If one tries to reduce the redundancies, using disks with a size (a diameter) proportional to the length of the repeated sequence, one will obtain, dropping the 1^{st} disk, which, in this case, has no information content : one nucleus (the former 2^{nd} disk containing 1s) with null "diameter", then one layer with two "entities" 0 and 1 of opposed values (that we may call "spins"), then two layers with 4 entities in each, and with a double "diameter" if one compares with the previous layer; altogether, this pair of layers has 8 entities. Any chemist will immediately notice a surprising analogy with the way electrons are assembled in the first rows of Mendeleev's table, known as the periodic classification of the elements : the first electronic shell "K", complete for He(lium) has 2 electrons; the second electronic shell "L", complete for Ne(on) has 8 electrons, altogether shells "K" + "L" have indeed 10 electrons (see, in the **synapse** section, the hypotheses about the sodium ion Na^+ which exhibits the same electronic configuration as Ne.)

But, now, as far as vision is concerned, the cylindric rod model becomes a pseudo-conic model. Although the role of cones, which see colours, is not well-understood, we know that **retinal** plays the same role as in the rods; the sensitivity to 3 different colours for humans and European monkeys - while American monkeys can only see 2 colors - comes from proteins (the genes of which lie on the X sex-chromosomes); these proteins, when bound to retinal, exert some constraints on its shape, modifying its maximum spectral sensitivity. These proteins also exhibit a double-helix structure, like DNA (desoxyribonucleic acid) and RNA (*idem* ~ 'desoxy' i.e. ribonucleic acid).

The small matrix, displayed hereabove, may be also used to clarify the connection between the special double-helix shape and the properties of information in such a data structure.

If one isolates D the 2nd diagonal of matrix P, as well as DD, the opposite parallel bit string, using simple *APL* expressions :

```
      ⎕←D←0 0⍉⊖P    ⍝ origin is 0
0 1 0 1 0 1 0 0 0 0 0 1 0 0 0 0

      ⎕←DD←0 0⍉8⊖P
0 1 0 1 0 1 0 0 0 1 0 0 0 1 0 0
```

one has extracted a double helix from the periphery of the rod (cylinder).

First, both left halves of D and DD have the same content :

```
      D[;⍳8] ≡ DD[;⍳8].
```

Second, the logical difference (or modulo-2 sum) of both right halves equal this left half :

```
      D[;⍳8] ≡ D[;8+⍳8]≠DD[;8+⍳8]
```

Third, if D is considered as a new information sequence, then is integrated iteratively 16 times as `⎕←D←≠\D` , the matrix which will be displayed will contain the old B (i.e. 'AP' in bits) as its second diagonal; such a property will be true for any length of information which is a power of 2, after the same number of integrations; so, D is an orthogonal transform of B, which was named, for this reason the *helix transform* of B; (hence the hypothesis, emitted in Blois by the author, at the International Encounters on Chaos and Complexity, June 1993, that the observed genetic code, present in DNA sequences, could be thought of as some equivalent of the Fourier transform of what it really means).

The last (16^{th} column) of matrix P above contains C the cognitive transform of B : if C is difference-scanned iteratively 16 times as : `⎕←C←≠\C` , the old B (i.e. `'AP'` in bits again) will be read as the 16^{th} column of the displayed matrix.

Sequences D and C are connected via the fundamental theorem (a kind of Maxwell law for information processing) :

The cognitive transform of any sequence is the reversed helix transform of the same sequence, reversed.

expressed in *APL* as : `(COG B) ≡ ⌽ HEL ⌽B`
or, by symmetry, as : `(HEL B) ≡ ⌽ COG ⌽B`

if COG and HEL are *APL* functions which compute respectively both transforms.

Several algorithms were published and commented in the past for these functions, especially, modulo-2 matrix products by fractal Sierpinski matrices (which connected the theory to fractal geometry, using, for the first time, fractal constructs as matrix operators); however, the fastest algorithm we know results from the hereabove-given identity, (which also corresponds to what biologists observe when DNA double helices are built from separate strands by the polymerases), combined with the COG vs HEL relations. We have, in general :

```
D[;⍳K] ≡ D[;K+⍳K]≠DD[;K+⍳K]
```

with K∊1 2 4 8 etc... i.e. a power of 2.

This relation is recursive : it applies to both halves of the left half, to both halves of the left quarter, etc...

Here are the detailed rules with the rationale :

The helix transform of a sequence with length (shape or size) 1 bit is the sequence itself :

> In the P matrix, the leftmost bit of the last row which contains the sequence, is also the leftmost bit of the 2nd diagonal which contains the helix transform.

The helix transform of a sequence with 2×K bits is the helix transform of the left half (the first K bits), catenated with the helix transform of the itemwise logical difference of both left and right halves.

> The theorem (and building algorithm) results from the property of P-matrices - paritons - cut into 4 quadrants (square sub-matrices) :
>
> North-West   North-East
> South-West   South-East

The NW and SW quadrants are identical; any quadrant among NW, NE or SE is the logical difference of the other two; this results (in a proof by recurrence) from the symmetry of the truth table of the Exclusive Or alias ≠ .

Example : Given B as 0 1 0 0 0 0 0 1 0 1 0 1 0 0 0 0 ('AP'), a double recursion (as in some Fibonacci or Hanoi Towers famous algorithms) would allow to write an "elegant" APL program which would be inefficient for a large dimension of B. Derecursion can be achieved, using something related to the "baker's transform" (Arnol'd), or to what illusionists (magicians) do when they apparently cut and mix playing cards with dexterity, and miraculously find the card you had chosen; (by luck, regular card games have 32 cards, i.e. a power of 2) : Let us take a binary mask M with the same length (shape) as B, and AM (Anti-M) its logical negation which is also 1≠M. Initial B is supposed to have been reshaped as a 1-row matrix :

```
D←B          : 0 1 0 0 0 0 0 1 0 1 0 1 0 0 0 0
M←,(⍴D)⍴1 0 : 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0
AM←1≠M       : 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1

X←M/D        : 0   0   0   0   0   0   0   0
Y←AM/D       :   1   0   0   1   1   1   0   0

Z←X≠Y        : 1 0 0 1 1 1 0 0

D←X,[⎕IO]Z : 0 0 0 0 0 0 0 0
               1 0 0 1 1 1 0 0
```

Note. ",[⎕IO]" is also "⍪" in many implementations.

```
AM←1≠M←(1↓⍴X)⍴M

X←M/D         : 0   0   0   0
                1   0   1   0

Y←AM/D        :   0   0   0   0
                  0   1   1   0

D←X,[⎕IO]X≠Y : 0 0 0 0
                 1 0 1 0
                 0 0 0 0
                 1 1 0 0

AM←1≠M←(1↓⍴X)⍴M

X←M/D         : 0   0
                1   1
                0   0
                1   0

Y←AM/D        :   0   0
                  0   0
                  0   0
                  1   0

D←X,[⎕IO]X≠Y : 0 0
                 1 1
                 0 0
                 1 0
                 0 0
                 1 1
                 0 0
                 0 0

AM←1≠M←(1↓⍴X)⍴M

X←M/D         : 0
                1
                0
                1
                0
                1
                0
                0

      ⎕←D←,X,[⎕IO]X≠Y←AM/D
0 1 0 1 0 1 0 1 0 0 0 0 0 1 0 0 0 0
```

D is indeed the **second** diagonal of matrix P (given 3 pages back). Was *APL* designed for wizards ?

Altogether, 4 iterations only, i.e. 2⍟⍴,B have been performed. This "magician's algorithm" allows to obtain both transforms in a PC, for sequences with millions of bits; only 20 iterations are necessary for 1 Megabit.

As forecast by the "APL-TOE" theory, no other scalar dyadic primitive than ≠ is used. This algorithm is faster than what the electrons can do with ≠\ but these electrons are able to compute, as a fantastic holographic parity check, **all** the helix transforms of all the integrals of the 1-kilobit sequences in each of 100 million rods, 55 times a second, in each eye !

When the sequence is periodical, e.g. with the bit translation of 'AA', the repetition of the same information will be detected and the transforms will be shorter (i.e. will contain 0s on the left or on the right) :

```
    BIN 'AA' : 0100000101000001
HEL BIN 'AA' : 0101010000000000
COG BIN 'AA' : 0000000000111111
```

0s appear right of the helix transform, and left of the cognitive transform, in the general case of `16⍴?8⍴2` in 0-origin.

These transformations may compress more (e.g. here, to 6 significant bits only). The compression effect becomes more striking if one uses the hexagonal topology observed in the retina receptors, because it induces a drastic economy of excited (coded 1) neuro- or bio-receptors; in addition, periodicities and internal symmetries of information become visible, as one can see it the last figure (cf. the Annex) in the "fanion" i.e. the ternary model of `'AA'` : If one drops the first 0-bit of the sequence as well as the left oblique row on the left side, one obtains a vertical -symmetric fanion for 15 bits. When a sequence B is symmetric (so that `B≡⌽B` holds), both transforms produce the same result.

Already, since about 1989, I suspected that **everything** in physics, biology and computer science (at least) could be studied, modelled and, perhaps better understood if not completely unveiled, with `≠\` (since that time, many mathematical proofs converged and allowed to develop faster and faster and, at the same time, shorter and shorter algorithms in a variety of fields). I could have chosen any other subject, e.g. electrocardiography, puzzle solving, turbulence or music. I chose vision because it is a thrilling subject, that would interest quite a lot of people, by pure curiosity or professionnally, and on which, in fact, although numerous books exist, we knew very little. I was lucky to be, first, a chemical engineer, then a theoretical crystallographer, which gave me the possibility of detecting similarities, hidden symmetries and apparently-bizarre properties **visually**, just looking at bitmaps - every image being the equivalent on just one screen of a cheap microcomputer, QL Sinclair, Atari ST or Macintosh, of a paper listing with thousand lines of grim either 0s or 1s.

This work would not have been feasible 10 years ago, for a couple of reasons : **0)** Cheap *APL* implementations did not allow to handle huge matrices, e.g. to find their matrix inverse, without using virtual memory, with not even a single bit of error so that the inverse of the inverse exactly matches the original matrix, even when this matrix contains several million items as bits; (the same holds for the modulo-2 equivalents of Fourier, Laplace, Hadamard, Walsh and wavelet transforms, namely the Cognitive-Helix transform); **1)** it was impossible to look - as said in the last paragraph - at the internal structure of such huge matrices, as bitmaps, so as to simplify the software.

No other programming language than *APL* and APL2 handles fast enough logical data as large structures which can be also considered as numeric data at will. No other standardised programming language provides **scans.**

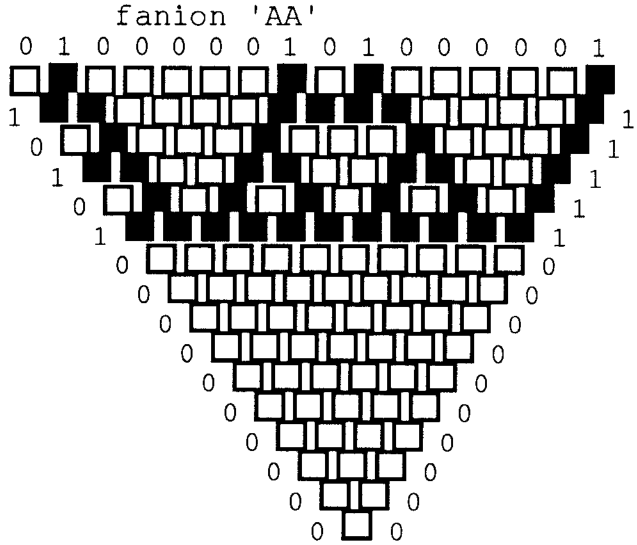
The **scan** operator is both an integrator and a parallel-algorithm maker (in arrays). No other programming language provides the fantastic monadic and dyadic symmetry primitives `⌽ ⍉ ⊖` which allow, just to see what happens, to explore mirror-images, circular shifts and diagonal cuts - a real dream for a crystallographer.

One can use (when matrices are small enough and with a non-0 determinant) the *APL* domino in order to solve quite a lot of problems in modulo-2 algebra and discover new methods of solving the same problems which use symmetry properties instead (cf. [**Lan**M]); these new methods may now be applied to much larger problems for which the domino, as well as all the known algorithms in floating-point arithmetics would alas fail, because of truncations, or because the domino is unable to find the sub-basis of independent vectors when the determinant of a matrix is exactly 0 or very close to 0. In this respect, refer to [**Lan**Q], [**Lan**S] and to the Workshop about *binary /Integer-Modulo-2* algebra at APL94.

Annex. Equivalence with a physical model

In a special *APL* WS, function "`fanion`" produces the ternary parity output for a character string : a fanion contains the information of the lower right half of a pariton, arranged in trigonal symmetry.

```
     fanion 'AA'
```



The triangular or hexagonal model for retina parity difference-scanning is equivalent to an **Ising** (or percolative) model with infinite nearest-neighbour and finite next-nearest-neighbour interaction, used in physics for antiferromagnetism (cf. eg. the slow-dynamics study for glasses by Shore [**Shore**] in which randomness had to be excluded from the spin Hamiltonians). The model, extended to 3 dimensions, as a stacking of successive plane layers, already reproduces very stable crystal-structures, such as the hexagonal packing (e.g. of graphite) or the cubic (face-centered) one, that is observed in solid sodium and potassium chorides, in iron at high temperature (γ-Fe), or in stainless-steel alloys and in gold.

Hypotheses about information in DNA

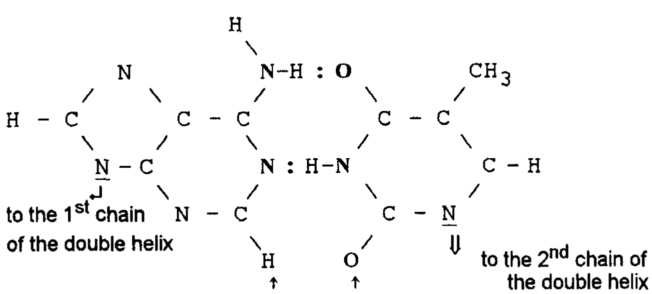
In DNA, information is kept as sequences of chemical base pairs : four letters form the genetic alphabet in which all words - just like old semitic roots, have three letters (Chinese names also have 3 monemes). Among the 64 possible combinations of 4 letters 3 by 3 i.e. 64, only 23 have different meanings (20 for amino-acids and 3 for punctuation in the general case). Note that we have 23 pairs of chromosomes and that most natural alphabets (old Roman, Greek, Arabic, Hebrew also have such a number of letters, around 24; Braille without "w" has 25).

In fact, there are only two letters, because the other two are each symmetric mirror-images the first two. Compare the symmetries in shape and pronunciation of our consonants :

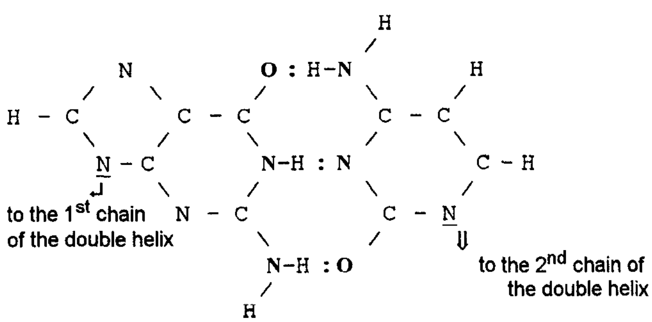
|p q|	|labial	guttural|	|front	back (palatal)|	
|b d|	|labial	dental |	|front	front	|

Symmetries hide everywhere, always with the same rules. If we note pair AT (Adenine-Thymine) as letter "A", then, its mirror-image is letter "T". If we note the second pair GC (Guanine-Cytosine) as letter "G", then its mirror image CG is letter "C". Let us have look at their inner chemical symmetry, in parallel on both columns of the page :

Adenine **Thymine** (Letter "**A**")



Guanine **Cytosine** (Letter "**G**")



In pairs AT and TA, there is no 3rd hydrogen bond (colon symbol) between O and H below, pointed on these figures by the *APL* up-arrows : they are much two far (about 3 Ångstrøms) from each other. (A coincidence is that chemists use, for hydrogen bonds, symbol ⊕, which is the one of + modulo-2 then of Exclusive Or in mathematics).

One clearly recognises a symmetric of a geniton, this time **N..O** (bolded) which corresponds to the self-inverse **1 0** / **1 1** famous matrix, in AT.

N..O	**1 0**
N..N	**1 1**

Pair TA (code "**T**") is pair AT (code "**A**") turned over easy, like a fried egg in the pan.

The underlined N (nitrogen) atoms of every pair are bound each to one strand (chain) of desoxyribose which forms the double helix. The line which joins these points is not horizontal on the mirror images so that TA is not simply ⌽ AT (10 successive letter stackings form a whole turn).

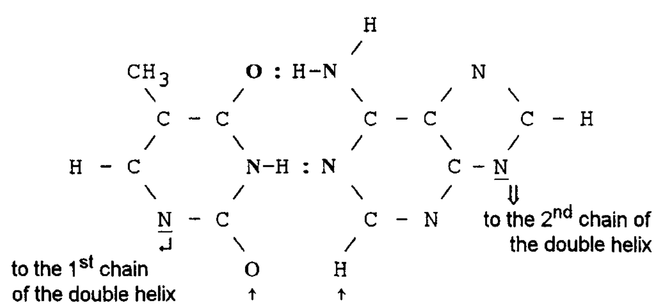
O..N in pair TA, is the modulo-2 cubic root of unity	**0 1**.
N..N	**1 1**

Seen from below (by ⊖ symmetry), one matrix is a square root, the other one a cubic root again. No confusion is possible.

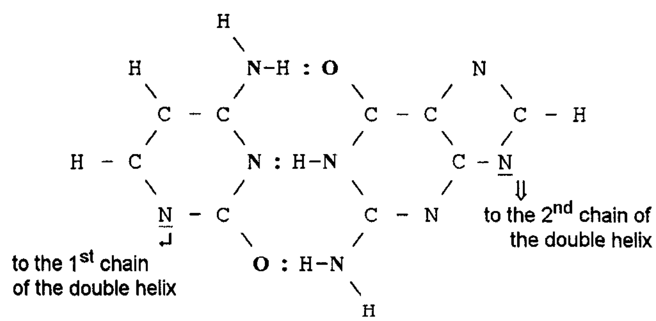
For letters "**G**" and "**C**" respectively, we may see the 3-by-2 matrices (exactly as in the braille code for the blind) :

O..N	**0 1**	**N..O**	**1 0**
N..N	**1 1**	**N..N**	**1 1**
N..O	**1 0**	**O..N**	**0 1**

Thymine **Adenine** (Letter "**T**")



Cytosine **Guanine** (Letter "**C**")



Now, in order to make these matrix square and with a non-0 modulo-2 determinant, let us catenate a column of 1s left of "**G**", then, by symmetry, right of "**C**", then study what we find : for "**G**", the first row 1 0 1 is ≠\1 1 1 i.e. the second row , while the third row 1 1 0 is ≠\ 1 0 1 i.e. the first row. Is there no way to escape the ubiquitous rule ?

Both matrices for letter "**G**" and "**C**", as well as their ⊖ and ⍉ images (molecular models seen from below the paper), have the following property : if I is a unit matrix with rank 3 given by I←3 3⍴4↑1 , then the following identity holds :

I≡**G**≠.∧**G**≠.∧**G**≠.∧**G**≠.∧**G**≠.∧**G**≠.∧**G**

A new magic number has appeared : 7. All these matrices are modulo-2 (complex) seventh roots of matrix I, then, their successive modulo-2 matrix powers form a regular heptagon on a trigonometric circle; these numbers (the successive modulo-2 matrix powers of **G**, as an example, are expressible with only nine bits, exactly, without trigonometry or double-precision waste. "*Nature is really thrifty in all its actions*", was set by Maupertuis in 1744 as the original (not reduced to classical mechanics) formulation of the least-action principle. This baron from St Malo could not guess his principle would become true also, 250 years later, in computer science... as well as in genetics. Nature knows, by symmetry, how to solve equation $x^7-1=0$ as $e^{2k\pi i \div 7}$ with k≡⍳7 while mathematicians and computer scientists first need to compute **e** and π before (which is impossible... exactly).

⊖**G** is the modulo-2 matrix inverse of **C** (and, of course, conversely), and the 6^{th} modulo-2 matrix power of **C** ipso facto. Refer to a recent paper **[LanB]** as well as to [**Lan**M] for details (and fast algorithms) in modulo-2 algebra, connected to Galois fields (Abelian groups), and to problem solving by pure symmetry-methods.

An hypothesis was that the properties of the genotypes (magnificent information sequences) hidden in DNA within the chromosomes, which program sex, vision, language, as well as all aspects (phenotypes) of our species - and of all living species - can be found by the properties of such products; especially, the symmetries of genotypes should be the same as the symmetry of phenotypes. Since genes are modulo-2 entities (either *dominant* i.e. active or *recessive* i.e. inactive but transmissible), it was urgent to study models in the corresponding algebra (what *APL* allowed to do). The main law of genetics states : *a dominant genes acts, a recessive one does not*; when expressed as a least-action principle for information, it becomes, written in PASCAL : **IF A THEN B:=NOT B**; because **NOT B** (in *APL* ~**B**) on one bit is the least-action. (There is nothing less, as an action, than the unique logical monadic function, applied to the quantum of information, one bit).

Entity **A** is the controller of the action, the actor if 1, the no-actor if 0. Then, for any initial couple **A**,**B** of scalar parities ∊0 1, the final result after execution of the **IF** statement, is, again, ≠**A**,**B** i.e. reduces to the same parity law as the one the electrons like to play with in electrodynamics, as shown in another section.

So, no other *genetic algorithm* than this idiom (one can invent plenty of genetic algorithms which have in general no deep rationale) will be able to explain... genetics, if it does not first explain what is indeed observed as the basic rule for genes.

Many more investigations as well as theoretical developments on the properties of information, seen in modulo-2 integer matrices and other topologic structures, (shapes which will reflect the observed shapes) for the spatial distribution of the quantum charges, the "electrons", will be necessary before we may understand the whole of the DNA code; however, many observations and mathematical properties of **Z/2Z** matrices converge, so that one may have the feeling that this new way may prove at least as fruitful, in the future, as other more sophisticated approaches, such as those of quantum mechanics.

Conventional molecular dynamics is based on energy minimisation. On molecules which process information, the law which rules information self-processing itself with no increase in entropy, will allow to find new paths that energetic considerations alone would not solve.

Continuous fields (and their equations) are in fact an approximation; they would have no meaning at quantum scale, since the simple idea of a quantum should imply that no infinitesimal quantity should ever been thought of, for any plausible mathematical model in physics or biology.

It is impossible to understand a process such as vision without trying to understand the action of one quantum on another quantum.

If this action can be modelled by ≠\\ ,then the successive 1,048,576 integrals of a modulation expressed in a one-megabit signal, are all computable with no error, easily, e.g. in APL* PLUS II or III, or APL2 on a PC. All these modulations are strictly equivalent to what one would obtain with formulas involving *sin* and *cos* (ωt+φ) at a high frequency, with truncated results. For higher frequencies, our computer techniques would fail, while algorithms resulting from the new mathematics for the computer, in bits and in bits only, will never cry for mercy.

In order to take an axample, suggested as a last-minute proof, by Eugene Mc Donnell's paper about the 10,000,000,000th prime number, then 252,097,800,623 in 0-origin ("*At Work and Play with* J", VECTOR, Vol. 10, No 4 (April 1994) p. 110), how long does it take to compute modulo-2 matrix power 1,228,200,000,001 for a bit-matrix MAYA the bee (15 15≡⍴MAYA) in a tiny but almost full WS (over 400 *APL* fns), with TryAPL2, on a PS2 machine at 33 MHz ? {The answer is 2.7 s}.

And one can check that the result is, as it had to be, (for symmetry reasons), the original matrix exactly.

Main Conclusions and Hypotheses about Information coding and processing

a) Our eyes, senses, brain and nervous system process information in bits only (and not as continuous electric potentials which are measured as macroscopic consequences of individual actions of quantum charges coded 1 while the absence of charge is coded 0).

b) The responsible mechanism cannot (and may not) be described using either the theory of continuous functions or number theory in classical algebra. On the contrary, it may be described and modelled, e.g. in *APL*, by the mathematical construct which is written ≠\ known as "difference-scan" or "unequal-scan" (cf. **ISO8485**, 1989).

c) ≠\ is the correct mathematical expression at least of the quantum law of electrodynamics, as far as information processing is concerned. (The intersection of the set of all physical and biological systems with the set of systems in which information plays **no** role is the empty set ∅).

d) Inventors reproduce the way they are themselves programmed - of course by DNA. (DNA has a structure which is, as an example, isomorphous with what it produces, e.g. human language, protein sequences as well as encephalograms and music : all these are **1/f** i.e. fractal signals).

e) Topologies (i.e. shape of organs) which process information in living organisms are not random : they possess special (until-nowadays-unknown) properties as collective data structures, that one may express in **Z/2Z** i.e. modulo-2 integer algebra and simulate with only one logical function. Examples of such topologies are, for vision and genetics : ternary bit networks, cylindric and conic bit structures, double helices, and rings (*cognitons*).

f) A theory must take into account observed facts and be somehow predictive as well : **Then,** our genetic information would be coded in DNA within the hydrogen bonds of the two complemetary base pairs (AT and GC). It can be expressed as matrices containing parities with shape 2 2 or 3 2 respectively, in correspondence with the nature of atoms (either N for nitrogen or O for oxygen, the most abundant elements of the Earth's atmosphere) which bear these essential labile hydrogen bonds. The matrix found in the AT pair, the 2-geniton, is a symmetric matrix in which any row or column is ≠\ of the other one, isomorphous with the sex matrix, with the spin matrix, with the blood-agglutinogen matrix and with the synapse matrix, inter alia. This matrix has the property to be the accurate code of ***j***, the symmetry operator of the Universe's 3D Euclidian space, when it is considered in the algebra of **Z/2Z**, and is the nucleus of the giant Sierpinski fractal and Fibonaccian matrix (infinite geniton) which, for all sizes and shapes, has the same astonishing property.

g) ≠\ is the correct mathematical formulation of the *least-action principle* (expressed in decision theory as well as in genetics). This mechanism never introduces noise into the data it processes, and operates on a constant volume (global shape, size) of data; therefore it represents the conjunction of an *adiabatic system* - which never produces heat i.e. entropy i.e. disorder - and of a system whose evolution would progress at *constant volume* in thermodynamics. With the usual criteria of classical thermodynamics - which does not take information into account as the essential factor, but postulates continuity, simultaneity, numeric additivity of actions together with some randomness, however modulated by mysterious statistical distributions, the 2nd principle of thermodynamics cannot be respected by living organisms ! ≠\ now brings a magnificent counter-example. So, if the arguments we have brought here are recognised as valid, a consequence would be that ≠\ represents the expression of absolute optimality for information processing in Nature's very clever (though in fact simple) and ancient technology.

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