Biochemistry

2014-03
www. u5d.net

CONTENT

Biochemistry

- some elementary data viewed with aspects from the background model -

Files

See also file "The Cell" under menue Biology, first pages

1. Some first general aspects

1b. Phases

1. A dimension chain in the model here has 5 steps, 6 "borders"

5 → 4 → 3 → 2 → 1 → 0/00

There are 5-4 bases in the genetic code.
There are 5-6 atoms forming the rings (C, C-N) in carbohydrates and bases.
There are 4-5-6 elements as the essential building stones for the structures of life chemistry (P-C-N-O/S-H) with valences 5-4-3-2-1.

- 4-5 or 5-6 cyclic processes have been regarded as condition for life (Marquand: Life, 1970).
- 4-5 cells in the development of the fertilized ovum becomes the embryo, according to some source.

Hence, there is a lot (and more than these things) to be said in favour of counting on 5 primary dimensions.

Why "dimensions"? Here is assumed that numbers ultimately, at bottom, are rooted in dimensions, and a transformation through dimension steps to dimension degree (d-degree) 1 for instance give 5 x 1 units. (With d-degree 0/00 substantiated 6.

2. There are the millions of chemical substances - all the butyric acids, malic acids, formic acids of the chemists and thousands of other unpronounceable molecules which change names and identity only because they exchange an atom or move a group, all becoming a brushwood for non-chemists. Perhaps it could be regarded as an attempt to describe a forest through its spatial forms instead of in terms of trees, earth, stones?

Perhaps all substances are as matrices to what in reality is simple; perhaps it is the processes as matrices to the individual substances that draw the simple patterns, or the gist of these processes?

Dimension chains on a field level may be imagined working as fretsaws in the molecular substance as at production of jigsaw puzzles, a dimensional process of inward / outward developments where the small pieces get increasingly complex to interpret in comparison with the whole, the entirety.

3. The aspect from the entirety towards the parts has in the dimension model the same validity as a view in the opposite direction, the synthesizing aspect from parts toward the more complex units.

If so, one should at a "pre-material" field level have mass numbers, virtual weights, which get distributed on atoms, translated to differentiated molecules and compounds. We have also that most elements in practice are found in the form of molecules.

(Is it possible to imagine that nuclear fission and molecular structures could occur simultaneously under certain density and temperature conditions? A differentiation of a whole mass to a multi-centre molecule? Atoms interpreted as "poles" out of a bigger unit in a process of varying fragmentation and simultaneously creating of bonds?

It's probably only imaginable on an underlying level where the Time axis still is double directed? In macrocosm however, double and multiple stars seem to differentiate more or less simultaneously out of cosmic clouds: a fragmentation into bound systems as through "development inwards".)

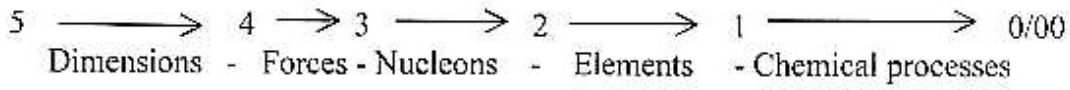
Atoms can also be analysed as wave functions, as matter waves (in d-degrees (3)--2--1-- according to our model here). This makes it perhaps easier to understand their mutual connections as through underlying fields - and processes of disintegration and association as results of such things as diffraction and interference..

4. A conclusion of the dimension model is that the mass numbers ought to have a much bigger importance for which chemical compounds and molecules that are created than the common biochemistry is willing to count on.

Levels:

5. A dimension chain where each step develops to whole new secondary dimension chains and steps in these to tertiary dimension chains, is equal to what here is called a level chain. It surely implies the same as"fractals".

A first level chain:



We should imagine that a level chain is double directed at bottom, between outer poles in d-degree 4 or between macrocosm and microcosm, between a part, a unit and its surrounding, centre and anticentre.

An alternative aspect is to regard a counterdirected unit O → ← O with equal energy level) from outside, from the environment, as a condition for new level steps.

Another aspect is to look at the dimension chain in right angle to the main axis, polarization steps as 5→4/1, 5→3/2: the development evolving through step 3--2 when the analysis concerns the dimension degrees of material units.

Possibly too one could imagine underlying levels "inverted" to superposed ones as expression for the pole exchange 0--00, centre --- anticentre and change of direction.

6. According to first hypotheses in the dimension model the level development also implies
- centre displacement where anticentre becomes a new centre, as a kind of growing "strangeness", and
- a process towards increasing ***unidirection***, differentiation to more and more specified addresses.

The chemical substances become connected over increasing distances as a result of this secondary development of new chains in each step of earlier dimension chains, connected via underlying levels in the same way as people's journeys over geographical distances and distant contacts may have roots in their earlier relationships and underlying psychological levels.

(An illustration could be the cutting of mRNA before the translation process as redundant information. Back to the relevant level of connection?)

Energy levels (as numbers) could function as addresses. Each step in a dimension chain or level chain may be assumed as representing a certain energy level, and molecular structures as complex results of dimension processes then get different energies. Interpreted as numbers (equivalent with personal code numbers) could then represent addresses to equal (complementary) poles or structures on a related level.

7. Assumptions in the dimension model is also that number of motion moments increases towards lower degrees and higher levels. "Lost" d-degrees in structure become translated into motions (and/or meeting "the other way around").

This becomes also related to the optional level of analysis: the more dimensions attributed to the structure, the less to motions. In one formulation the number of "freedom degrees" should increase with increasing complexity of the molecules.

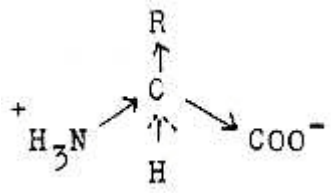
If a simple atom or ion only has an unsophisticated pathway motion in its local area before it gets bound, a more complex molecule can be assumed to move in 1-2-3 dimensions, move on and between others keeping its unbound freedom with a more or less differentiated address (~ receptor) - as human beings on floors, between walls, through streets towards their destinations.

8. Level development could also imply displacements in roles of the involved atoms and molecules, a rising or lowering of the dimension degree or d-degree step that the unit, atom or molecule represents in relation to others at a certain stage or in a bigger context? A displacement in its role, expressed through displacements and angle changes on its underlying levels, as changed binding directions, variations in their relative electronegativity, changes in oxidation numbers etc.

Coordinate axes - directions - angle steps:

9. It should follow from the analysis of electron shells that all electrons involved in molecular bonds, orbitals and directions in space around an atom differ mutually, represent different dimension degrees and steps and levels or different poles of a d-degree. No coordinate axes can be equivalent in the sense that they are all the same, the magnetic polarity N-S included.

One example is the central C-atom in amino acid tetrahedrons.



In addition to the division of the 4 directions into 3 + 1 (1 for the side chains) one has the R-H-axis in opposition to the axis NH2 -----COOH with character of inward / outward direction respectively, poles of d-degree 4, e. g. hydrophobic versus hydrophilic directions in Glu, and the axis of the peptide bindings, secondarily polarized in + and -, $NH3^+$ and COO-, a polarization in the property charge.

Atoms direct the space.

It should be possible to regard them as micro-codes for dimension chains, therewith also for biochemical processes on superposed levels: codes similar to the genes in DNA for the proteins of cells, although of a more directly involved character.

And different levels within the atoms should act on different superposed levels in the chemical processes via the orbitals as "field lines" in the environment?

10. The coding language on the chemical level is also an angle language. Compare for instance sp-hybridizations, boat- and chair forms of carbon rings etc. One may wonder if perhaps within the atom as "autonomous" a dimensional process is going on as a kind of "standing wave", then through the angle steps in repetition.

The magnetic poles of the Earth reverse now and then, a "pole exchange". Then perhaps the magnetic coordinate axes in atoms do the same? Of the same obscure reason. With the result that bonds get broken. (Perhaps an answer to why substances age, break down, have to be renewed?)

If there is a connection between mass and angles, perhaps mass numbers - and valences - not unambiguously are integers (in number of u or e-). Binding capacity or potential could lie between integers and this become a factor in the force driving chemical processes. (Also to regard as a consequence of the assumed secondary development of new dimension chains in steps of the first one. Cf. fractals.)

11. In the parts about physics here it's suggested that we have a kind of polarity matter - antimatter on all levels. Then L/D-forms of amino acids would be one example on the molecular level. (Fungi and eventually some bacteria contain both forms, so it's said, but all higher organisms only the L-forms.) This would be one example of increasing unidirection in the development towards lower d-degrees and superposed levels.

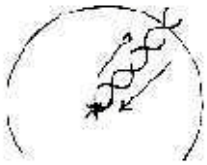
Perhaps, mentioned only as a speculation, the D-form of amino acid tetrahedrons in its elementary form exists as part or interval structure within DNA, as the complementary picture, its "negative" - regarded from a certain angle in the DNA-helix? Analogous then to the hypotheses (some decades ago) about a p --- anti-p-relation in the centre of atomic nuclei. (Cf. a pyrimidine ring as ring structure, in relation to two B-chains of an amino acid as a zigzag-way in the ring: C-C-N.)

12. Many amino acids and some nucleic acids too can spontaneously be formed in a soup of smaller molecules with the supply of energy in some form (*Miller* 1953 and many subsequent experiments). One may then imagine that the lightning or the other energy supplied defines a centre, that is a 0-pole as the condition for a dimensional development according to primary laws: a centre equivalent with a pole of d-degree 5. Or that it defines the main axis in a dimensional chain which also represents the energy steps?

Processes:

13. A general aspect on biochemical processes is to regard them as efforts by a fragmented matter to recreate entireties - and at the same time solve number demands of dimension chains (probably with different types of mathematics in different d-degrees).

The metabolism of the cell, its energy transports, copying processes, feedback mechanisms etc. should according to the hypotheses here be possible to describe as dimension chains through all levels from the elementary particle level to the cell level, to and fro, out- and inwards, in a certain similarity with standing waves.



14. With a Time aspect, we could adopt the description that what is "quantum jump" happenings on an underlying level, more and more develops in time toward superposed levels to increasingly more of processes in several steps.

That which in the centre of an atom eventually may be called a "pole exchange" or an inversion, can on a biochemical level have developed to a long process (while other "jumps" still may be more as jumps, not yet have had the time to a secondary development in many steps)?

Perhaps one example is the move of one oxygen atom from one end to the other in the aldehyde part of fructose: a process in about 10 steps in the glycolysis (from Glycerin-aldehyde to Pyruvate).

(Even if the cell chemistry seems fully developed from "the beginning", it may have taken some important seconds, equivalent with the creation of a material Universe after Big Bang.)

Interpreting processes as a fragmentation into several steps, it could also motivate a summation of the stages as in opposite direction, with exclusion of the Time axis.

Different stages - in simultaneous existence - becomes also free actors in different other processes.

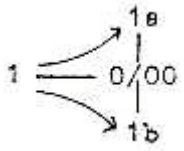
15. Further, it has been assumed in this model that there is a gradual substantiation of the last steps in a dimension chain through counterdirection from other units. This could be one way to regard the covalent bonds, where atoms (as 0-poles) with their free valences as virtual lines or field lines are saturated with corresponding "field lines" from other atoms and chains as linear and get bound to surfaces and further to volumes through folding.

The chemical principle *addition* (through condensation of similar units to "linear" chains) may generally be regarded as such a substantiation of the 1st d-degree on a superposed macromolecule level. Carbohydrate chains as n x glucose is one example, protein synthesis another.

These additions could probably be interpreted as expressions on the biochemical level for longitudinal waves on the level of physics.

Other additional processes are in reality summation of different stages of "the same" substance, as Acetyl~ and Malonyl~ in the fatty acid synthesis. (See Fatty acids.)

16. In the biochemical processes the wanderings or migrations of 2H are central.
The last step in a dimension chain, 1 →0/00, as a polarization into poles 1a/1b gives the sum of poles 2, 2 "E" as a potential value in the d-degree of Motions, the processes.
This according to our assumptions in the model.



In each step outwards 2 E are debranched, corresponding with the 2H-migration.
(Cf. the way to write NADPH+H: indicating a difference between the 2 H, as between poles 1a and 1b, or roles of poles 0 and 00 in d-degree 0/00.

On the elementary geometrical level the poles 1a and 1b represent virtual (haploid) lines - presumably for catching and aggregating from the environment. Representing possible connections with other dimension chains.

17. "Activating" of a substance, a molecule, could hypothetically be interpreted as a displacement half a step, corresponding to 1/2 dimension degree (perhaps from a pole to

the main axis) or between interval and border in the dimension chain, (towards a binding or polarizing centre). The activation implies reasonably also a displacement of charge within the molecule - perhaps analogous with the depolarization in a nerve cell which releases a nervous signal when charge over the cell membrane becomes zero.

18. A consequence of the dimension model could be that also processes as motional patterns, as structures, could appear as 1-2-3-4-dimensional.

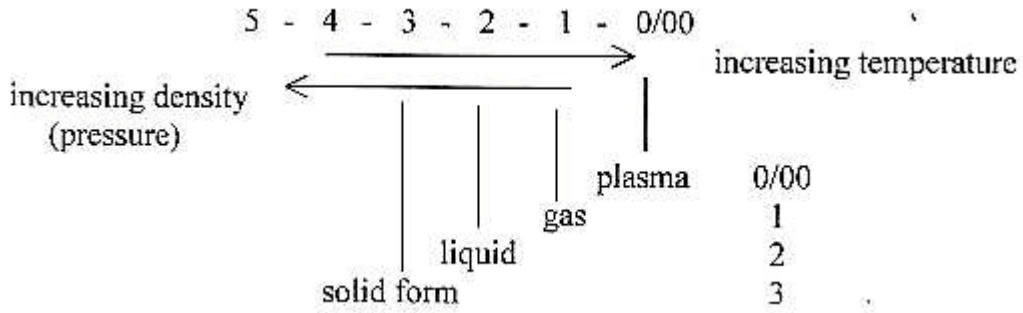
It would be possible then to have "linear" processes and cyclic ones, rotating processes (as that in the porphyrine synthesis), wavy ones (as the synthesis of fatty acids could be described), double-directed versus unidirected processes, pole exchanges (as perhaps in the move of the COO-group in Pyruvate to Malonyl~ via Acetyl~). We could also find the geometrical opposition between radial versus circular/spherical structures when processes on a macro level are studied more closely, as between glycolysis and citrate cycle.

19. Cyclic processes can be interpreted in several ways, departing from our dimension model: as an expression for rotation, appearing in d-degree step 4→3, but also as the development of the 0-pole through steps -4-3-2-1 with angle steps in the same direction, re-coupling to the start. In this respect also an expression for the 00-pole, the pole of repetition and for manyfoldness. (Cf. perhaps the respiration cycle "within" the citrate cycle. ?)

In general terms cyclic processes becomes expressions for the increasing unidirection towards lower d-degrees as towards higher levels.

1b. Phases

20. The aggregation forms of matter, its different phases, may be regarded as steps in a dimension chain:



There are the 3-dimensional crystals of minerals and the 2-dimensional, plane H2O-molecules of water for instance. Identifying gases as 1-dimensional in structure seems perhaps a bit more problematic. However, in 2-atomic gases there is just one linear relation and most gases exist in the forms of molecules. Inert gases should more correctly perhaps be described as 0-dimensional ("points"). The gas phase appears in steps 2→1→, and it's reasonable to see plasma as a phase of type 0/00, where even the elementary link between charges, protons and electrons, are broken.

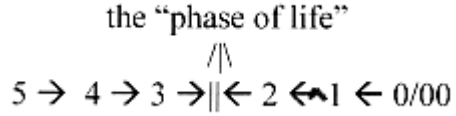
According to first aspects on our dimension model, there are in direction outwards a stepwise decreasing d-degree of structure, increasing d-degree of motions as translation of the lost d-degrees in structure. In the opposite ("synthesizing") direction, an increasing number of structure building bonds.

- Temperature = motions (as vibration, rotation, translation) as polarizing "force" from d-degree 0/00, breaking structures towards lower aggregation forms.
- Density gradients = assumed here as the "physical quantity" in d-degree step 5→4, decreasing towards lower d-degrees. (Pressure one factor.)

21. Phases corresponding to d-degrees 4 and 5?
The state of matter in neutron stars is of course another phase, but hardly of the same structural kind as the other "phases", sooner as a compressed form of plasma, the antithesis to plasma, individual neutrons without external relations, total lack of an expressed outer structure, through pressure.

A 4- (or 5)-dimensional aggregation form of matter of the structuring kind would simply oppose the definitions adopted in this model that mass (or matter) isn't defined as property before d-degree 3. The property disappears in black holes and at Big Bang there is only a mathematical point or singularity.

However, in life chemistry it seems as if we could talk about a new phase, of underlying elementary phases appearing in a new combination. Inverted to a superposed level, through d-degree step 3-2. All "phases" represented, even 4-dimensional "vector phases" as gradients of different kinds.. The plasma phase for instance appearing in photolysis, the separation of e- and H+, united again in the respiration cycle. The higher d-degrees are of course inherent in mass.



Using the term "phase" here is of course only one way to look at the creation of structures.

The co-ordination of processes to serve the unit as a whole implies or looks like building 4-3-2-1-0-dimensional structures of pure motions as "building stones". (Perhaps, regarding the dimension chain of motions, counterdirected to that of structure and with our simple assumption that number of motion moments agree with lost d-degrees in structure, it would be possible to identify 15 elementary kinds of motions in a cell?) In any case the number of motional moments would increase on superposed levels.*

[*About motion moments in different aggregation forms on the elementary non-life level: The hypothesis that lost d-degrees in structure should be looked for and found in external motions may often seem too primitive even if well-founded, when looking to type and number of motions. Yet it may perhaps throw light upon some behaviour of matter in the different aggregation forms:
- Solids: There is of course no 2-dimensional motion of "rotation" in parts of solid matter on earth - as the rotation of celestial bodies and atomic nucleons in macro- and microcosm. But growth of crystals with new layers of surfaces - and oscillations in lattices.
- Liquids: Through surface tension creeping by capillarity; liquid Helium creeping 3-dimensionally over all surfaces… Other 3-dimensional streams in liquids have been detected and studied.
- Gases: The different, well studied motional moments of 1-2-atomic gases: vibration, rotation and translation in 3 dimensions…Expansion and contraction (as it seems in celestial hydrogen clouds)…
- Plasmas: In the behaviour of plasmas it sounds quite possible to identify motions in 5 dimensions according to fusion research: spiralling, pumping, elevation anti-gravitationally, pole turning etc.]

*

2. Chemical bonds

The chemists talk about 5-6 types of chemical bonds, 5 within the organic chemistry plus the "metal bonds" within the inorganic one:

- Metal bonds

- Covalent bonds (electron pair bonds)
- Methyl bonds (hydrophobic bonds)
- Ion bonds
- Dipole bonds (hydrogen bonds)
- van der Waals bonds

Is there anything besides the number of them which indicates that these type of bonds or chemical "forces" in their schoolbook formulations could correlate with a dimension chain?

Any such unambiguous identification seems difficult to find (as when it regards the known 4 forces of physics). Yet, here some aspects in that direction:

All chemical bonds are said to be manifestations of the electromagnetic force of physics, perhaps while that is the only force scientists have the feeling they almost fully understand?

According to the general postulates in our dimension model underlying levels are to interpret as binding forces on superposed ones as higher d-degrees in relation to lower ones. This implies that all forces of elementary physics should be involved as complex components on the chemical level even if only the electromagnetic one is mentioned.

Any closer explanation of the hydrophobic bonds is not given in here used sources, and it's said that the covalent bonds are not "fully explained" either.

Concerning the nuclear force it was said some decades ago that it seemed to include both gravitational, inertial like components and electromagnetic potentials. The theories and views have changed since then, but still it's said for instance that the nuclear force may be totally analyzable in spin-spin- and pathway dependencies. From the viewpoint of our model this just means that "forces" as a concept for d-degree 4 are translated into lower d-degrees - into mass, charges and linear relations and in a general sense may be expected to appear in molecular interactions.

Even Mass becomes a force with this view.

$\mathbf{H^+}$ and $\mathbf{e^-}$ as elementary particles on the underlying level, become forces - and very central ones - on the chemical level and should be identified and regarded as such, mediators as they are in most chemical bonds. They become counterparts to π-mesons and other quanta of forces which the physicists call "carriers of forces".

In physics the distinction is made between polar and non polar forces, between the electromagnetic force and the weak force as polar ones, gravitation and nuclear force as non polar The same contradiction appears among the chemical bonds:

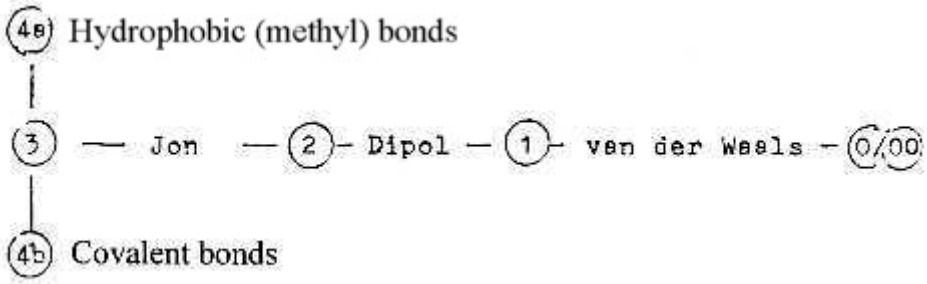
Hydrophobic bonds become of the type +/+ between CH3-groups for instance, where the "plus sides" of the H-atoms are turned towards each other: that's "methyl bonds".

Covalent bonds are of the -/- type, electron pairing as essential feature. Hence, both these types are non polar from the viewpoint of charge.

On the other hand ion, dipole and van der Waals bonds are all three polar, built upon

the attraction between opposite charges.

Here a first sketched suggestion of how to look at relations to the dimension chain:



Hydrophobic← →Covalent bonds (4a --- 4b):

It should be underscored that none of these bonds are fully understood which may imply that other forces than the electromagnetic one (EM) are involved. In the model here we have assumed the EM-force developing first in step 3→2 in a dimension chain of forces (see that file in Physics).

As (-/-)-bonds the covalent electron pairing bonds may be regarded as complementary to the the nuclear force between protons in the atomic nucleus, which translated to the superposed molecular level gets expressed in hydrophobic bonds, type (+/+).

Compare the covalent bonds, "explained" with the octet rule on one hand (more about this below) and on the other the number 8 in the nuclear force: according to older views on this strong force one could find three times 8-9 potentials in it. And the strength of that force is roughly said developed first at 8 Z (with about 7,6 MeV per nucleon.) Even if maximum is reached first at 26-28 Z.

(Are there eventually virtual positrons in the electron pairing bonds, as one have speculated about virtual anti-protons in the depth of atomic nuclei? Virtual positrons out of the negative energy of empty space?

If so it would be in accordance with the here adopted general aspect: the stepwise building-in of the opposite pole, the 00-pole, on different levels.)

The relation between the two types of bonds becomes that between outward and inward directions, from 0-pole and 00-pole respectively: the covalent bonds outwards the surface, the electron shells, and the hydrophobic bonds inwards, analogous to protons inwards the atomic nuclei.

(Hydrophobic bonds may also be regarded as consequence of the covalent ones, developed from them, as there is always an anticenter (~ a 00-pole) for a unit as 0-pole, in the same sense that the 00-pole represents the end of a haploid dimension chain in relation to the 0-pole as start, and represents lower d-degrees and levels in relation to higher ones.)

Both types of bonds may be characterized as mutually counterdirected, cf. d-degree 4 as double direction, while bonds of the ion and dipole types gets rectified:

The electron pairs in the covalent bonds have opposite = counterdirected spin. Cf. double direction in d-degree 4 and increasing unidirection towards lower d-degrees according general views in our model.

Hence, in these both forces or bonds we find features of the "FA" and "FG"-forces from the physical level, FA as the outward acceleration force, FG as Gravitation.

General definitions in the dimension model say that the 0-pole represents first binding, integrating force, the 00-pole the primary polarizing one, but in d-degree 3 turned to circular geometry becomes an "aggregating" one. It's easy to state as a fact that covalent bonds are integrating, the outward opposite directions leading to bonds building bigger and bigger molecules and increasing order towards superposed levels. It's the foundation of life chemistry, the shared lack of completeness.

How a hydrophobic "force" primarily may act as polarizing in a cell, is here left as an open question. (Maybe the methylation, marking inward direction, of positions in genes should be studied from this aspect?) Yet, like gravitation it appears as aggregating on a weaker, superposed level.

The results of these forces could be seen as expressed in next step, the poles of d-degree 3, proposed as radial versus circular in elementary geometrical terms: The covalent bonds may be regarded as radial in their main valences. The hydrophobic bonds are described by chemists as if they had "circular structure", that's with feature from the 00-pole, the anticentre pole. They are demarcating a "sphere" within which water is driven out; the non polar methyl groups repelling the polar water molecules. (One may after all ask why?)

The hydrophobic bonds are also central for the building of cell membranes - a "circular" structure, shell creating, related to d-degree 2 of surfaces.

Cell membranes could perhaps be regarded as expression for the nuclear force on this superposed level, (inverted to anticenter or expanded).

Mass ←→Space, the complementary concepts regarded as the poles in terms of physical entities in d-degree 3 in our model can also be one aspect on the relation between hydrophobic and covalent bonds: Mass is on the atomic level connected with the nuclei and *protons* (H) and may as an expression for gravitation appear in the hydrophobic aggregations which have got the name of "bonds".

The covalent bond are built on *electrons*, most closely related to Vacant Space and outward acceleration, the complementary force to gravitation (see interpretations in Physics). The covalent bonds may be regarded as the essential space-building ones.

Covalent bonds - some more aspects:

Covalent bound molecules are more mobile than metals and salts. In outward direction the number of motion moments increases towards lower d-degrees and higher levels. And the level development - eventually through counterdirection from other units outside - gives increasing degrees of freedom (as for instance in the OH-groups of carbohydrates). Life as motion.

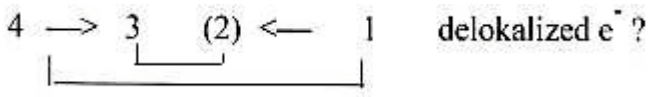
The covalent bonds develop outwards toward lower d-degrees as in -4→3→ 2→1- steps in several ways:

- Molecules get ionized - that is polarized in charge, a kind of parallel to the ion bonds in what could be seen as a secondary developed d-degree chain within covalent bonds.

- The bonds get differentiated into main valences and side bonds, in ∑- and π-bonds, a structural relation of 180° to 90° between overlapping orbits which implies coordinate

axes corresponding to a d-degree step 4 →3 in a dimension chain interpreted in terms of angle steps.

- The development from sp3 to sp2-hybridization (as in diamond in relation to graphite), from 4 bonds around a C-atom to 3 with delocalization of 1 electron, implies a step from 3-dimensional spherical structures to 2-dimensional plane ones: a step towards lower d-degrees which also implies more motion moments.



(The step from sp3- to sp2-hybridization has been regarded as a condition for life.)

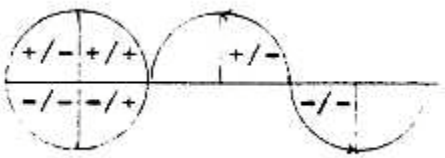
The covalent bonds become increasingly unidirected - as through angle steps - towards lower valence numbers as in the atomic sequence C → N → O with valences 4 - 3 - 2. The molecules get more and more of a dipole character, a development which becomes a condition for the dipole bonds.

Ion, Dipole, van der Waals bonds:

These bonds are explained by the electromagnetic force between charges plus and minus but a condition for the ion bonds is the octet rule behind the covalent bonds which isn't explained by this electromagnetic force.

Ion bonds (3 -- 2):

There is a gradual changeover between ***covalent bonds*** and ***ion bonds*** according the Pauling's curve for the electronegativity of atoms, between bonds of dominant covalent character and those of dominant ion character. This curve has however an inflexion point which may be interpreted as a border, representing a structural change of dimensional character. (Cf. a sinus curve as projection of a rotating vector in a unity circle:



Ion bonds have traits of both the metal bonds and the covalent ones, both inward and outward directions. (Cf. poles 4a--4b of d-degree 3.)

In typical ion bonds as salt crystals for instance the structure building extension is principally unlimited as in metals, in opposition to the "individual level" of covalent bound molecules and differentiation in structures. In this sense the ion bonds are characterized by continuum in relation to the feature of quantum jumps of covalent bonds - an opposition continuum - quantified which we have seen as one aspect on the poles 0 and 00 (part Physics).

However, the ion bonds in opposition to metal bonds are quantified in steps +/-/+/-/+/-. polarized in charge. But the transition of electrons from metals to non metals, creating the charged ions, is totally dependant on the octet rule.

In which sense 3-2-dimensional? Ion bonds build 3-dimensional regular space structures, volumes as in salt crystals, and grows "spherically", with addition of layers (d-degree 2).

Polarizations of Charge:
With the model of a dimension chain through polarizations it becomes natural that also charge as property and physical quantity gets polarized further from units of +/-. On the atomic level the *d*-orbital for instance have been illustrated as with single electrons divided on the half axis around the origin in the coordinate system. With polarizations as the basis for distribution of charge this should principally be quantified and possible to express as a series of the type e →1/2 e →1/4 e… or e^2 →e → √e, with the electron as a wave function or the like and secondarily still more complex divisions on a molecular level. (See further files *Chemical Elements*.)

"Activation" of molecules within biology may be assumed as more or less partial displacements of charge - as partial or "half steps" from border to interval or the inverse, also here regarded as the basis for the concept discontinuity.

In ion bonds one can talk about whole charge transitions, in dipole bonds of half or partial ones as of the H-atoms in H-bridges. Hence, in a step from ion bonds to dipole bonds we have a polarization step outwards in the dimension chain.

Chemists talk about "delta charges" in connection with *dipole bonds*.

Dipole and van der Waals bonds (2 → 1 → 0/00):

The dipole bonds may be regarded as developed from the covalent bonds when small molecules become more and more polar towards lower valence numbers of atoms as C, N, O (suggested to be read as d-degrees).

While ion bonds create solid volumes of aggregation, the H-bridges are unidirectional and linear and bind molecular chains to one another, laterally as in the H-bridges of DNA and between protein chains, creating "ladder" structures and layers.

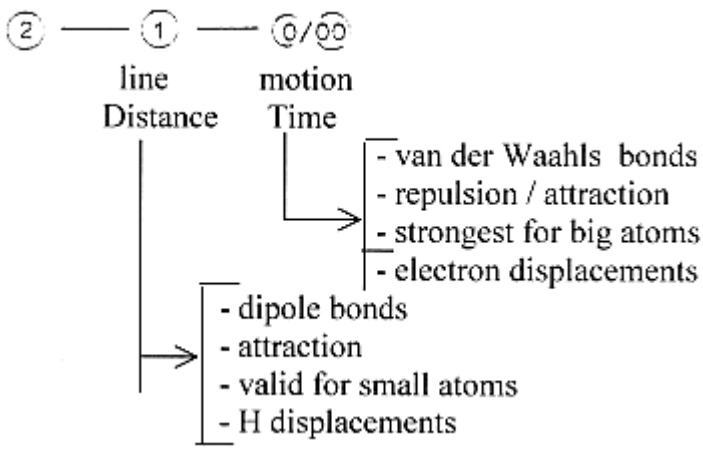
Hence, they can be connected with d-degree step 2 - 1, also with regard to the structures they create.

The dipole bonds between H2O-molecules in water render the water molecules the flat form - a reason to identify the phase of liquids as of d-degree 2.

Distance and Time
This pair of concepts may be applied to the dipole bonds in relation to van der Waals: .

Dipole bonds,
- out of unsymmetrical distribution of charge in space,
- linearly:
- entity: Distance.

van der Waals bonds,
- out of "unsymmetrical" distribution of charge in Time.
In dimension steps:



van der Waals bonds:

These bonds depend on the rotation of the electrons, derive from "induced dipoles" or "temporary dipoles", represent time-dependant couplings.

The poles 1a and 1b of d-degree 0/00 in our dimension model have been defined as "motions towards each other" and "motions from each other" respectively. Expressed in terms of charge that's attraction and repulsion. Both moments are included and alternate in van der Waals bonds.

The bond as a "line" between the atoms is polarized in these motions to and fro as in a dimension step 1 →1a/1b. Change of signs are also included in this type of bonds according to the chemists. Compare the description in our model: motions towards each other, derived ultimately from inward direction in d-degree 4, defines a new centre, a new 0-pole and therewith outward direction. While "motions from each other", ultimately derived from the 00-pole and outward direction in d-degree 4, defines a new anticentre and therewith new inward direction. This implies a sign exchange as direction change in terms of the dimension model.

The van der Waals force is generally prevalent between atoms and molecules close to each other. Hence, in this force an aggregating multidirectional force seems to turn up again and it would perhaps be possible to identify a gravitational component of inward direction in this force. Primary poles of d-degree 4 "meet again" in d-degree 0/00, which makes it reasonable that the force of d-degree 4a (inward direction and the pole of manyfoldness) reappears at the end of the chain of charge polarizations.

Like the gravitational force in microcosm, the van der Waals force is also very weak.

With the assumption that all forces on the physical level should reappear in some form on the biochemical one, the question may arise how the weak interaction could manifest itself in biochemistry? May it be found somewhere in the development of the covalent bonds towards biological levels, perhaps as interaction between levels? Or as a factor in the spiralling of nucleotides and proteins? Or just as one cause for the curious fact that proteins are broken down and have to be built up again all the time? (This some vague speculations.)

The octet rule:

Covalent bonds depend on what is called the "octet rule" and are usually explained as the "endeavour" of the atoms to reach filled *s*- and *p*-orbitals towards the environment, 8 electrons as the border for a whole shell.

This octet rule goes beyond what is explained by the electromagnetic force which implies balance between protons in the nucleus of an atom and number of electrons in the shell.

With a more general aspect we could imagine the atom alternate between two roles, as an entirety in itself, a relative 5-dimensional whole, in proton-electron-balance, and its other role as part in the entirety, a 0-pole in relation to its surroundings. This in the same way as human beings alternate between states of sleep, closed in themselves as entireties, and states of being awake, the role of being parts in relation to the surrounding world.

Number 8 - some interpretations from the viewpoint of our dimension model:

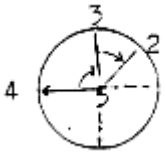
- In the $2x^2$-series behind the periodic system from which whole shells and orbitals can be derived, we have number 8 in d-degree 2.

	5		4		3		②		1		0
$2x^2$:	50	--	32	--	18	--	8	--	2	--	0
							|		|		
							6		2		
				orbitals :			p		s		

D-degree 2 represent surfaces, the demarcation of a unit from the surrounding, a shell.

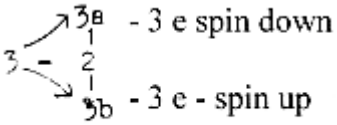
- In the 2^x-series, which hypothetically has been assumed valid in direction inwards, we have after 3 polarizations (from 0/00) number 8 at d-degree 3
- In a 3-dimensional coordinate system there are 8 space quadrants: The number 8 could be traced back to the 3rd d-degree of space.
  (The coordinate system is also defined through 6 outer poles, and with the polarity "origin versus anticentre", represented by the s-orbital, added it gives number 8.)

- In angle steps 360°→180° → 90° → 45°, a circle is divided in 8 parts.



- Another aspect: In our model we have assumed that Charge as such is a property (the physical quantity) defined in d-degree 2 in relation to mass analysed as 3-dimensional. Here at d-degree 2 this property of Charge would possibly appear as still unpolarized. In this sense "complete".

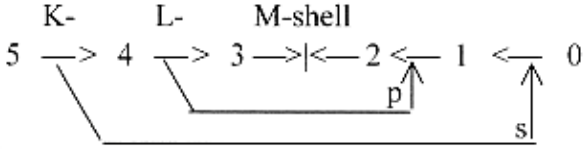
- In a dimension chain the outer poles of d-degree 2 is 3a and 3b. Compare perhaps what becomes the 6 electrons divided in 3 + 3 with opposite spin in the p-orbital.



|_ read as 2 + 6 ?

- Outer poles of d-degree 3 is 4a 4b, representing the opposite vectors of d-degree 4 on an underlying level. Sum of poles = 8. In this way we can trace the octet rule back to d-degree step 4→ 3 according to our suggested views on covalent bonds above.

- The "loop version" of our dimension model implies that orbitals in steps 0/00-1 and 1-2 (*s* and *p* orbitals) are regarded as debranched from higher steps outwards, and the opposite directions in the chain meeting in step 3--2:



We have *s*- and *p*-orbitals as debranched from inner shells and remember that H belongs to the K-shell, C, N and O belong to the L-shell, P and S to the M-shell.
(More about the octet rule in files Chemical Elements.)

Metal bonds - in inorganic chemistry:

How interpret the inorganic metal bonds in this suggested scheme?

a. They may be regarded as the *collective* correspondence to an *individual* atom with protons assembled in the centre, electrons "displaced" to a shell. Delocalized electrons described as uniting "clouds" around the positively charged metal ions.
The polarity *individual - collective* has the feature of 0- and 00-poles, defining d-degree 4.
Generally the 00-pole represent manyfoldness and anticentre in relation to centre. It's the source for inward direction. This vector aspect could be one factor in the metal bonds where the atoms get closer to one another: the ionizations and delocalization of outer electrons as a means or a result.
The common cloud of electrons is said to act "uniting" on a collective atomic level, but such an explanation is hardly convincing. Why do the electrons get delocalized - and in which sense do they appear as clouds? Is there really reason to interpret the metal bonds as purely an expression of the electromagnetic force?

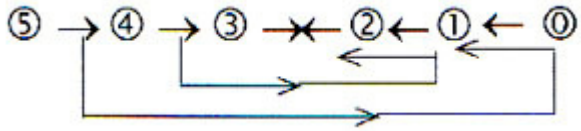
b. Metals dominate more and more toward heavier elements and all elements in higher orbitals as *d* and *f* . In atoms Mass is concentrated to the nuclei and Mass is connected with gravitation, the FG-force; electrons in the shell are closest to Vacant Space, connected with the FA-force. We could in this respect connect the metal bonds with the gravitational force. The growing number of neutrons in heavier elements emphasizes also the Mass property of nuclei. Hence, in metal bonds one factor could be an example of Mass as binding force in relation to lower d-degrees as Charge, interpreted as of d-degree 2, a factor which should be part of the interpretation.

c. Metal bonds have similarities with other bonds as if they represented the collective complementary poles to bonds developed from individual atoms:

- With hydrophobic bonds, in its non polar type, its aggregation of similar atoms with a relative surplus of electrons and in the gathering of plus-charges and "driving out" of electrons, as hydrophobic bonds drive out water. But the hydrophobic bonds develop from covalent bonds on an individual level.

- With ion bonds in building solid structures and in the aggregating type, characterized by continuum like ion bonds in salts but in opposition to these not quantified with respect to charge. Here the ion bond has the individualized crystal structure of +/- variations, possible to regard as radial in relation to metallic bonds with their "spherical" (?) clouds. (Poles of d-degree 3.)

- With dipole bonds in the character of layers which the delocalized electrons give metals, surface layers that may glide over one another. A corresponding form in the development of individual covalent bonds is what is explained through the term sp^2-hybridizations, with "delocalized" common electrons giving plane molecular structures.
Again we remind of the coupling between d-degree step 4→3 and the step 2 → 1 in the loop version of a dimension chain in our model.



- Finally, there are a certain relationship with the plasma phase in the mobility of the delocalized electrons. With the plasma phase as the ultimate separation of protons and electrons interpreted as the phase in d-degree 0/00, we get the connection between the outer poles of d-degree 4, 0 and 00, combined in last d-degree" 0/00" of motions.

In the "haploid" version of a dimension chain the pole 0 represent 5 and pole 00 the d-degree 0/00.

Hence, we could in a certain sense regard the development of phases and types of chemical bonds as occurring between the individual and covalent type outwards and the metal bonds inwards.

Some kind or kinds of metals should be an essential factor in the development of life structures - as they surely are!.

Connections between bond types and phases:

	Solids	Liquid	Gases	Plasma
5 - 4 -	3 -	2 -	1 -	0/00
Metal b.	Ion b	Dipol b.	van der W. b. .	
Covalent b.				

Above has been pointed to the connection between bond types and phases: Ion bonds in salts the solid phase, dipole bonds with the liquid phase of water. The van der Waals bonds could be connected with a gas phase if "induced dipoles" or its time-dependant combination of attraction and repulsion is translated into the more mechanical collisions (to and fro) between atoms or molecules of gases.

Some more general annotations about chemical bonds:

From the viewpoint of an atom, the bond to other atoms can be described as a centre displacement 0 → 00 (becoming a new centre 0'), from centre of the atom to the centre of the bond on its circumference - a virtual place for insertions from outside. Overlapping orbitals (counter directed = of the same sign) define a new centre.

However, the bonds may be imagined as derivations from a field level underlying the atomic level of chemical elements:
a) fragmentation - polarizations,
b) bonds "the other way around". (Most elements exist in nature as molecules at lower temperatures.)

From this aspect orbital centra could be regarded as the basic structures which orientate the atoms. Compare the precipitation of amino acids from mixtures of smaller molecules.

Release of energy at creation of bonds could be interpreted as (partial) depolarizations - a return to a higher d-degree.

[The molecule or the chemical compound could be compared to a linguistic phrase: The development of an underlying unit, in languages = the "sense", regarded as stepwise

polarizations into directions, words for directions, verbs for actions or processes, nouns and qualities…]

Assuming a development from fields to mass to particles representing charge etc. through polarizations, inversions, angle steps, then one branch of the fields may be thought of as expressed in the coordinate axes of the atom, as drawings in the surroundings, in the negative energy of "vacant space". The other branch, that from the 00-pole, imagined as meeting "the other way around", from outside, as potential counterdirections ...

...
[The reactive rope ends of molecules are called radicals, a word which originates from the word "root".]

*

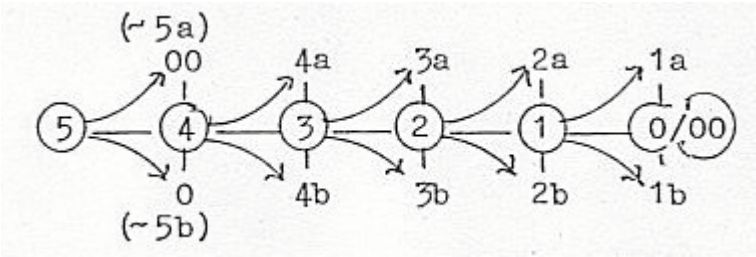
3. Protein synthesis

- Why does it look like this? –

From DNA to protein chains - some general aspects

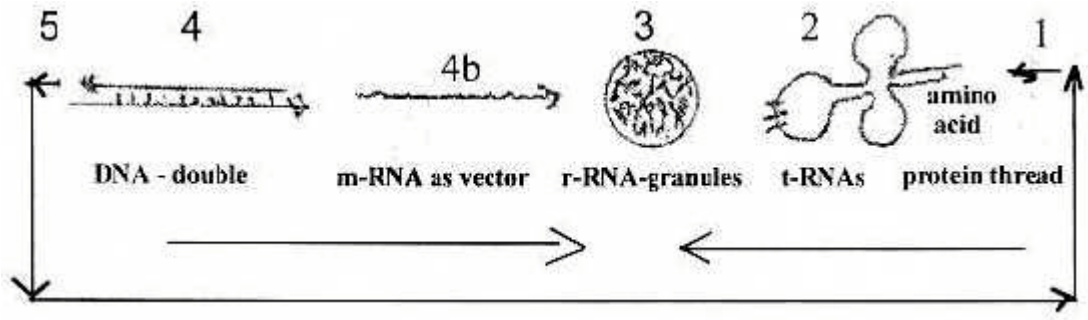
At this high, very complicated level there are some remarkable simple features, which seem to illustrate a dimension chain of the kind suggested in the pages about physics:

Dimensional development from D5 to D"0/00" in the model:



There are about 5 steps in the process:
from DNA→ mRNA → rRNA →tRNA →single amino acid → peptide chains.

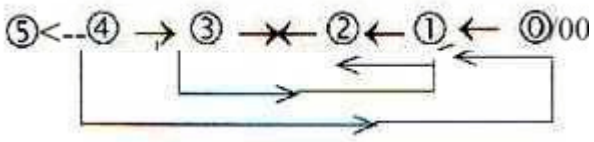
Dimensional geometrical forms in the protein synthesis regarded on a macro-scale:



Dimension degrees (d-degrees or Dx) shortly:
4 - DNA: double-direction, double strands, opposite directed "vectors" united,
4b - mRNA, the outward directed"pole" of d-degree 4, with vector character,
3 - rRNA, the ribosomes, as "balls", volumes,
2 - tRNA, as "plane" forms ("clover leaf" forms) on a macro-level.

In these forms, it's also possible to see the one of higher d-degree as binding force in relation to the one of lower degree in accordance with the model: mRNA binding (or attracting) ribosomes, ribosomes binding tRNAs, tRNAs binding their special amino acid.

The loop model of a dimension chain, where debranched degrees in first outward steps "meet the other way around":



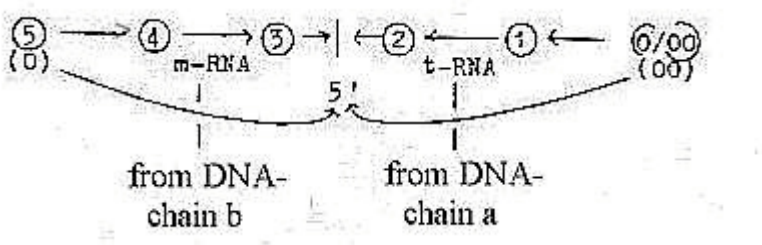
The 5-dimensional chain could be interpreted as double-directed from, 5→4→3 →etc. and "the other way around" from 5 to 0/00 and inwards

D4. We have the **double DNA-spiral** in the central nucleus of the cell, a double-directed chain, as a vectors of opposite directions, primarily in the model defined as outward/inward directions of d-degree 4, with bonds between complementary code bases A--T, G--C. These pairs may on this underlying level be regarded as expressions for the outer poles "0 - 00" in d-degree 4. (About the complementary character see here.)

D4b -3:The double chain gets "polarized", the chains separate - and one gets copied through counterdirection from the manifold of single code bases in the surrounding (as anticentre") to **mRNA,** pole 4b of polarized d-degree 4. As a single stranded vector it acts like an outward directed force when moving outwards to the cytoplasm to the ribosomes located between the "centre and the anticenter" of the cell, between the nucleus and cell wall.

Cutting of the mRNA, implying loops, may on this macro-level be regarded as an geometrical illustration of the step 4 → 3 with partly circular forms.

D3-2: **rRNA,** the **ribosomes**, have the 3-dimensional form of small spherical balls where the mRNA gets attached, however also divided in two parts as in a step 3 --2. and consisting of both nucleotides and proteins.



Here the meeting between tRNA and rRNA occurs (at right angles, of natural reasons, but compare the assumed angle 90° in d-degree 3 in the model).

D2-1: **tRNAs, transferRNAs**, are usually described with the form of "cloverleaves", principally as such "plane" structures, partly loops, partly linear, as 2-1-dimensional forms on a macro-scale; the wavy form (convex/concave as poles of d-degree 2) are also in the model connected with the lower d-degrees.

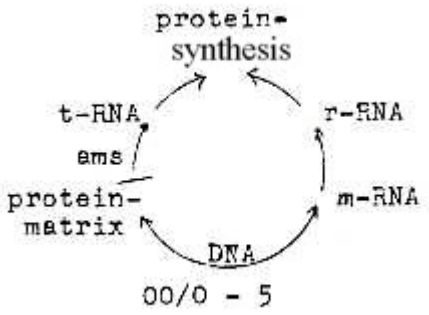
These shorter chains of nucleotides, different for different amino acids, represent a manifold as each lower dimension degree is a manifold in relation to the higher d-degree. In the middle of the central loop the anti-codon for a certain amino acid is located.

The anti-codons of tRNAs represent the complementary strand to mRNA, the 00-pole with inward direction, meeting here in the middle step 3→2 of the chain.

D1-0/00:
In the opposite end of the tRNA, at the linear end (bases A-C-C which is similar in all tRNAs), the individual amino acid gets attached.

Then the similar parts of the amino acids, here called the "B-chains", get bound through condensation to protein chains.

In this sketch of the process the amino acids (ams) come perhaps to represent the first 00-pole, meeting "the other way around", while nucleotides of RNA represent the 0-pole. DNA-nucleotides + Amino acids as primary poles of a d-degree 5?



00-pole ~ multitude of separate units

Hypothezised is the start in a "whole" made up of DNA or RNA nucleotides and amino acids combined. A similar direct combination is part of one of the many theories among scientists trying to explain the genetic code. Within the "poles" of this assumed unit, when polarized, the protein synthesis develops.

Some single amino acids take an essential part in the synthesis of the codon bases.

Counterdirections in the process and the relation mRNA - tRNA:

The difference between T- and U-bases represent the opposite directions:

T-base the inward direction towards the DNA-strands when not activated. It's replaced by the U-base when a DNA-strand is copied to mRNA (outward direction) in the synthesis.

The only difference is a CH3-group in the T-base, obviously the chemical expression for inward direction. (Cf. hydrophobic bonds.)

Many bases in tRNA have got this group added too, as a fundamental chemical sign for "inwards" (+ 14 A).

Coordinate axes of the DNA-spiral:

Counting in the first place on three coordinate axes, the first main axis may be regarded as the one along the base pairing H-bonds: inwards toward the H-bonds / outwards at copying. An axis of type d-degree 4 as from a step 5 →4.

Nucleotide pair, e.g. A-T-bases

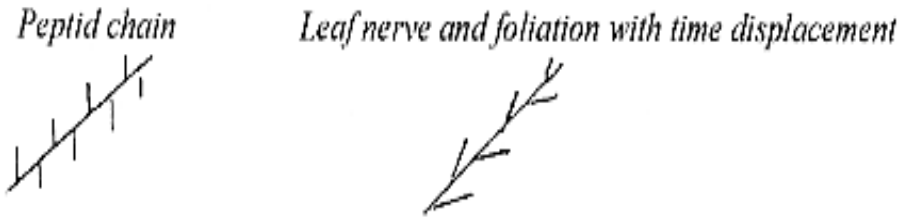
P-group—deoxiribose—base/R....H ..l. . R—base—(deoxi)ribose—P-group
----------> <----------
↓
<----------
outwards towards nucleotides as separate units, e. g. AMP...

[Somewhere in the "potential groups" in the H-bonds (*Löwdin*) would perhaps the d-degree 5 be found, a representation of "the whole". (!)

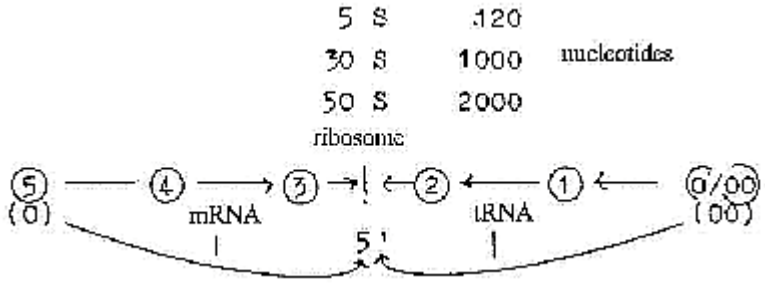
Second axis will be the one along along the strands, representing a d-degree step 4 →3. Secondary H-bonds along the individual strands curve the strands into helix structures, as we in the step 4→ 3 in the model get a transformation toward circular structures and rotation.

The third axis, as a *z*-axis, should reasonably be expressed in the relation between mRNA and tRNAs in step 3 → 2 (or more elementary, perhaps originally in the evolution of the genetic code?) between RNA-nucleotides and proteins or singular amino acids. (Examples of close relations: Basic amino acids among others are His and Arg. His derives from the A-base. Arg's R-group derives from the G-base. Compare the proteins "histones" on which the DNA-spiral gets rolled up in steps of storage.)

In addition; the opposite directions of side-chains of the amino acids in the protein chains could eventually be regarded as a forth coordinate axis:



rRNA - ribosomes:
More details:



Sketch of a dimensional interpretation:

- We can note the locality of the small "spheres" on the "endoplasmatic reticulum", a structure of membranes in cytoplasm - 3-dimensional forms on 2-dimensional surfaces and, as said above, in "the middle" between the poles centre - anticentre of the cell. rRNA is produced in nucleoli, also a spherical organelle.

- It is said that "groups of 5 or 6 individual ribosomes are held together" by a molecule of mRNA. Why just 5-6? As a number determined by the dimensions in the model.
  It's said too that bacteria has 5 ribosomes! Why exactly 5?

- We can also note that ribosomes are made up of two parts (50 S and 30 S) with a mass relation 2/1: "50 S" and "30 S": 1,1 x 10E-6 u and 0,55 x 10E-6 u,

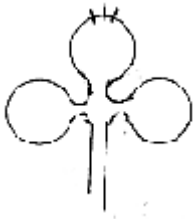
- Still another thing about numbers:
Ribosomes consist of **about 40 - 60 %** RNA, **60 - 40 %** proteins, a 3-2- or 2-3 relation
  Another reference says the relation is 64 % RNA, 36 % protein: That would be a relation 8^2 - 6^2 : compare "E-numbers" as sum of poles in d-degrees 3-2 squared, in d-degree 3 = 8, in d-degree 2 = 6.

- How to look at the fact that the ribosomes only act as a kind of enzymes, a meeting place for mRNA and tRNA and not are involved in themselves? Doesn't this fact contradicts the general, suggested interpretation here in terms of the dimension model?
  The ribosomes with their close combination of proteins (amino acids) and bases

(nucleotides) seem to illustrate - on a secondary level - the "whole" hypothezised at start. The poles from polarized d-degree 5 meet in the middle of the chain. Hence appear as a secondary evolution of the underlying whole and as representing a superposed level "detached" to a solely enzymatic function?

tRNA:
More details.

1. Forms of tRNAs on the macro-scale resemble the 2-dimensional "clover leafs" with 1-dimensional (partly paired) end chains and illustrate the geometries convex - concave of poles 2a /2b suggested in the model.

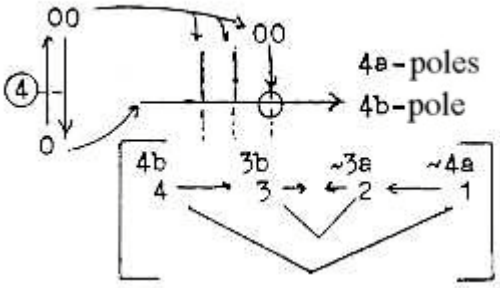


2. tRNAs represent a coordinate axis at straight angle to the the RNA strand - of natural reasons of course but illustrating the angle of 90° assumed in d-degree 3.
Further the tRNAs represent a **multitude** in relation to the mRNA-chain, a relation connected with poles 00 versus 0.

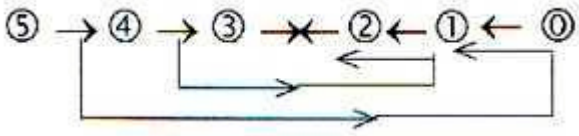
3. As said above, bases in tRNAs are **often methylated**, as the T-base in relation to the U-base, a fact which also points to the inward direction of tRNAs.
[In the four examples of tRNA given in the used reference here (Ala, Ser, Phe, Tyr), there is also a T-base in position 23 from the A-C-C-end, a single one. Rather odd. And at this position appears the same order of the 5 bases: T - U - C - G - A.]

4. The U-base in tRNAs appear in an angled attachment to ribose as **pseudouridine**. This fact could be one expression of the assumed angle steps through the dimension chain. (3 - 2 hypothetically an angle change from 90° to 45°?)

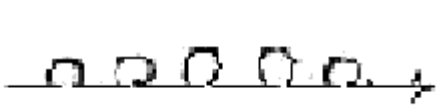
5. In an alternative form of the dimensional interpretation the **mRNA and tRNAs could be identified with poles of d-degree 4**; polarized to perpendicular relation in d-degree step 3-2: : 4b as outward direction ~ mRNA, and pole 4a as inward direction ~ tRNAs:



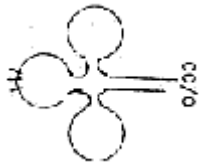
6. With the loop model of the dimension chain the step **4→3 outwards is also coupled with step 2←1** inwards.



The anti-codons of tRNA corresponds also to the anti-strand of DNA in relation to mRNA. One could question **if the cutting of mRNA has any inherent connection with tRNAs?** Cf. perhaps the cutting as loop forms and the cleaver leaf form of tRNAs? With its 2-dimensional, partly wavelike form tRNAs have similarities with the stage where mRNA on its way to rRNA undergoes change: "irrelevant" (?) parts of the chain are cut off.



4 → 3 mRNA



tRNA 2←1

This similarity could be read as a relation between step 4 → 3 outwards and 2←1 inwards, the dimension chain seen "orthogonal" as double directed with a meeting in step 3-2.

According to the model we have a 2-dimensional *motion* resulting from step 4 → 3, which could be thought of appearing inwards as a 2-dimensional structure.

	0/00–1 – 2 – 3 – 4 – 5	D-degrees of motions
D-degrees of structure:	5 – 4 – 3 – 2 – 1 – 0/00	

7. **Numbers of nucleotides in tRNAs:**

It seems to be around 75 - 77: (A little more in tRNA for Ser which have a beginning of a 4th loop in the leaf. Four examples, counting from anti-amino acid end to the anti-codon 34 +/- 1 bases, with anti-codon 37 +/-l.
Including anti-codons:

Ser 85 = 33 + 3 + 49
Tyr 78 = 35 + 3 + 40
Phe 76 = 33 + 3 + 40
Ala 77 = 35 + 3 + 39

One should note that there isn't generally any even number of triplets in tRNAs, but 26* codons including stop codons times 3 bases give the number 78. Theoretically one tRNA in a ring form could code for all amino acids without frame shifting.

*(With the way of counting codons, see files about The genetic code.)

In the 4 examples the **quotient G+C / A+U** ≈ 1,4 ≈ 45/32.

This relation is the opposite to the quotient between codons for G+C-coded (10) and A+U-coded (14) amino acids respectively Same figures in 1st and 2nd base order.) The opposition - if valid for more tRNAs - could eventually be an expression for an original opposition in directions between mRNA and tRNAs if the aspects on codons on this home page are applied.

8. **Why this -C-C-A-end of tRNA**, similar in all tRNAs, to which the amino acids are attached? One aspect concerning mass numbers:

Triplets of a dimension chain inwards and mass numbers (A) of the bases:

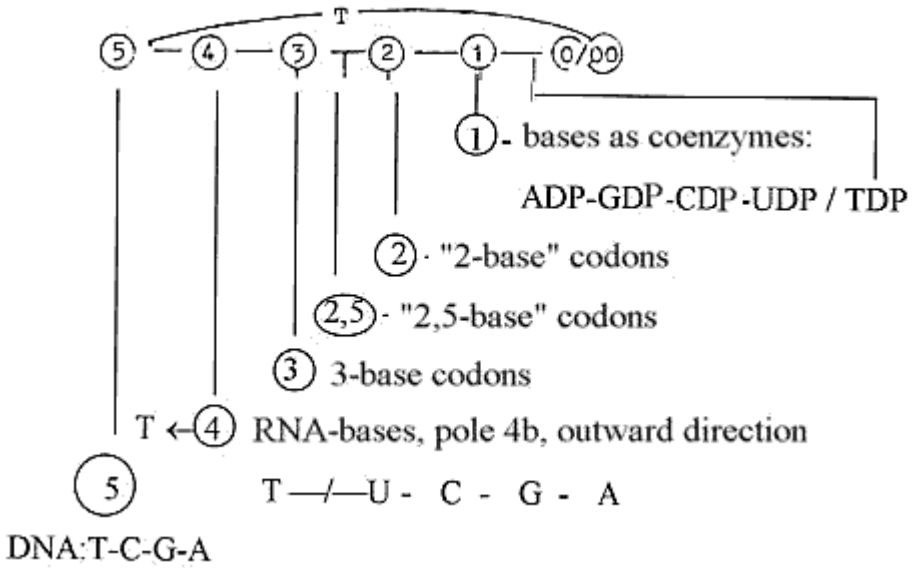
012
111---
123... sum: 135 = A-base
111----
234... sum: 357 = A+C+C. Sum of the bases with +1 for the bond to ribose.

Intervals between the triplet numbers = 111 = mass number of the C-base.

345, the last triplet inwards, happens to be the mass-number of the G-nucleotide in chain binding, also = cGMP.

Compare the triplet series outwards, approximating the sum of side chains of 20 plus 4 double-coded amino acids:
543, + 1 = G+C-coded ams,
432 + 321 + 210 = 963, - 3 = A+U-coded ams.

Number of bases:



1. 5 bases - 5 dimensions: number 5 returns.
This doesn't mean to say that the bases in any unambiguous sense represent dimensions or dimension steps. It rather seems as if they could represent different dimensions in different contexts.

2. 5 bases becomes 4 in DNA, RNA:
T-base in DNA representing direction inwards towards the "mirror", the H-bridges in the DNA helix. T-base with its CH3-group added to the U-base made chemically hydrophobic.
U-base in RNA, outward directed towards the protein synthesis and passing from the nucleus to the outer cell plasma.
Hence, the polarity T/U corresponds to the poles of d-degree 4, inward / outward directions, DNA←/ → RNA.

3. 4 bases becomes 3 in the codon triplets identifying amino acids in the protein synthesis. Or 3 - 2: the 3rd base only differentiated one step in 16 ams, indifferent in 8 ams.
There are other features in the protein synthesis at rRNA, the ribosomes, which point to the interpretation that this synthesis occurs in d-degree step 3 - 2.

4. The bases then becomes 1, singular ones, as coenzymes GTP, CTP, UTP, ATP. Each dimension step implies one d-degree debranched, transformed to external motions with the step 1 → 0/00 according to postulates in the model. This means stepwise increasing motions, revealed in the copying process and protein synthesis - and the activity of the H-transporting coenzymes.

5. Dimension degree 0/00 (equivalent with 5, as 5') = the d-degree of Motions, of processes.

Bases as coenzymes as specially connected with elementary kinds of substances ?

Carbohydrates - Lipids - Proteins - Transportation
T - U C G A

T- and **U**-bases in their role as coenzymes, TTP and UTP, are used for bonds in carbohydrates (different kinds). The difference may be seen in UTP(-DP...) active in binding/breaking of carbohydrates within cells, TTP(-DP...) when it concerns cellulose, the outer "anticentre" shell of plants.

Note too that all amino acids with U in first or second position in their codons are derived from stages of the glycolysis where carbohydrates are broken down.

C as coenzyme CTP is active in synthesis of lipids, in amination of phospholipids.
G as coenzyme GTP(-DP) takes part in the protein synthesis.

A as coenzyme represent a central energy storage, as such corresponding to a lot of transportations.

A dimension chain, according to the model here, implies steps towards growing amount of kinetic energy (motions).

Compare the similar order of the bases in tRNA at position 23...: T-U-C-G-A!
(If the four examples should be typical.)

Triplets of bases in codons - why?

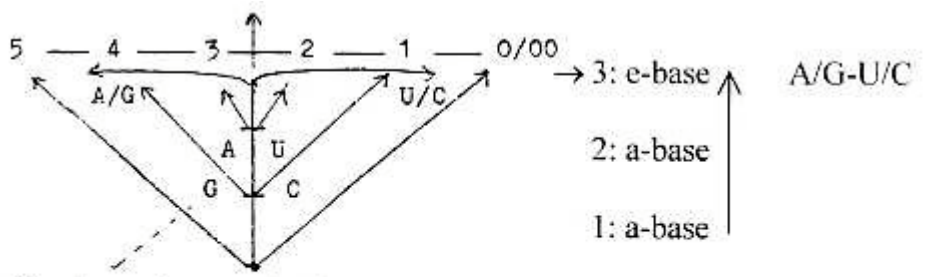
a) The suggested view could be one elementary answer to the question of why triplets in the codons. There may be others connected with the number of coded amino acids.
5^3 — 4^3— 3^3— 2^{33} gives the number chain 125 - 64 - 27 - 8 - 1.

64 theoretically possible different codons becomes 27 in "d-degree" 3, transformed into 19 + 8 (2-base-coded) ams. 16 ams differentiated in 3rd base + stop codons...(See further *The genetic code*.)

b) Another aspect is that the "loop model" of a dimension chain implies 3 polarization steps:

5 / 0-00 —> 4 / 1 —> 3 / 2.

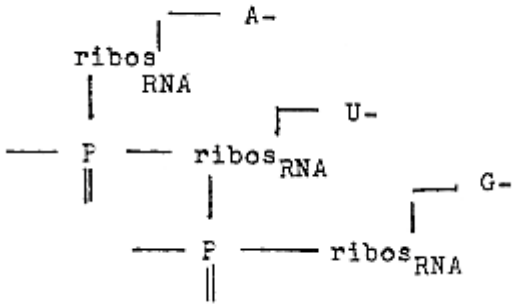
(There are also 3 steps in the protein synthesis from DNA to tRNA:
4 — 3 — 2 — 1: DNA —> mRNA —> rRNA <— tRNA.)



The bases here marked according to their mass number and intervals:

G - C = 40 (151 - 111) G 4 ——— 1 C
A - U = 23 (135 - 112) A 3 -- 2 U

c) Triplets of *nucleosides* connected by only 2 P-groups?
- Sum of the triplet AUG corresponds to sum of triplets in the elementary number chain.
RNA: Starting code for the protein synthesis = AUG = amino acid Meth:



P-groups	ribose groups	bases bound
126 A + 2H	394 A	395 A (A + U + G)

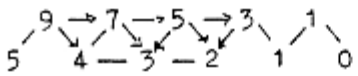
Nucleoside part in chain bonds 2 x 395 -1 = **790 -1** = 792 - 3
Corresponding nucleoside part in DNA with bases T-A-C = 715 = **714 +1**
Sum: **1504** equals sum of side-chains of 20 + 4 double-coded amino acids.

Triplets in the number chain 5 - 4 - 3 - 2 - 1 - 0:

543 345
432 234
321 123
+210 + 012
1506 — **714** Interval **792**.

T-A-C-nucleosides: T-A-C-bases bound = 369 = **012+123+234**.
Ribose part in DNA: 3(150 - 18 - 16) - 2 H =345 + 1.

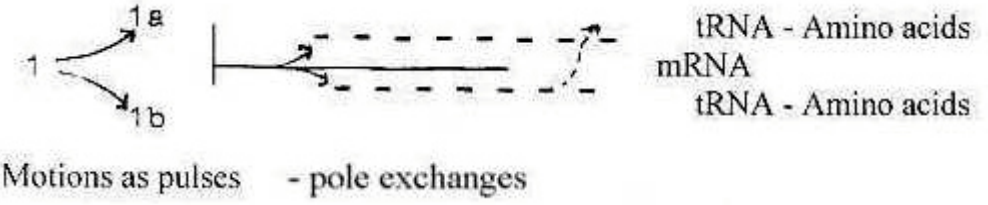
d) Numbers from the elementary chain with superposed odd figure chain:



975 753 Superposed odd figure chain
+ 43 + 32 Numbers for the steps
= 1018 785
| └→ 785 ≈ 3 base pairs DNA unbound (3 x 261,67.)
|→ = 2 x 509. → 509 = the 4 RNA-bases unbound.

2 x 753 -2 = 1504 = sum of 24 ams R

[A vague association:
The polarization of a line in d-degree 1 into d-degree 0/00 of Motion has in files about physics been illustrated as in the figure below, a splitting in steps as virtual lines. This step 1 → 0/00 may be regarded as occurring in each higher steps.



Cf. opposite directions of side chains in the peptides?

Could we look at the picture as 3 "phases" in the process of synthesis (?), the balance line + two half steps)

There are also 3 positions A-P-E for a tRNA at the ribosomes, d-degree 3 in our interpretation, during the process, the tRNA displaced from A to P to E.

(Groups of 3 half-steps besides the "balance" line give the picture of B-chains of amino acids with side chains in opposite directions.)

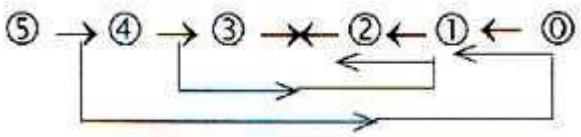
5-6 as reappearing numbers in steps and storage:

Bonds during the protein synthesis:
5 DNA: H-bridges
4 DNA / mRNA: at copying
3 mRNA / rRNA
2 rRNA / tRNA
1 tRNA / amino acids
00/0 amino acid / amino acid (peptide bonds)

Circa 5 levels of storage of DNA:
Diameter (Ø) = 20 - 100 - 300 - 2000 - 6000 Å):
5 → 4: The double helix of anti-parallel strands of base-pairs, H-bridge. Ø 20 Å
4 →3: This thread winded up on balls or cylinders of proteins, (histones), Ø 100 Å
3 →2: This strand of balls drawn up in a big spiral, Ø 300 Å
2 → 1: This in its turned drawn up in a thicker spiral, Ø 2000 Å
1 → 0/00: In last step this thicker spiral drawn up in a still thicker spiral, Ø 6000 Å, making up the arms of the X-formed chromosomes, and as a centre of this the centromeres, with a structure of the type 0/00. Centre - anticenter, ~ 5'.

D-degrees should be viewed as a suggestion. Alternatively we could see the d-degree of motions, from linear (1), 20 Å, to rotation (2) on "balls", 100 Å, to winding spirally (3 dimensions), 300 Å, to windings spirally of higher orders in d-degrees 4 to 5, 2000 Å - 6000 Å.

There are 5 histones too, proteins of a certain, fundamental kind, on which DNA is rolled up: one of these 5 seems to have a function related with the "all-embracing" character of "the other way around",



Cf. too 5 bonds between the two pairs of bases:
3 between G- and C-base,
2 between A and U-base.

Helix structures:
H-bonds between protein chains and along the main axis of the chains are in one reference classified in number of steps:
310-helix: 4,5 steps
α-helix: 3,5 steps
π-helix: 2,5 steps

Protein structures 1 - 2- -3 -4 -:
1 - Primary structure linear chains,
2 - 2-dimensional sheets of parallel protein threads bound laterally, plane or pleated
3 - 3-dimensionally folded proteins, globular proteins
4 - gathered globular chains with centres of coenzymes as expressions for the 4th d-degree equivalent with forces. (Often 2 or 4 similar proteins together.)
5 - The cilia or centromere structure perhaps interpretable as the 5th level ?
The centromere structure (and centrioles, cilia) with central and anticenter filaments (as 0- and 00-poles, in number 9 + 1 or 9 + 2) is probably the way the 5th d-degree is realized in a visually 3-dimensional world: The d-degree of motion, 0/00, is also equivalent with 5', the 5th dimension degree transformed into pure motions. Cilia represent on the macro level of cells the motional organs.

Protein fibres as collagen have also 5 levels of structure:
1. Amino acid chain - the collagen molecule.
2. Protofibril of 3 such chains spiralled.
3. Collagen fibrils with protofibrils stored both after and besides one another.
4. Packets of these fibrils.
5. The collagen thread.

(Perhaps noteworthy too is the information that the mean molecular weight of proteins are about 10^4 - 10^5 u à la 4-5 ten-power steps.)

Chromosome as "lumosomes":
Could the DNA-spiral be perceived as a kind of "built-in light wave", chromosomes as "lumosomes" on this much higher level of complexity? Structured through the help of electromagnetic (EM) waves?
The DNA-helix seems to have some fundamental properties common with light beams. Its **self-sustaining** ability, its self-preservation capacity, its self-supporting process, its "endogamy", is of the same nature. As a light wave may be interpreted is self-supporting through "breathing of vacant space" (see file about EM-waves), levelling the negative energy of vacant space up to zero, in the same sense the complementary principle may be seen working when DNA-strands gets copied from individual complementary nucleotides in the environment as anticentre, the 00-pole.

[A corresponding breathing of "emptiness" could eventually be found in the atomic nucleus as a kind of proton → anti-proton-relation (an old hypothesis among

physicists). H-bridges of DNA as corresponding to a *p*-/ anti-*p*-relation on this higher level?]

What should in that case correspond to the E- and M-factors in the EM-waves?
On the most fundamental level perhaps the basic NHx-groups, inwards, ~ M, versus the acidic OHx- or =O-groups outwards, ~ E ?
On a secondary level perhaps the chains of amino acids as "radial" (~ E) versus codon bases as "circular" (~M) ?
On a third level the polarity between U-C-bases and A-G-bases ?
Is there any way to connect the complementarity between purine and pyrimidine bases with the relation electric versus magnetic fields?
Codons G and A in 2nd position code mostly for polar amino acids, U and C in 2nd position for non-polar amino acids, hydrophobic ones, probably connected with magnetic fields, closed structures. (?) The question is left open, but the DNA-spiral seems more than just a metaphor for a ray of light.

It's said that a magnetic monopole (if any) should have the mass 137 times that of the electron. Mean value for an unbound amino acid is 136,5 u. Mean value for pairs of amino acids = 273 = the mass of charged π-mesons in electron units exchanged in the nuclear force.

Perhaps the 4 codon bases should be apprehended similar to complementary colours?
Three elementary colours (A+U+G) plus 1 (C) for the formation of two complementary pairs?

Spectral lines of H-atoms:
In the "Lyman-, Balmer-, Paschen-Brackett-series" for spectral lines of hydrogen, quotients between the spectral lines happen to give numbers for the mass of codon bases:

The Balmer series: m = 2, n = 3, 4, 5 within the visual area:
m = 2, n = 5, 4, 3 givesλ = 4341, 4863, 6565 Å:

$$\underset{a}{\underline{R(1/4 - 1/25)}} \qquad \underset{b}{\underline{R(1/4 - 1/16)}} \qquad \underset{c}{\underline{R(1/4 - 1/9)}} \qquad \rightarrow \text{wavelength}$$

a/b x 10^2 = 112 = U-base
b/c x 10^2 = 135 = A-base
a/c x 10^2 = 151,2. ~ G-base (151)

And what about the C-base?
The lowest spectral line of oxygen is 4368 Å. Quotient to the the middle spectral line here for H 4863 Å = 111,3. x 10^{-2}. (?)

[Quotients between spectral lines could in some sense be apprehended as related to phase-waves, said to carry no information ! ?]

As mentioned before: Behind all aspects here lies the thought or hypothesis that DNA or RNA and the coded amino acids on some deep biochemical level made up a unit (a whole which could be called DAP, P for proteins). An entity perhaps belonging totally to an underground of mathematics? A whole which then got polarized through different phases and angle steps etceteras and developed to all processes of the protein synthesis between primary poles.
There is DNA with a protein matrix, there is rRNA consisting of both proteins and nucleic acids and there is tRNA carrying amino acids transported by the A-base as AMP. And the bases are mainly constructed by and of amino acids.

4. **RNA / DNA-bases**

Synthesis, complementary traits, first annotations about mass.

The DNA-RNA-bases G and A versus C-U-T do indeed represent complementary "poles", with several polarities in origin and their synthesis.

The 6-5-member-rings of G- an A-bases originate from Inosinic acid,
the 6-member-rings of U-C-T-bases from Orotate.

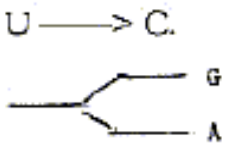
In original papers G and A are called "00"-bases, U-C-T "0"-bases. Yet the G- and A-bases in their construction have the character of 0-poles of the dimension model here, U-C-T the character of 00-poles (anticentre poles).

a) G- and A-bases are constructed from a centre outwards, the U-C-T-bases inwards:The centre in G- and A-bases is made up of the smallest amino acid Gly, whose branches outwards are filled with small molecules from the surrounding anticentre.
We have a "c - ac"-relation.

The U-C-T-bases on the contrary are created through the meeting from outwards of two bigger molecules, the amino acid Asp and carbamylphosphate, binding to form the 6-atom rings.

Principle of synthesis for the opposite codon bases:

b) Further, G and A then are formed along a branched way from the resulting Inosinic acid, while U, C and T are differentiated along a "linear" path of changes.



c) Also the relation to the P-ribose groups of the nucleotides are opposite:
construction of A- and G-bases occurs on the P-ribose group which comes first,
U-C-T bases are constructed separately with the P-ribose group added afterwards.

d) Gly and Asp, the amino acids making up parts of the polar types of bases have mass numbers which are inversions to one another:

Gly,	75 A,	/\ 133 x 10^x.	75 = 3/4 x 100	A-G-bases
Asp,	133 A,	/\ 75 x 10^x	133 = 4/3 x 100	U-C-T-bases

(Cf. sum of 133 and 75 = 208, numbers reappearing in the *Exponent series*.)

e) Mass number sums of "0"- and "00"-bases are inversions:

G + A = 286 = 151 + 135 A (with +1 for bonds to ribose)
U+C+T = 349 = 112 + 111 + 126 A

286 Λ 349. x 10^{x}

Also, more intricate:
2 bases with exponent 2/3 give their opposites if inverted.
(Cf. the exponent 2/3 to an elementary number chain 5-4-3-2-1 related to codon distribution to amino acids in the genetic code, see files *The genetic code*.)

2 x G-base 151 A = 302. $302^{2/3}$ Λ x 10^{4} = **222,**16. ~2 x C-base 111
2 x U-base 112 A = 224. $224^{2/3}$ Λ x 10^{4} = **271.**12 ~ 2 x A-base 135

2 x A-base 135 A = 270. $270^{3/2}$ Λ x 10^{6} = **2 x 112,7** (~ U-base, 112)
2 x C-base 111 A = 222. $222^{3/2}$ Λ x 10^{6} = **2 x 151,2** (~ G-base, 151)

The branched paths of synthesis for G- and A-bases:

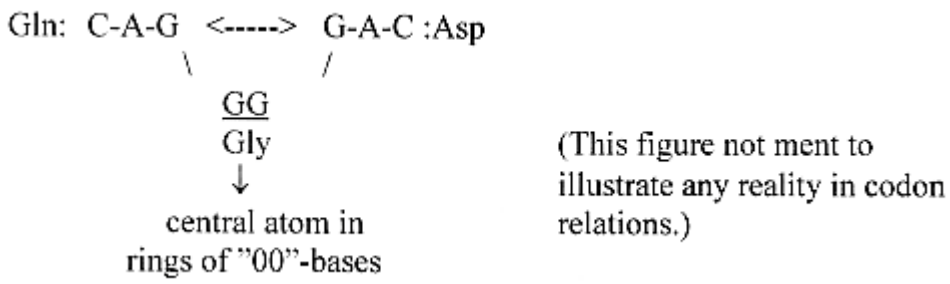
Here we have something like a secondary polarity:

A-base gets its free N-group from the amino acid Asp,
the N-group in the B-chain of this. (There is of course no other.)
G-base gets its free N-group from Gln,
the N-group in the R-chain of this.

We can note too:
Asp, 70 Z ——> A-base 70 Z
Gln, 78 Z ——> G-base 78 Z

Codons as a mirror relation:

Asp G-A-C <——> C-A-G = Gln
(but G-A-U <——> U-A-G = one of the Stop codons.)

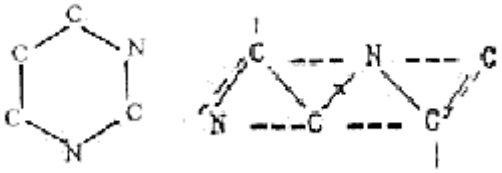


(This figure not ment to illustrate any reality in codon relations.)

Complementary forms of bases versus amino acids (ams):

There is a relation in their forms like centres-anticentres, (c—ac), as 0-00 in the model - or radial versus circular as geometrical poles of dimension degree (d-degree) 3 in our model:
- Amino acids as tetrahedrons have central C-atoms and direction outwards in 3-4-directions,
- Bases are rings as if the central atoms had got inverted to anticentre positions.

Formally, 2 amino acids N-C-C-N-C-C could be restructured to the 6-rings of the bases (if chemically possible is another question):



Actually, the contribution of the amino acid Gly to A- and G-bases corresponds to half a 6-ring (1/3 of the C-N-atoms in the 5-6-ring), and Asp with C-C-C-N, 2/3 of the 6-rings of U and C, T: 7 out of 15 C + N in purine and pyrimidine rings.

(Also Glu and Asp contribute with singular atom groups (NHx) to the Inosine, the parent to A- and G-bases.)

Polarization in end-(R)-groups of the bases:
In the G-C-pair the bases have both O and N, keto-oxygen and nitrogen groups, while the opposition O-N is polarized to separate bases in the A-U-pair (A-base with only a NHx-group, U (and T) with only 2 oxygen groups.

This fact points towards the A-U-pair as expression for a secondary step or level from the viewpoint of our dimension model. Many other facts do the same in the arithmetical analysis of codons and amino acids (see those files). (That the opposite is true about the order of synthesis, representing the opposite inward direction, is natural.)

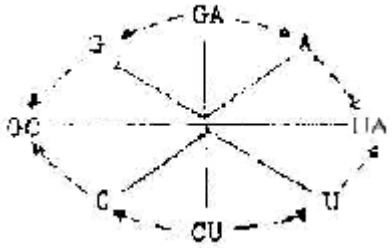
The base pairs may be ordered along 3 kinds of polarities:

a. GA <——> UC type of bases
b. GC <——> UA complementary pairing
c. GU <——> AC defined as keto-bases versus amino-bases.

The GC <—> UA- polarity is here suggested as the first one, an expression for opposite, complementary directions, i.e. d-degree 4.

The GA <—> UC-polarity could be the second one. Compare features of "radial" versus "circular" in the forms of synthesis as poles of d-degree 3. Also a certain polarity heavier — lighter in the property Mass.

The GU <—> CA polarity, founded in the O <—> N-polarity, refers to a hydrophilic-hydrophobic aspect, which concerns Charge as a property. Charge in this model assumed as a property defined in d-degree 2.
Illustrated as coordinate axes:



3/2/relations among bases as a polarization of 5:

Number of bases:

5 bases, divided 3 →←2 in types: T-U-C / G-A,
divided 1←→4: T versus U-A-G-C. (DNA / RNA)

3/2-division in number of atoms in the rings:

A, G: 9
T, C, U: 6

Z-number in rings including directly bound H-atoms:

A, G: 60 Z
>3/2-quotient
T, C, U: 40 Z

Bonds:

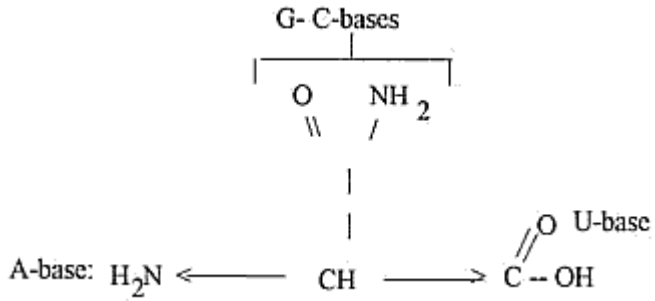
5 H-bridges between the 2 pairs divided 3/2:

3 for G ≡≡≡ C
2 for T ═══ A

Type of bonds:

3 of the O ...N-type: =0.....H-N
2 of the N...N-type: N-H.....N

Free end-groups of the 4 RNA-bases as illustrated in end-groups of amino acids Gln and Asn:



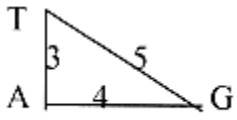
About mass numbers (A) and atoms in the single bases:

Intervals in mass between A-T-G-bases:

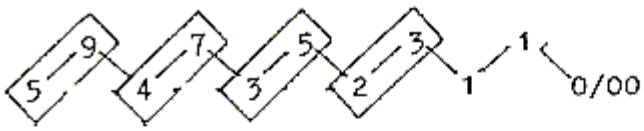
Intervals are squares illustrated by the Pythagorean' triangle.
G 151 u, A 135 u, T = 126 u. (Including +1 for bond to (deoxi-)ribose:

. Intervals:

G - T = 5^2
G - A = 4^2
A - T = 3^2
U - C = 1^2



Approximate mass numbers of T-A-G-bases from quotients in the dimension chain with superposed odd-figure-chain:



59/47 x10^2 = 125,5. ~ T 59/47 ⟶ √ x 100 = 112,0 U-base
47/35 x10^2 = 134,3. ~ A
35/23 x10^2 = 152.2. ~ G....sum 412.
59/53 x10^2 = 111,3 C (53 - ? - a number read inwards)

543/432 x10^2 = 125,7 ~ T
432/321 x10^2 = 134,6 ~ A
321/210 x10^2 = 152.9 ~ G....sum 413 Real sum 412.

594/473 x10^2 = 125,6. ~ T
473/352 x10^2 = 134,4. ~ A
352/231 x10^2 = 152.4 ~ G....sum 412.3.
594/537 x10^2 = 110,6. C (537 - ? - , a number read inwards)

Sum of the 4 DNA-bases with +2H for the double bonds added = 543:
543: the first triplet in the elementary number chain:

A-base:	4	double bonds: ~ 8 H,	+	135	A =	143
						> 300
G-base:	3	double bonds: ~ 6 H,	+	151	A =	157
C-base:	2	double bonds: ~ 4 H,	+	111	A =	115
						> 243
T-base:	1	double bond: ~ 2 H,	+	126	A =	128
				Sum:		543

[Mass of side-chains of G+C-coded ams (R) = 544. The same number division appears there between Z- and N-numbers: 300 Z, 244 N (-/+1 in 2nd base order)]

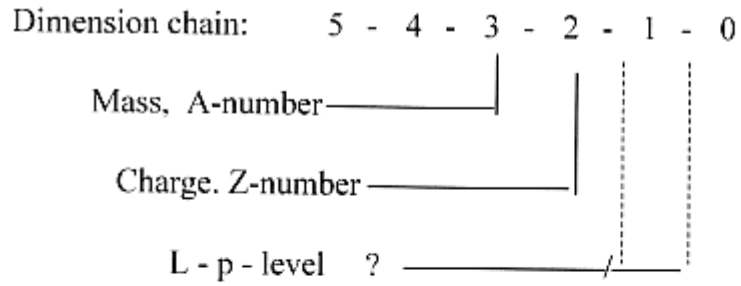
A mass relation between base types as connected with sum of ams:
Pyrimidine ring without H: 4 C + 2 N = 76 A
Purine ring without H: 5 C + 4 N = 116 A

76/116 = 2 x 3275,9. ≈ **3276**. x 10^{-4}. 3276 = sum of 20 + 4 double-coded ams.

A - Z - L/Lp - p - numbers as different levels in the bases:
The starting point here is the thought that activation ("excitation" ?) of an atom or molecule may imply a stepwise approach towards more superficial levels as suppression of deeper ones and therefore different number of levels in the electron shells are engaged in different stages of processes.

Here we assume that in first steps the orbitals of the K-shell are suppressed first, designated L-level, in next step the *s*-orbitals of the L-shell, designated *p*-level. It doesn't include H-atoms of course.

Addition of different stages could then be regarded as an operation for getting the time aspect inherent (only virtual).



Adding different stages with H-atoms excluded:

Base:	N /Z - H	L	p	Sum: N/Z-H + L + p	
G:	73	51	29	153 = A-number	G-base +2
A:	65	45	25	135 = A-number	A-base
T:	60	42	24	126 = A-number	T-base
U:	54	38	22	114 = A-number	U-base +2
C :	53	37	21	111 = A-number	C-base

L-level: - 2 in each atom C, N, O.
p-level: - 2 again in each C, N, O.

Here it seems as the deeper level of atomic Mass is "disintegrated" in different stages of more superficial levels - as Charge and the electron shells - in a way that agrees with the general principle in the dimension model of higher d-degrees transformed to lower ones. There is a similar, rather remarkable pattern among the coded amino acids, see *The genetic code*.

Number of atoms in 2 x 24 codon bases, 1st and 2nd position:
Cf. table of 20 + 4 double-coded amino acids. in files The Genetic code.
- Equal number divisions +/-1 in 2 dimensions, horizontally and vertically.

	C	N	O	H			
A	75	75	-	75 =	210+15	= 225	
							> **401**
G	55	55	11	55 =	176	= 176	
U	52	26	26	52 =	144+12	= 156	
							> **273**
C	36	27	9	45 =	117	= 117	
	209+9	176+7	44+2	218+9			
=	218	183	46	227			
	\ **401** /		\ **273** /				

A+G-bases: atom numbers ~ **C + N**
U+C-bases: atom numbers ~ **O + H**

Total sum of atoms = 674 = 2/3 x the sum of the exponent series 1011:
With 3rd base in codons included, assuming equal distribution, 6 of each base, 336 atoms are included:
6 G = 6 x 16 = 96,
6 A = 6 x 15 = 90,
6 U = 6 x 12 = 72,
6 C = 6 x 13 = 78
Total sum of atoms should then become ~ the sum of the exponent series 1011.

$5^{2/3} — 4^{2/3} — 3^{2/3} — 2^{2/3} — 1^{2/3} — 0 \quad \times 10^2$ = Sum 1011, 3 x 337.

Numbers abbreviated to integers in the exponent series:

292 + 252 + 208 + 159 + 100
544 467

Atoms then in the bases paired:
A+U-bases: **544 atoms -1** = 292 + 252 -1
G+C-bases: **467** atoms = 208 + 159 + 100

Including stop codons, UA-A/G and UGA, first two bases = + 2 U, 1 A, 1 G:
The same equivalence vertically and horizontally appears +/-1:
A+G-bases: 432 ~ C + N = 433.
U+C-bases: 297 ~ O + H = 296.

23 amino acids, without Ileu2 (same 1st and 2nd base in the codons):

	C	N	O	H	Sum of atoms
7 A1 + 7 A2 = 14 A:	70	70		70	210
					> 386
5 G1 + 6 G2 = 11 G:	55	55	11	55	176
5 U1 + 7 U2 = 12 U:	18	24	24	68	144
					> 261
5 C1 + 4 C2 = 9 C:	36	27	9	45	117
	209	176	44	218	
	385		262		

a. A+G-bases: atom number ~ C+N atoms (A ~ C, G ~ N)
U+C-bases: atom number ~ O+H atoms.

b. Number 385, which guide one 12-group among amino acids, is equally divided here in the numbers 209 - 176 (among the Cross- and Form-coded ams +/-1).

Numbers 262-261 is the mass number of a DNA pair G + C and A + T respectively.
Note perhaps the inverse relation between numbers around 260 and 385.
There is also the relation in number-base systems (nb-x):
261 in nb-10 = 405 ~ 385 rewritten in nb-8.
(From files The genetic code.)

The schemes above seem connected with the function the bases have as coenzymes in relation to the different classes of substances. Roughly:
U-base (UTP) with carbohydrates (dominating atom O),
C-base (CTP)- with lipids (characterizing atom may be said to be H)
G-base (GTP) with proteins (typical atom N).
A-base, less specific, most connected with energy storing and transportation.

Sum of products in the dimension chain with superposed odd-figure level gives mass numbers of bases and amino acids:

94x47+73x35+52x23+31x11 = 851 x 10 ⌊ **1504** x 10
49x74+37x53+25x32+13x11 = 653 x 10 ⌋ ↓
24 ams R

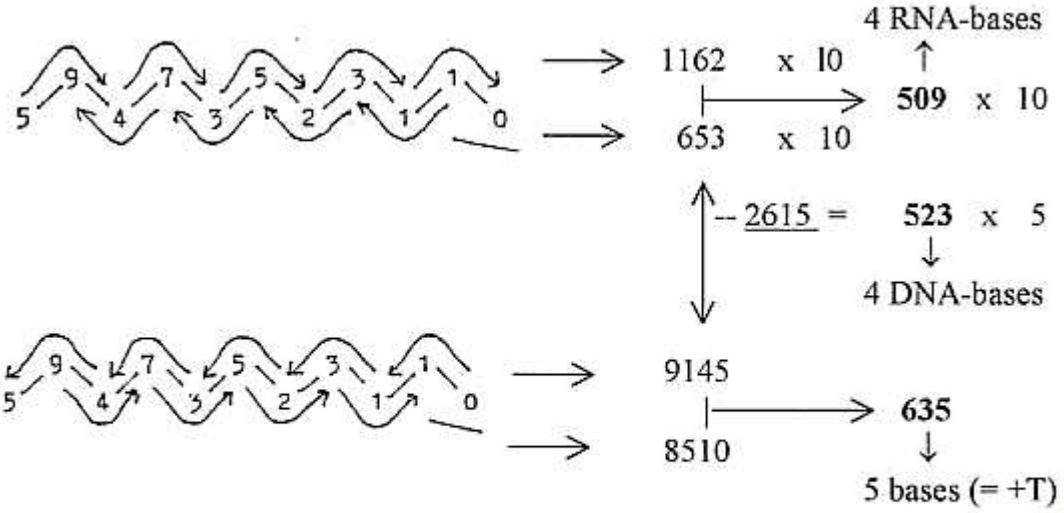
C1 + A1-coded ams = 850 (U2 + G2: 848)
U1 + G1-coded ams = 654 (C2 + A 2: 656)

Difference 8510 - 6530 = **1980**
= **4** coenzymes $^{4-}$ ATP^{4-} +UTP^{4-} +CTP^{4-} +GTP^{4-} (-1)

Products - illustrated in the same way with bowed arrows below:

59x94 etc, sum of 5 products = 11620
95x49 etc. " 5 products = 9145

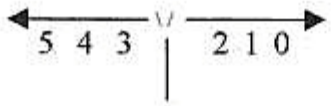
Difference 11620 - 9145 = **2475**
= **5** coenzymes TPT^{4-} + ATP^{4-} +UTP^{4-} +CTP^{4-} +GTP^{4-}



Difference 5 respective 4 products in inward direction above:

9145 - 6530 = **2615** = 10 x mean value for a base pair A+T, G+C.
= 5 x 523, 4 DNA-baser.

A-base and nucleotides - some number readings in the elementary chain:



135

A-base - mass number

AMP^{2-} = 345 A, - P-ribose-group^{2-} 210 = 135

135 Λ 74 0 74 0 74 0 74 0 ...($x10^{x}$) = series of B-chains before binding.

A-base as coenzyme transports the ams to t-RNA. in their B-chains at the protein synthesis..

135 = Meth, 149 A, without its end group CH2, 14 A, which it leaves when acitvated by ATP: 149 - 14:

Meth, codon A-U-G, starts the RNA-synthesis.

The odd number series 1-3-5-7-9 of the superposed dimension chain:

: 1 3 5 — 7 9

Mass numbers: A-base P-group (PO_3^{2-})

5 7

+ 7 5

= 132 ⟶ + 79 = 211

RNA-ribose

PO_3^{2-} : the group in coenzymes of the bases = 79 A:

79

O_2 x P=O

32 x 47 = **1504** = 24 ams R

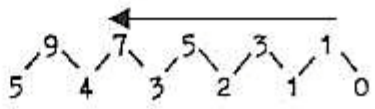
9 7 5 3 1

5 - 4 - 3 - 2 - 1 - 0/00

47 also the R-chain of Cys, CH2-SH, responsible for many bonds between peptide chains.

Sum of masss numbers (A) of 4 coenzymes; uncharged P-groups:

GMP:	363	- 1357
AMP:	347	
UMP:	324	
CMP:	323	



$\sqrt{97531}$ = **312**,3. = DNA-nucleotide of A-base

Tables: Codon bases DNA RNA - Nucleotides

DNA/RNA: nucleic acids: A-, N-, Z-numbers, including +1 for bonds to (deoxi)ribose:

DNA:	A	N	Z
G-base	151	73	78
C-base	111	53	58
G+C	262	126	136
A-base	135	65	70
T-base	126	60	66
A+T	261	125	136
4 bases	523	251	272

RNA:	A	N	Z
G-base	151	73	78
C-base	111	53	58
G+C	262	126	136
A-base	135	65	70
U-base	112	54	58
A+U	247	119	128
4 bases	509	245	264

P-ribose-groups PO_2^--- C_5 --$O_{4/3}$ -- H_8 --:
In chain binding:

DNA:	A	N	Z
Ribose	115	54	61
P -group	65	32	31
Sum	178	86	92

RNA:	A	N	Z
Ribose:	131	62	69
P -group:	65	32	31
Sum:	194	94	100

Sum of 5-4 bases: A-Z-N-numbers:

5 bases:	a) unbound:	A: 635	Z 330	N: 305
	b) bound:	A: 630	Z 325	N: 305
4 bases: DNA	a) unbound:	A: 523	Z: 272	N: 251
	b) bound:	A: 519	Z: 268	N: 251
4 bases RNA	a) unbound:	A: 509	Z: 264	N: 245
	b) bound:	A: 505	Z: 260	N: 245

G+C-bases, unbound = 262 A equivalent with (~) Z - 2.
A+U-bases, unbound = 247, ~ N +2.

Nucleotides: DNA. RNA: A-. Z-. N-numbers:
(In chain binding with charge -1 in the P-groups.)

DNA	A	N	Z
G	328	159	169
C	288	139	149
G+C	616	298	318
A	312	151	161
T	303	146	157
A+T	615	297	318
Sum	**1231**	595	636

RNA	A	N	Z
G	344	167	177
C	304	147	157
G+C	648	314	334
A	328	159	169
U	305	148	157
A+U	633	307	326
Sum	**1281**	621	660

Mean value: DNA = 308 (307,75)
RNA = 320. (320,25)
Middle value 314, (~ number of π), x 4 = 1256 ≈ 20 ams R-chains -2H.

5. Mass numbers of bases and nucleotides in relation to the dimension model and to coded amino acids

Experimental calculations
Partly from files The genetic code.

Used abbreviations:

Ams = amino acids.
R-chains = the different side chains of ams.
B-chains = the similar part, which bind through condensation.
- Here it's calculated with 24 ams, the four double coded included, where nothing else is mentioned. See table over ams **here**.
/\ , sign indicating inversion.
nb-x = number-base system, e.g. nb-10, nb-8 etc.

1. **Two sets of the 4 bases give the mass sum of coded amino acids in nb-8:**

a. The elementary number chain 5 - 4- 3- 2- 1- 0 with exponent 2/3 x10^2 called the ES-series:

The Exponent series - the whole chain

$$\mathbf{5^{2/3} - 4^{2/3} - 3^{2/3} - 2^{2/3} - 1^{2/3} - 0^{2/3}} \quad \mathbf{x\,10^2}$$

= 292. 252. 208. 159. 100. 0

\ / \ /

544 460 |- 2 x (292 + 252 + 208) = **1504 = 24 ams R.**

544 - 159 =**385**, 208 + 159 =**367**.

*Numbers 292-252...etc. below referred to as "5", "4" etc. elementary figures within quotation marks.

Transformations of base numbers to nb-8:

	G-base	C-base	U-base	A-base	2 x (G+C+U+A)	
nb-10:	151	111	112	135	1018	
	↓	↓	↓	↓	↓	
nb-8:	227	157	160	207	**1772**	= 24 B-chains unbound
Σ:	**384***		**367**			
=	544		208-1		→ the ES-series, 292+252 — 208.	

*If transformed together 386.

2. **Division of the sum 1504 in 714 - 792**-2**:**

Mathematical operations performed in nb-10.
Sum of 24 ams, R-chains = 1504 divided in numbers 792-712,
related to the sums of triplets of a dimension chain through rewritings:

	nb-10		nb-8
2 G	302	-->	456
2 C	222	--->	336... **792** = interval outwards-inwards

2 x U	112 x 2		160 x 2 = 320 ~318 = - 2 (rewritings)
2 x A	135 x 2		207 x 2 = 414 ~394.....sum **712**

↓

543	345	[Note: With additions and multiplications inside
432	234	the 8-power system, we get the sum
321	123	**1772** = sum of the B-chains of the 24 ams.]
+ 210	+ 012	
1506 <------->	**714**	

↓

792

3. **Mass numbers of bases read as in nb-8, separately translated to nb-10 - and the triplets of a dimension chain:**

	4 DNA-bases nb-10		nb-8
G	**105**	<---	151
C	73		111
T	86		126
A	93		135
Sum:	**357**		**523**

	4 RNA-bases nb-10		nb-8
G	105	<---	151
C	73		111
U	74		112
A	93		135
	345		**509**

Triplet series 0f 5-4-3-2-1-0 "inwards"

↓

4 RNA-bases =	**345**	=	**345**	+ 012 = 357
4 DNA-bases =	**357**	= -|	**234**	|
		|	**123**	|
			012———	|

Difference **012** = 14 in 8-power system = + $\mathbf{CH_2}$
added to U-base giving the T-base in DNA..

4. **Mass numbers (A) of the bases read as 6-power numbers:**

	nb-10		nb-6	
	67	<---	151	G-base
	43	<---	111	C-base
	59	<---	135	A-base
+	54	<---	126	T-base
=	223			

|----------> **1011** = sum of the whole Exponent series

(223 is also U+C bases as **10**-power numbers.)

5. **The bases bound with exponent 2/3 give numbers of the ES-series:**

G: $150^{2/3}$ x 10 = 282,31.
A: $134^{2/3}$ x 10 = 261,86...sum 544,17 = **544.** = 292+252 = "**5 + 4**"

U: $111^{2/3}$ x 10 = 230,97.
C: $110^{2/3}$ x 10 = 229,58...sum 460,55 = **460.** = 252+208 = "**4 + 3**"

T: $125^{2/3}$ x 10 = 250
C: $110^{2/3}$ x 10 = 229,58...sum 479,58 = **480.** = 960 x ½
= ½ x("**5 + 4 + 3 + 3**")

G + A give together the A-number sum for amino acids coded G or C,
(first and second base ordering).
T + C give half the sum of amino acids coded A and U. "
Number 100 and 159 in the Exponent series::

$150^{2/3} + 134^{2/3} + 111^{2/3} + 110^{2/3} = 100{,}5. \approx$ **100**. ("1").
$282{,}31^{2/3} + 261{,}86^{2/3} + 230{,}97^{2/3} + 229{,}58^{2/3} = 159{,}10 \approx$ **159**. ("2")

6. **Middle figure in the A-number of bases as a dimension chain**
between "poles" 1--1 as in the last d-degree of motions in the model:
Numbers 292 - 252 from the ES-series:

151 ---> **G-base**

292 < (Inosinic acid + Orotate = 292)

141

> 272 ---> 2 x 136, **A-base +1** (Inosinic acid = 136)

131

252 < > 252 ---> 2 x 126, **T-base**

121

111 ---> **C-base**

101

↓ ⟶ 292 - 252 is the beginning of the Exponent series:

↓ ↓

$5^{2/3}$ $4^{2/3}$ **(x100)**

With 2 times 131 + 121 + 111 = + 363 = 655 + 363 = 1018 = 2 x 509, the sum of 4 RNA-bases. All these numbers transformed to nb-8 give the sum of the 24 ams divided 973 - 531 (as triplets of the odd-figure chain 9-7-5 (-2) —531.

Products between bases

7. **Products between bases and (approximate) sums of amino acids:**
Number of bases in 1st and 2nd position times A-numbers of the pairs, inverted:

14 x (A+T =261) = 3654, Λ = 2736,7. $x10^{-7}$

10 x (G+C =262) = 2620, Λ = 3816,8. $x10^{-7}$

Sum 6553,5 "

↓

= 2 x **3276,76** $x10^{-7}$

(Inverse number of A+T 2736,7. ~ 20 ams (= 2735).

8. **Products of bases and number 3282 - 3282 as an approximation?**

The triplet series 543-432-321-210 expanded gives approximately R+ B-chains of the 24 amino acids:

Sum of 24 ams, unbound, R+B-chains, = 3276: There is a loss of one H in B-chains of 4 ams, Arg 1, 2, Lys, Pro. when Arg and Lys have charged N-groups in the R-chains. Could there eventually be a stage where there is +2H in some R-chain, giving the sum 1506? Cf. the triplet series of the dimension chain:

987 + 876 + 765 + 654 + 543 + 432 + 321 + 210

3282 <----------> 1506 = 24 R-chains + 2H

|

1776 = 24 B-chains à 74 A

1776 = B-chains before reduction of 4 H in B-chains of Arg1,2, Lys, Pro,

Difference between base products of base pairs:

G-base: 151 A
> 2 x 151 x 111 = 33522
C-base: 111 A ↑
|-----> **3282**
A-base: 135 A ↓
> 2 x 135 x 112 = 30240
U-base: 112 A

U x C = 112 x 111 = 12432
A x G = 135 x 151 = 20385
→ Sum = 10 x 3281.7 ~ 3282.

9. **Products of bases DNA divided with 4 π:**

A x G = 135 x 151 A = 20.385
| < diff. 6399 =79 x 81. [$(H_2)PO_3$ = 79-81 A.]
T x C = 126 x 111 A = 13.986
Sum 34.371

Difference 6399 / 4 π = **509**,2. 509 = A+U+G+C, the 4 RNA-bases
Sum 34371 / 4 π = 2735,15. 2735 = 20 ams, R+B

Various other kinds of operations.

10. **Four times the base number with displacements in the 10-power positions:**

A-base: 135, x 4 = 540
T-base: 126, x 4 = 504
G-base: 151, x 4 = 604
C-base: 111, x 4 = 444

4 A x 10
4 T x 1 + 4 G x 1
4 C x 0.1
Sum 6552,4
↓
= 2 x 3276.2.
= 24 ams, R+B

11. **24 RNA-bases, as if equal use in the codons in one position:**

6 x 509 = 3054, -2, Λ = 3276.5. x10^{-7}
↓
Λ = 3274,4 x 10^{-7}

12. **Natural logarithm *e*:**

4 DNA-bases = 523 A: 10^{e} = 522,7 ≈ 523.

13. **Dimension chain numbers as n x 111-numbers, times π:**

$1665 = 555 + 444 + 333 + 222 + 111 = 1665.$
$\pi \times 1665 \times 10^{-1} = \underline{523,}075.$ 523 = the 4 DNA-bases

14. **Number 32 and connection with the π-number?**

$2^5/2\pi, \times 10^2 = \underline{32 \times 10^2}/2\pi = 509,3.$ $\underline{509\ A = \text{the 4 RNA-bases.}}$

4^{th} root out of $\underline{32 \times 10^2} \times 100 \approx 752,12$ .752 x 2 = $\underline{1504 = \text{sum of 24 ams R.}}$

[Quotient $10^5 / 2^5 = 3125 \rightarrow \log 3125 = 3,49$. Inverted (Λ) = 286,1. x 10^x.
Cf. the hypothesis in the model that 10 could be the log-base as sum of poles in d-degree 4 and 2 the log-base in polarizing direction as sum of poles in d-degree 0/00.]

15. **How to show that sum of the 4 bases ≈ 31-32:**

7 <	6,6	—> Λ =	151,5151	x 10^{-3}	G-base	= 151
	7,4	—> Λ =	135,1351	x 10^{-3}	A-base	= 135
8 <	8,0	—> Λ =	125	x 10^{-3}	T-base	= 125, bound
9 <	9	—> Λ =	111,111	x 10^{-3}	C-base	= 111
Sum:	31					

The other way:

G-base	151	Λ	6,6225	x 10^{-3}
A-base	135	Λ	7,4074	x 10^{-3}
T-base	126	Λ	7,9365	x 10^{-3}
C-base	111	Λ	9,0090	x 10^{-3}
			30,975.	"

↓

Λ re-inverted = 32,28.

With U-base instead of T: 31,96 x 10^{-3}

↓

Λ re-inverted =31,28.

Hence: 4 DNA-bases $\sim 2^5 = 31 - 32.$
4 RNA-bases $\sim 2^0 + 2^1 + 2^2 + 2^3 + 2^4 = 32 - 31.$

16. **Number 63:**

$$63 = 2^0 + 2^1 + 2^2 + 2^3 + 2^4 + 2^5$$

$$63 = ([5/4 + 4/5] + [4/3 + 3/4] + [3/2+2/3]) \times 10$$

- Sum of 5 bases bound = 630 = 1/2 x 1260,
- $(6,3 \times 4)^2 = 635,04$. 635 the sum of 5 bases.

- Mean value of a base = 126 A = A-number of the T-base unbound.
- Mean value for a side chain of ams ≈ ½ x 126 = 63 (62,75),
  counted on 20 + 4 double-coded ams.
- 1260 - 2 = A-number for side chains (R) of 20 ams.
- 63 = the difference A+G <—> U+C = 286 - 223.
- 63 = PO2 -group, connecting the nucleosides in DNA/RNA.

17. **Bases divided with number steps,**
read in the odd-figure chain 9-7-5-3-1:

G/97 + A/75 + T/53 + C/31 = 9,3147.
↓
√ , Λ = 3276,5. x10^{-4}

18. **The 5 bases according to their mass: G-A-T-U-C divided with the elementary number chain 5-4-3-2-1:**

G/5 + A/4 + T/3 + U/2 + C/1 = 272, 95. ≈ 273*. = mean value of 2 ams:
↓
x 12 = 3276
24 ams, R+B

*A+G = 286, T+U+C = 349: 286 /349≈**0,819**.
819 = 273 x 3 = 1/4 x 3276, sum of 24 ams R+B

19**. A more odd operation:**
First figure in the A-number of the bases regarded as detached from the last figure:

G: 151 → 52
A: 135 → 36
U: 112 → 13
C: 111 → 12

(Quotient G/U= 52/13= 4/1
Quotient A/C = 36/12= 3/1

G x C: 52 x 12 = 624
> **1092** = 1/3 x 3276
A x U: 36 x 13 = 468 24 ams, R+B.

G+C: 52 + 12 = 64 = 8^2 (Oxygen, Z-number squared)
A+U: 36 + 13 = 49 = 7^2 (Nitrogen Z-number squared)

R-groups: U-bas: =O + OH: = 33 A
A-bas: NH_2 = 16 A -- 49 = 7^2
G-bas: =O + NH_2 = 32 A
C-bas: NH_2 + =O = 32 A -- 64 = 8^2

Nucleotides — and mirrored numbers

20. **Triplet of nucleotides in RNA with mean value 320 - 321 = ¨960 - 961:**
Cf. sum of triplets in the elementary chain: 432+321+210 = 963.
960 = A+U-coded ams R.

21. **The 4 bases bound = 505 give the sum of their nucleotides through nb-transformation:**

nb-16		nb-10
505	—>	**1285**

22. **Nucleotides with P-groups charged -1:**

4 DNA-nucleotides = 1231 A
4 RNA-nucleotides = 1281 A
-- mean value: 1256 A , 20 ams, R -2
$\sim 4\pi \times 10^2$

With uncharged nucleotides 1260 A: 20 ams R = 1258 ≈ the middle value.

23. **Mirrored number relations?**

a. Mass sum of RNA-nucleotides read backwards as in a mirror relation to DNA:

DNA → RNA ←

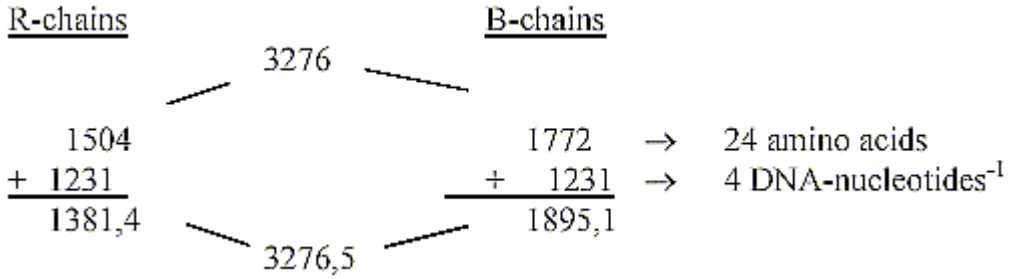
1231 + 1281 = 1231 + 1821 = 3052
↓
Λ = 3276,54. x 10^{-7}
↓
24 amino acids total mass, R+B-chains

b. Mirrored numbers for separate nucleotides RNA:

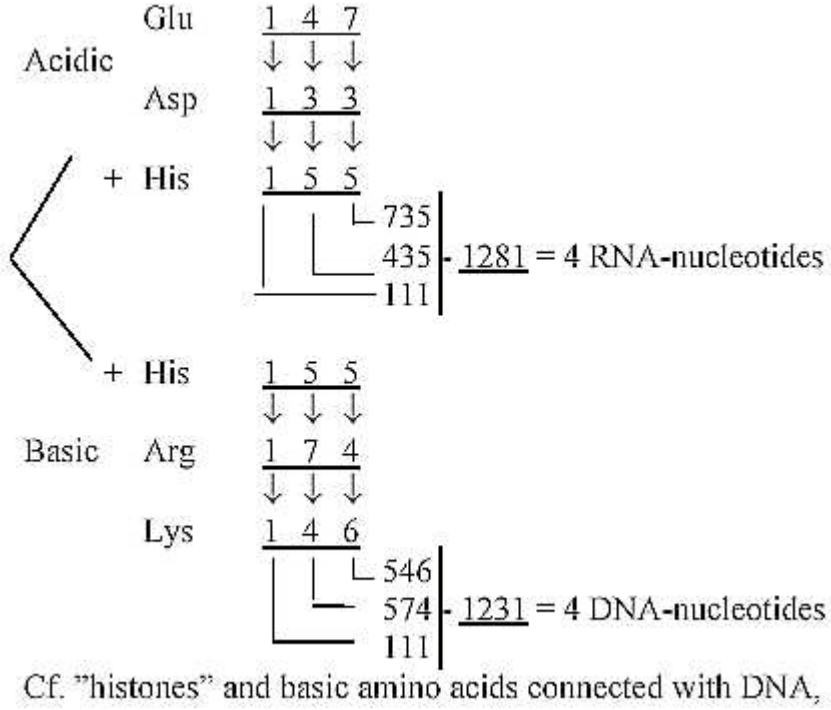
305	+	304	+	344	+	328	
←		←		←		←	
503		403		443		823	= 4 x 543

543, the first triplet number in the elementary dimension chain.
543 also the sum of the 4 bases when +2H for each double-bond in the rings are included but this concerns the 4 DNA-bases.

24. **Amino acid sums, R and B chains added with displaced DNA-nucleotides:**



25. **The four DNA- and RNA-nucleotides 1231-1281:**
The sums derived from an angled reading of acidic and basic amino acids (R+B-numbers), His included in both groups:

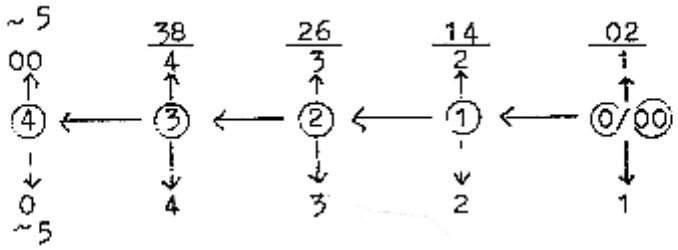


Cf. "histones" and basic amino acids connected with DNA,

Miscellaneous other operations

26. **The sums of 2 purine and 3 pyrimidine bases, 286 and 349;**

a. Numbers for dimension steps "inwards" with sum of poles of next higher degree added, for instance step 4 ← 3 = number 3-4, + poles 0 and 00 worth 5 = + 10, read as 350:



285,7.Λ ← 350 (T+U+C) ÷1 ← 238 (T+U) ← 126 (T) ← 014 (-14 = U)

A+G

Interval in the steps of this type = 112 = mass number of the U-base.

b.

$4321/1234 = \underline{350.16}.\ x10^{-2}$

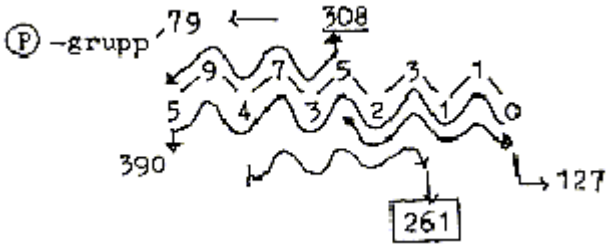
Λ

$= 285{,}58.\ x10^{-5}$

27. **Division of 20 ams in accordance to their weight in three groups gives sums which -1 corresponds to grouped bases.**

Light	Middle weight	Heavy	
Glv ----Cys	Leu ----Meth	His ---- Trp	
224	524	510	A-numbers of R-chains
223	523	509	A-numbers of codon bases
= U + C	= T+G+C+A	= U+ G+C+ A.	

28. **Numbers from 2-figure-reading and additions in the "2-figure-chain":**
Example: 59 + 94 + 47 + 73 + 35 = 308 etc.



308: Mean value of a DNA-nucleotide = 307,75. (charged)
261: Base pair A+T.
127: Mean value of 5 bases unbound = 635/5- = 127

29. **Mass number of the G-base 151 from inverted triplets:**

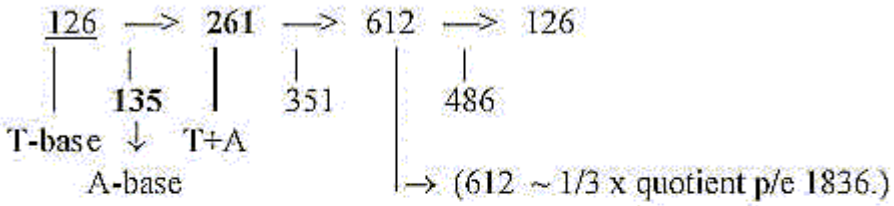
1/543+ 1/210, Λ = 151,4. ~ G-base 151.

30. **Mass number of C-base 111:**

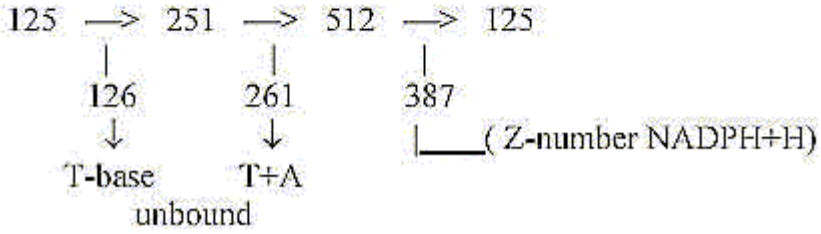
$\sqrt{1\text{-}2\text{-}3\text{-}4\text{-}5} = 111{,}1. \sim$ C-base 111

31. **Rolled numbers:**

T-base unbound =126 A



T-base bound 125 A:



*

6. Enzymes – Coenzymes

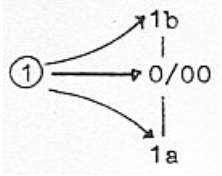
Some elementary views:

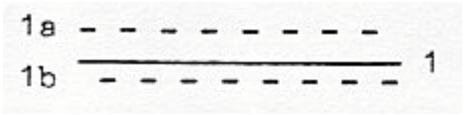
1. **How regard protein enzymes in relation to the dimension model?**

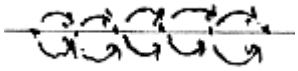
They are obviously acting as "forces", binding and breaking (~ polarizing) in relation to substrata, however, per definition, not transforming into other molecules, not involved in that sense.

Hence, the 0- and 00-poles defining Direction as d-degree 4, a vector geometry, which according to hypotheses in physics have been assumed transforming (possibly through inversions) to mass and particle structures (fermiones), is not the case here.

Instead we have to regard enzymes as expressions for these poles when they meet in last step 1 → 0/00 of motions, the enzymes here as "oscillating" between binding and breaking, expressions for poles 1a ("motions towards each other", defining a new centre) and 1b ("motions from each other", defining a new anticentre).







Chains of enzymes illustrate *metabolic pathways* (as such primitively seen as "linear"). There is however only one enzyme for each step on the way. Individual enzymes represent only the very jumps between stages (the metabolites): happenings in their active centra with just a few amino acids involved.

One example: the enzyme which breaks fructose dividing it in two parts, where His and Cys co-operate.

Last step 1→ 0/00 is represented in every step of decreasing d-degree in the dimension chain (or inwards increasing (1←0/00).

Hence, it would be possible to imagine that protein enzymes (Ep) originated from development of secondary dimension chains in each step of underlying chains, as the *level* development have been assumed in this model. In similarity with how new bubbles of economic activity and money circulation are developed through history and modern societies from more direct ways of "metabolism".

An immediate objection against these sketched views is of course that steps between metabolites or substratum/product(s) seldom appear as changes in d-degrees in any identifiable way. Why should they? The assumption here is that the enormous complexity in a cell and hierarchies of newer and newer levels out of earlier steps hide the origin in elementary dimension chains. Levels and distribution of charge and of energy may at higher levels be the only observable expressions for the different d-degrees.

2. Structure:

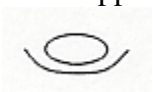
Keeping to the view on protein enzymes (Ep) as representing new levels developed out of d-degree steps, it could explain why enzymes geometrically enclose substrata as anti-centra in relation to centra. In the same snse that lower d-degrees represent manifolds

and anticentra (00) in relation to higher d-degrees, superposed levels become anticentra in relation to an underlying level.

Geometrically the relation is a typically complementary one, earlier called "*the lock and key*" model, later modified to "*the induced fit model*". It's a matrix relation and one expression for the complementarity between poles in the dimension model here.

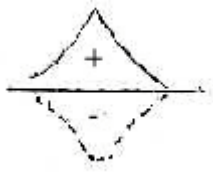
Cavities in enzymes with hundreds of amino acids are to a certain degree adapting to the small molecules of substrata, which also may undergo slightly changes in structure to fit in.

This main centre of the reaction could be described as positive/negative forms, similar to the opposition Mass/Space;



In terms of energy, this relation could be described as partly inversed:

If the needed activating energy for a reaction without enzymes is regarded as an energy wall, similar to the potential wall (+) around an atomic nucleus, the complementary principle would appear in negative energy (-) of space, as a hole.



The observations concerning activation energy levels (just decreased by enzymes) and speed of reactions should perhaps be regarded as only secondary results of the decisive complementarities in geometrical forms, in charge and hydrophobic / hydrophilic polarities.

Both the long chains of amino acids in the proteins, the "global structure"or complicated (stepwise) folding where each part has a special function - and the specificity of the enzymes, generally catalysing only one special reaction in their active centra, seems to agree with the view on enzymes as developed from the steps in the dimension chain.

Protein enzymes (Ep) with coenzymes (CoEp), including "prosthetic groups", appear as a new level with the same anticentre - centre relation as protein enzymes to substrata.

On this level the coenzymes as a kind of "substrata" are carrying mass, very small molecules beginning with H^+ and e^- as primary "carriers of forces" on the biochemical level. (About the coenzymes, see below.)

The coenzymes are mostly more or less closed ring-formed molecules and many are derived from the codon bases, the nucleic acids. If we regard the ring-forms from the aspect of $sp(d)^x$-hybridizations, they imply steps in the $2x^2$-chain for electron orbitals from the "end" towards the middle of the number chain. We find similarities between the *d*-orbital shape in some illustrations and the ac/c-relation of proteins to coenzymes, which also include several metals in the d-orbital of the periodic system.

We get enzymes illustrating anticentra on different levels and in relation to different dimension steps.

RNA has also been found to have a certain catalytic capability, and a central enzymatic function is performed by the ribosomes at the protein synthesis (step 3 - 2 in our earlier interpretation). The complementary polarity between the base pairs in the relation codons — anticodons at sites of ribosomes could perhaps be regarded as the first example of an enzymatic principle, generalized into all enzymatic activities by pure proteins?

In that context one could ask if there is a deeper connection between the

few amino acids chosen as active centra of Ep and the substratum, e.g. between His and Cys and fructose? Or if they just happen to fit the needed operation?

Mass numbers of side chains of His and Cys is 81 and 47 (uncharged). These numbers reappear in the distribution of 128 C-atoms to codon grouped amino acids as well as approximately between C-atoms of side chains and backbone parts of 20 + 4 double-coded ams (82 - 48). First two bases in their codons are anti-codons to each other when read in opposite directions. Could this have a deeper sense, a connection with the division of fructose in 2 C3-molecules in step 3 - 2 ?

With such facts and others it seems as the whole processes of glycolysis and citrate cycle should be regarded as in some way *"created"* by the proteins, developed from peptide relations or follow from analogous, connected schemes, not only the other way around. (Cf. e.g. that the sum of the 10 stations in citrate cycle + 8H from it amounts to the same sum as the side chains of the 20 + 4 double-coded amino acids.)

It's said that there are about 4000 catalytic reactions in a cell. It would be interesting to know how many of these that are performed by pure Ep-enzymes, how many through coenzymes. (An eventual number relation?) Another question concerns the relation between structure proteins and protein enzymes, if a border is possible to draw. The "walking" of molecules on microtubules in cilia for instance (and in ion canals?) have also been described as enzymatic. Correct? If so, we have an illustration of the last step in our dimension model from linear d-degree 1 to motions to and from as steps in walking.

Polarities reflecting complementary features between poles in the dimension model, a summary:
a. Protein part of enzymes versus coenzymes
b. Enzymes in relation to Substrata
c. Binding versus breaking enzymes
d. Activating versus blocking function (stimulating - inhibiting) in regulating systems

3. Origin of protein enzymes?

It would be much easier to believe that substrata or substrata relations create their own enzymes or in any case decide the folding of these long protein chains, than that they are synthesized independently and just happen to fit a certain catalysis. The "induced" adaptation possibility of the folding of enzymes seems to reflect a little of such a thought.

However, it should demand that proteins or chains of amino acids in some way could create their own codons for storage in DNA. Is there anything pointing to such a possibility in the earlier evolution. If possible, it seems left to the future to detect. (?)

More points to a similar but parallel evolution of amino acids and nucleic acids, following from related schemes. (Cf. in documents about the genetic code mass sums of amino acids, 2 x 544 + 2 x 208, derived from the "exponent series", and mass of codon bases in the same chain when transformed to number-base 8.)

We may remind of the arithmetical relations between sums of amino acids and bases in the figure here and ask if a similar relation could exist between more or less virtual chains of substrata or metabolites as pathways and the protein enzymes catalysing the steps?

(In a complex enzyme as *amino acyl tRNA synthetase*, binding both tRNA, ATP(AMP) and the single, specific amino acid for this tRNA, it has been shown that also all kind of organic bonds are included. bonds that are possible to interpret as steps in a dimension chain.)

The figure referred to above with arrow bows for multiplication could lead to another speculation:

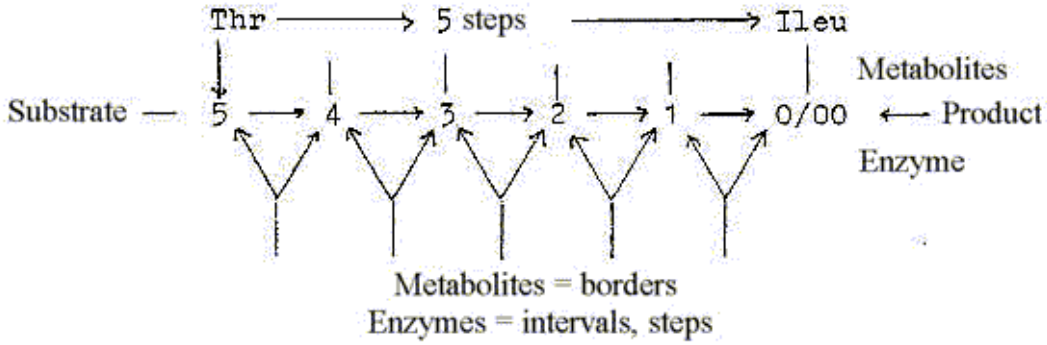
Frameshifts in decoding of a ring-formed RNA should lead to totally different proteins. Could such frameshifts be connected with the difference between protein enzymes and other structure building proteins?

Frameshifts may illustrate *the brick wall principle,* however not applicable to the relations between enzymes (Ep) and substrata, only to hierarchies of proteins.

One more question concerns the number of enzymes involved in the transformation of a molecule as substratum to the "end" product; for instance 5 enzymes for transformation of the amino acid Thr to Ileu, 10 for synthesis of the amino acid His, 8 for synthesis of Arg, according to a forgotten source.

Could these numbers of enzymes in their turn have a deeper connection with d-degrees?

One example of enzymes transforming the amino acid Thr to Ileu in 5 steps *:

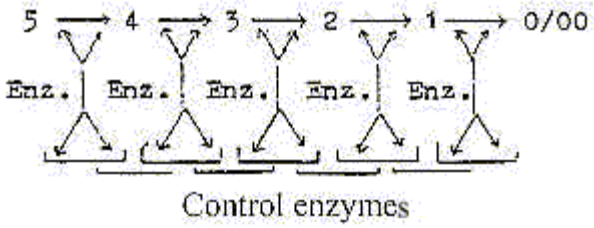


Intervals as expressions for underlying or superposed level - or secondary developed dimension chains in the steps? Representing other coordinate axes?
The process here in mass numbers: -2, +44, -32 as -16, -16, + 2.

4. Control enzymes:

They illustrate the hierarchy of proteins (as of genes) and represent still another level, a bureaucratization.

The brick wall principle, following from displacements in half steps between levels appears as the most natural for this relation between enzymes and control enzymes. (Possible to identify as such?) If they control not only individual steps but the order of steps, they represent changes of second order and may be interpreted as substantiations of the very process as such.



In the dimension model what is motion in one d-degree derives from a d-degree step and is structure in higher d-degrees. A process as a series of changes may be regarded as a chain of motions. The dimension chain of motions in the model here get the opposite

direction to the chain of structure. The motional patterns, the changes themselves, may be substantiated during evolution, saturated to structures.

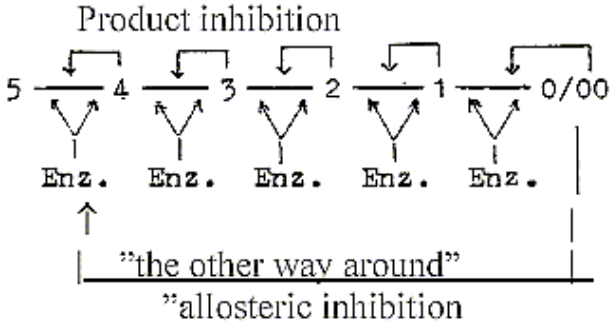
5. Activating enzymes and product inhibition of two types:

Inhibitors as products, or substances often similar in structure, act as a **feed back** mechanism. In the dimension model poles of each d-degree have character inherited from the 0- and 00-pole respectively as 4a ~ inward direction, 4b ~ outward direction.

Hence, the "*product inhibition*" could represent this inward pole in each step, affecting the active site of the enzyme. The complementary pole with feature from the 0-pole should represent the "**feed forward**" mechanism.

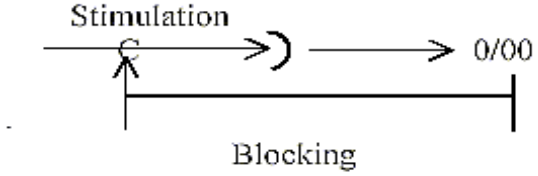
At the other kind of inhibition, the "*allosteric*" one, an enzyme in the start of the chain is affected and at another location than in the active site of this. It means that the enzymes also have the centre - anticenter polarity in themselves, centres as active sites, the anticentre expressed in the distant other location. With the suggested illustration below it could express a) the close connection between step 5 - 4 and 1 - 0/00 in the loop model of a dimension chain (the polarization steps 5 → 4/1 → 3/2), and b) the connection between anti-center at end of the chain (in d-degree 0/00 of Motions*) with the pole 00 of d-degree 4 (00 — 4 — 0).

* (The "d-degree 0/00" substantiated during evolution toward higher levels.)



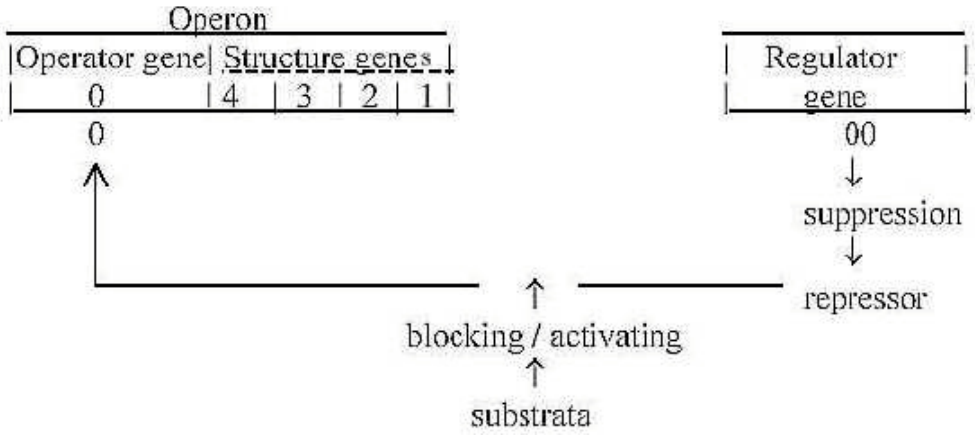
Regulating mechanisms of the types "product inhibition" and "allosteric" inhibition":

It seems as a congruent, similar pattern of inhibition is repeated on the higher electromagnetic level, in a developed **nervous system** where a cell nearby may inhibit a cell from activation through signals "- ½". Another system is the "lateral inhibition" which blocks incoming signals further away from the cell?



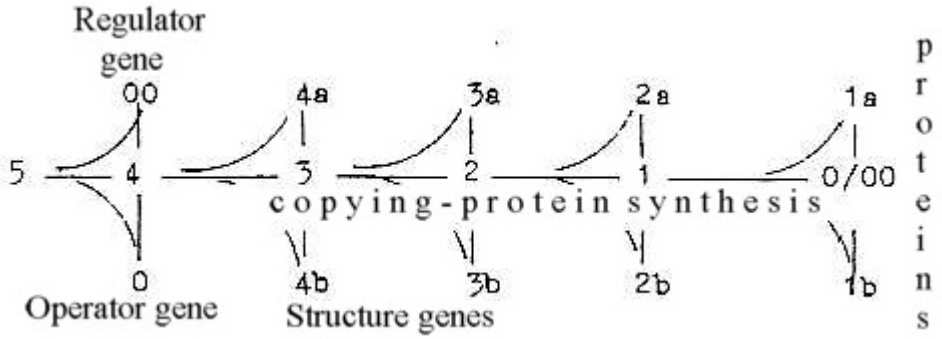
A blocking synapse on another location than in the pathway of the signal.

A corresponding regulating structure seems to appear between genes in DNA:



Operator gene and Regulator gene as a primary polarization in complementary poles:

With the aspect from the dimension model in mind:
- From 0-pole: quantified steps, structure building from inside outwards.
Structure genes connected with the 0-pole. (Cf. "feed forward" mechanism ~ outward direction.)
- From 00-pole, the pole representing continuum, repetition and multitude:
00 = anticentre, regulating gene in another location in the chromosome, reminding of the "allosteric inhibition" among enzymes. (Cf. feed back" mechanisms ~ inward direction.)

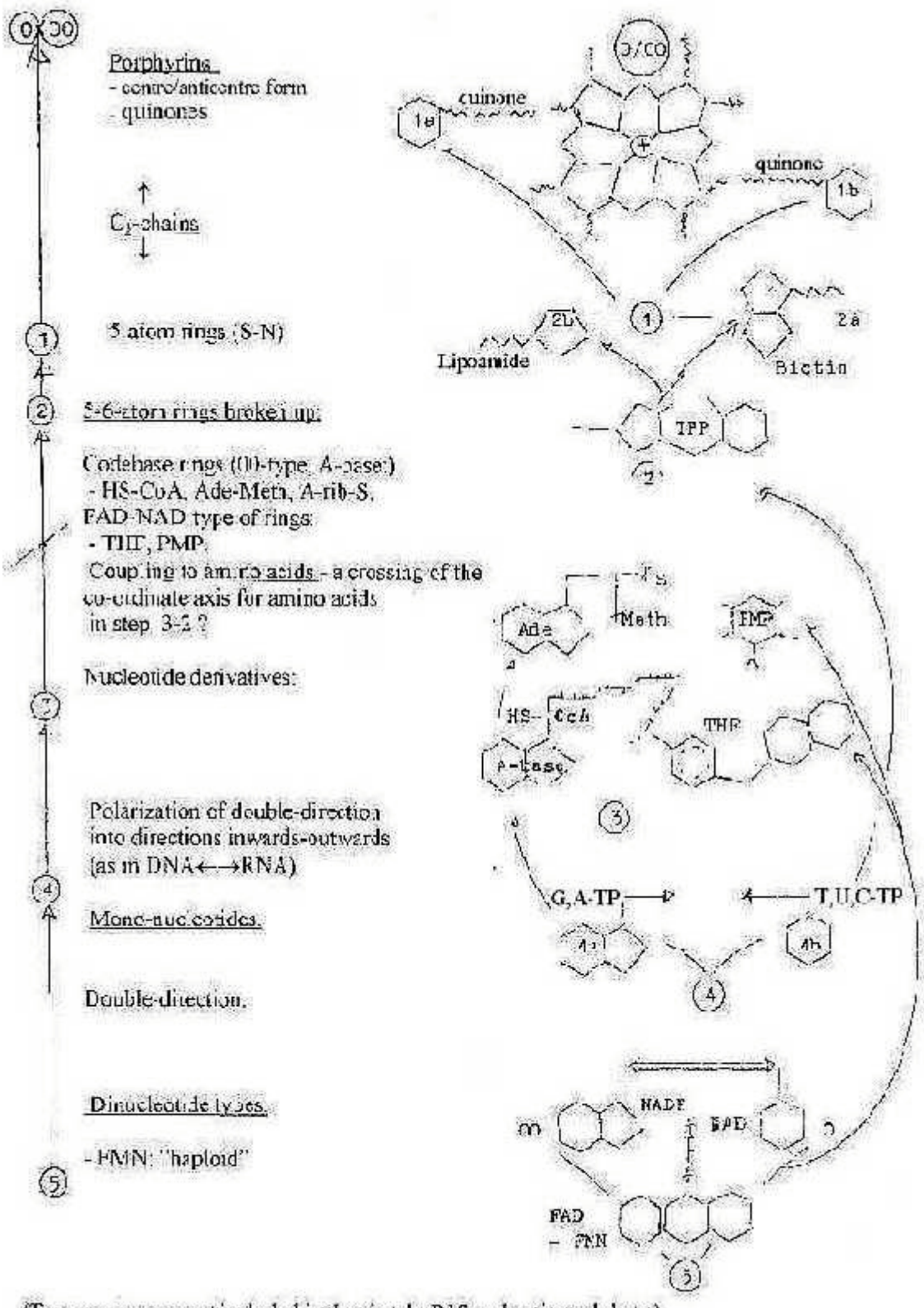


Coenzymes

Forms of the coenzymes?

An attempt to range the forms in a scheme of polarizing steps and in a certain degree according to heaviness is made below: Only giving a hint of eventually possible aspects.

Since most data indicate that nucleic acids and amino acids is coupled with d-degree step 4-3 as the step for "A-Z-numbers" of N, nitrogen, this position is kept in the sketch.



(Two coenzymes not included in the sketch: B12 and active sulphate.)

Calculations with mass numbers:

In the primary reference here (*P. Karlson:Biokemi 1976)* 25 coenzymes are mentioned, that's 5^2.

The simple number 25 became a temptation to study the coenzymes a bit closer to see if they in some sense could be interpreted as representing a dimension chain in agreement with this model. Such a task is of course a very suspicious one:

Firstly, the number of coenzymes may be just a selection out of many more. Secondly, regarding mass analysis, many of the coenzymes appear in different forms, for instance with or without carried groups or in -TP-, -DP-, -MP-forms etc. Following choices were made in the table below.

- Codon base enzymes in their -TP-form.

- THF, tetrahydrofolacin as formyl-THF

- PMP, pyridoxaminphosphate (PLP-form = -1 A)

- TPP, thiaminpyrophosphate

- Ubiquinone (said to include "6-10" isoprene molecules), here 8 supposed.
In mass numbers +1 are included for all negative charges and for bonds to other molecules, without regard to some (balancing?) positive charges.

25 coenzymes, A-numbers:

H-transporting enzymes. 5:				
FAD,		785	+2H	
FMN		456	+2H	
NADP		744	+H+H	
NAD		664	+H+H	
Lipoic acid		206	+2H	...Sum 2865
e-transporting enzymes. 5:				
Cytochrome	a	854		
"	b	616		
"	c	560		
Chlorophyll	a	614		
"	b	628		...Sum 3272
Codebase enzymes. 5:				
GTP		523		
ATP		507		
TTP		498		
UTP		484		
CTP		483		...Sum 2495

Cx-transporting enzymes 5:

C1-transporting enzymes:		
Formyl-tetrahydrofolic acid THF	474	
Adenosylmethionine	400	
Biotin (free)	244	...Sum 1118
C2-transporting enzymes:		
HS-CoA	767	
TPP	425	...Sum 1192
Transporting other groups*. 3:		
Active sulphate	507	
PMP	248	
Coenzyme B 12	1579	...Sum 2334
Quinones 2. regarded as meating places for H+ and e-:		
Plastoquinone	748 +2H	
Ubiquinone (if 8 isoprene parts)	726 +2H	...Sum 1478

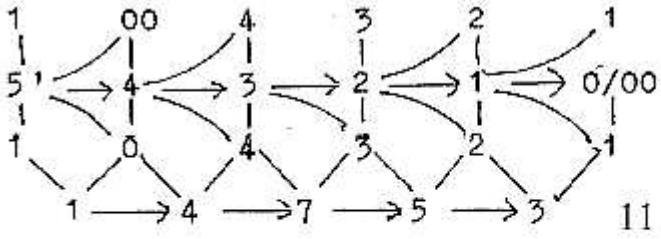
* (transport of S- resp. N-groups, and B 12 of H-, C1- or OH-groups among other things)

5 H+	2865
5 e-	3272
5 codon bases	2495
3+2 C1+C2	2310
3 other groups	2334
2 quinones	1478..... Sum 14754,

-1 if PLP = **14753**.

An alternative form of the dimension chain has been tested before (not published) in connection with amino acids. Here d-degree 0/00 as equivalent with 5' is the start, hence with outer poles 1a —1b. The superposed chain gets altered to the number chain

1-4-7-5-3:



11 x 4321 = 4-7-5-3-1

$54{,}321^2$ x 5 =
=<u>14753</u>, 86..

- Triplet 975 from ordinary superposed chain (9-7-5-3-1): $97{,}5^2$ = <u>2 x 4753,1</u> 25.

- 2 x 753 = 1475 + 31 = 1506 = 24 amino acids (R-chains) with +2H. (31 = Serin)
  (1475 + 4753 = 3278 = 24 amino acids, R+B-chains, with + 2H.)

- Quinones: 1-4-7-5 + 3 = 1478 A

- √543210 x 2 = 1474. = sum of quinones without 2 x 2H

- Quinones + e-group = 1478 + 3272 = 4750 A

```
1 - 4 - 7 - 5 - 3
|     4750      |
|               |
1 - 0 - 0 - 0 - 3  = rest
```

Mean value of a coenzyme = 14753/25 = 590,12.
590 is the sum of one of the "factor chains"

5 x 54 = 270.	x 25 =	6750
4 x 43 = 172	x 25 =	4300
3 x 32 = 96	x 25 =	2400
2 x 21 = 42	x 25 =	1050
1 x 10 = 10	x 25 =	250
590	**Sum**	**= 14750**

The coenzymes in 5 groups - as in 5 steps - in another way, where those transporting other molecules are split on the C2- and C1-groups.

Dividing the mass sums with factors 54, 43, 32 etc., gives a sum which is an inversion of the real total: (Sign for division here ÷.)

5-4:	H^+-group	2865	÷ 54	= 53,05
4-3:	Codon base group	2495	÷ 43	= 58,02
3-2:	C2 +NHx-group + kinones*	3177	÷ 32	= 99,28
2-1	Cl-group*	2944	÷ 21	= 140,19
1-0:	e^--group	3272.	÷ 10	= 327,20
	Sum	14753	Sum	677,749

↓

Λ

= 14754.7. $\times 10^{-7}$

* Explanations:
3-2: C2-group HS-CoA + TPP = 1192, + Active sulphate 507 = 1699.
+ Quinones as 0/00-centres meeting in step 3-2 = 1478. Sum 3177.
2-1: C1-group 1118, + PLP + B12 = 2944.

Step numbers 5 - 4 - 3 - 2: 53.05 + 58.02 + 99.28
= 210,359
Λ ⟶ 4753,778 x 10^{-6}

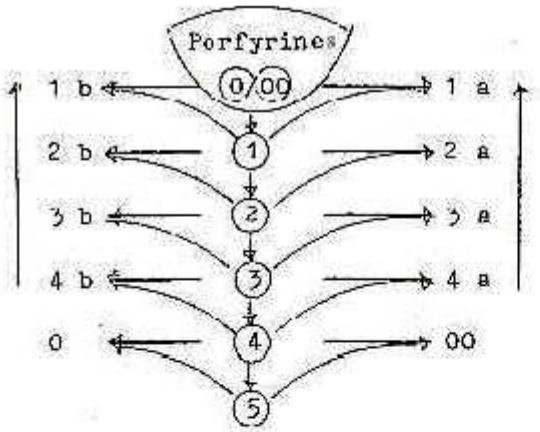
Porphyrines:

Mass sum of all 25 coenzymes with PMP: 14754.

Porphyrines, the e^--transporting coenzymes: 5 cytochrome and chlorophylls = 3272, + B12 (1579) = **4851**. 4851 = 21 x 231 or 11 x 21 squared..
Without +1 for bonds and negative charges in cytochromes and chlorophylls (=-6) the sum becomes 4845.

Without adding +1 for negative charges in the rest of coenzymes and only 2 H rolled in quinones and H+-group (= -12 H) we get the sum 9876 for the rest.

A dimension chain with poles:



3 vertical chains Sum

Outer poles outwards: 4 3 2 1 x 2 = 8642

\+

Centre line inwards: 1-2-3-4 x 1 = 1234

——> 9876
A-number without porphyrines

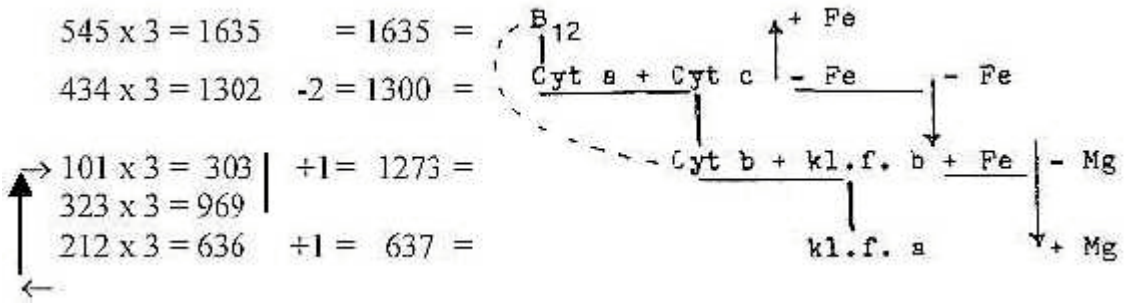
Horisontally "potentials" x 3

1-0-1
2-1-2
3-2-3
4-3-4
5-4-5

x 3 = 4845 ——> 4845
A-number porphyrines

(Difference 9876 - 4845 = 5031 = 3 x 1677. 1677 = sum of 4 RNA-bases as coenzymes in DP-form.)
Total sum here 14721 = - 33 (or 32,depending on counting with PMP or PLP.)

Divisions within the porphyrine group:
- The potentials of the dimension chain x 3:



(Here porphyrines as charged and in bonds, a part only from uncharged P-group in B12. B12 connected with activity of haemoglobin?)

Last potential 101 should here be imagined as appearing within the 3-2-step. There we get the border then between cytochromes and chlorophylls, a border between plant and animal life too.

If the thought above should have some sense, it could throw light upon why porphyrines are stored as piles (or columns), discs upon one another just inside cell membranes, d-degree 2 in form. (Cf. total number 4851 = number 21 for step 2-1 squared, x 11.)

And why the "virtual" displacements of the metal atoms (here illustrated as polarized in directions on level 4-3-4; poles 4a-4b representing opposite directions)? Illustrating some transition functions in a development towards higher d-degrees??

Sum of 5 code base enzymes in -TP-, -DP, -MP-form, uncharged:

$= 2495 + 2095 + 1695 = 6285 \approx 2\pi \times 10^3$

TP-form: 2495, Λ = 4 00 8 0 16 32 ... . = 2^x-chain $(x = 2 \rightarrow n)$

Mean value 499 Λ = 2 00 4 00 8...

(See further about these coenzymes here, part 2, Transformations between number-base systems.)

NADP - ATP, Z-numbers 256-260, 381-387:

ATP: 256 Z. charged -4 at P-groups.
260 Z uncharged

NADP: 381 Z, charged -4 at P-groups.
385 Z uncharged.

NADPH (+ H): 386 - 387 Z

NADPH + H:		ATP	
387, inverted Λ	=	258,40.	x 10^{-3}
387, lg: —>	=	258,77.	x10^{-2}
387. x 2/3 —>	=	258	(9 x 43 —— 6 x 43)

How many numbers exist that comply with all these three equations?

$1/b = a \times 10^{-3}$
$\lg b = a \times 10^{-2}$
$b = a \times 3/2$

If these arithmetical relations should have some hidden sense, it could imply that there existed some "dynamic balance" between charges of these molecules.
Or some principle between different parts of the molecules at the construction?

a. Allowed intervals:
Inversions: 384-387 —> 260,.. - 258,...
log-equation: 381-387 —> 258,...
3/2- equation: 384-387 —> 256 - 258

b. Triplets of the dimension chain: 543 / 210 = 258,57. x 10^{-2}, Λ = 386, 74. x 10^{-3}

b. $\sqrt{15}$ = 387,3. x 10^{-2}, Λ = 258,2. x 10^{-3}
15 = Z-number of P, phosphor = 5+4+3+2+1+0.

c. $\sqrt{2/3 \times 10^5}$ = 258,2. $\sqrt{3/2 \times 10^5}$ = 387,3.
(Another aspect on the 3/2-relation)

d. Group PO_3^{2-} = 39 Z, Λ = 256,41. ~ ATP^{-4}, Z. (as a periodic number)

e. NADP, mass number (A) as the inversion of that of the A.base, bound and unbound

	The part	inverted to	the whole	
A-base unbound	= 135	Λ	= 740 740 740...x 10^{-5}:	740 = $NADP^{-4}$
A-base bound	= 134	Λ	= 746,3.x 10^{-5}:	746 = NADPH+H

1/744 (NADP) = 1344,1. x10^{-6}. 1344 = B-chains of 20+4 amino acids bound.

Compare FAD: **Riboflavin** part — inverted — ribos-Adenine part

Mass-numbers: 375 /\ = 266 $x10^x$

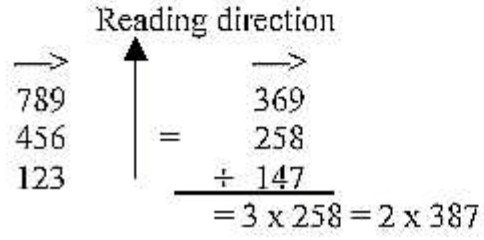
2 parts each others inversions

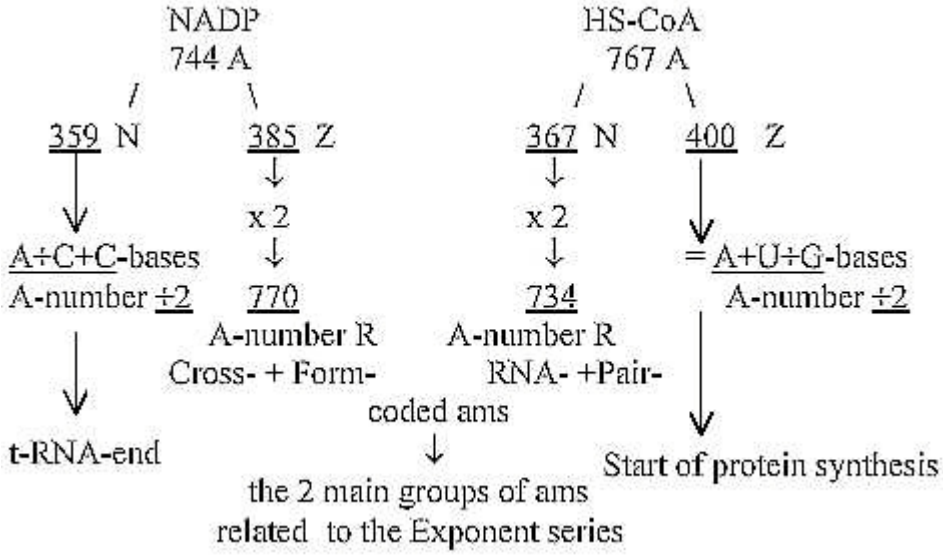
f. NADP, Z, uncharged = 385 is the sum of a "factor chain":

1x55
2x44
3x33 - 385 (också A-talssummor av korskodade ams R-kedjor)
4x22
5x11

385 as a mass numbr is also appearing in one of the 12-amino acid groups, "cross-coded" and "form-coded" ams (sidechains).

g. 9 figures 1-9 as triplets in angled reading:





(Both these coenzymes are involved in the glycolysis and citrate cycle, where amino acids have their origins - but these divisions in N-Z-numbers and mixed sums seem as a cruel violation of even the slightest possibility of a scientific theory?)

*

7. The chemical elements of life

Application of views from the dimensional mode:l
(*With some repetitions from other files.*)
See also file The cell, in Biology, first pages.

There are 5-6 elements primarily which build up the main structures of life as lipids, carbohydrates,.proteins and nucleic acids. The number worth noting.

H - C - N - O - P - S in order of weight

Valences :

P - C - N - O,S - H

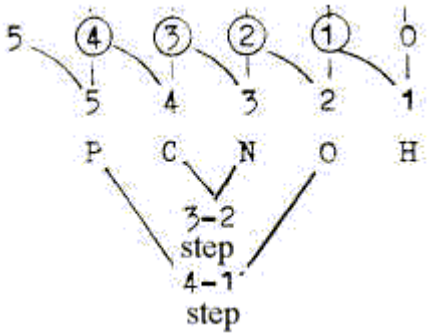
5 4 3 2 1 as numbers in a dimension chain.

P, with valence 5 in phosphate groups PO4 (to ~PO3) has a special function as a "binding force" in the other main substances - for instance in the DNA-spiral and in phospholipides and as energy storage in ATP. These functions could give arguments for interpreting the valence number 5 as an expression for dimension degree (d-degree) 5 as a first binding force. (See further P-groups below.)

In whch sense can the valence numbers represent d-degrees? Elements has been regarded as developed in step **2 - 1** in the underlying fundamental dimension chain, With development of a new dimension chain in this step (according to the principle of level development in this model) the different secondary d-degrees could be expressed **linearly**, that is in terms of d-degrre **1** - as valences, a number of potentially bond directions.

(In relation to properties of the fundamental chain --> Direction (vectors) --> mass/space --> charge --> distances , it would perhaps be possible to regard the C-atom as an expression for the vector character in directions (in its building of C-skeletons), and O-atoms as an expression for charge, but hardly the N-atoms in any certain sense related to the property Mass or Space!)

A figure connecting P---O and C---N, with the loop model of the dimension chain and "outer poles" indicated, here as valences:



Here the poles represent valences but the d-degrees the polarization of 5 in 4–1, and 3–2.

In the fundamental chain of the model mass and space are assumed as d-degree 3 in

relation to Charge as a property defined in d-degree 2. One could here see the uncharged C-atom as the space-building one, while N and O represent charges, in opposition to one anotheter: N plus as inward direction, the O-atom the negative charge as outward direction. So for instance in the peptide bonds (NH3 --- COO-).

Direction around the atoms:
The division of bond directions around the atoms seem to illustrate dimension steps:

C-atom: bonds 4 →3 + 1, e. g. the tetrahedron configuration in amino acids.
N-atom bonds: 3 →2 + 1, e. g. in peptide bonds or when bound in rings of bases.
O-atom bonds: 2 →1 + 1.
(The bond directions become stepwise more polar in order C → N → O,)

The P-atom with 4 O-atoms, one oxygen double-bound, crosswise distributed, seems to illustrate the step 5-4, 4 directions outwards, one complementary inwards, as illustrating a still unpolarized d-degree.
It ould be noted that the Z-number 15 of P-atom is the sum of poles in the dimension chain 5 -4 - 3 - 2 - 1.

Classes of substances:
The elements may be regarded as characterizing main classes of substances, connected

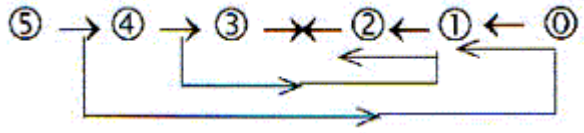
N with proteins (and coding bases),
O with carbohydrates,
H (in CH2) with lipids.

These classes could in some sense on a macro-scale level be regarded as equivalent with (~) following d-degrees in the cell:

lipids ~ surfaces, 2-dimensional,
carbohydrates ~ volumes, 3-dimensional,
proteins then ~ vectors, 4-dimensional.

Hence, as characterizing macro-molecules, the valence numbers of the atoms N - O - H as 3 - 2 -1 are increased 1 d-degree.

K-L-M-shells:
The elements H-C-N-O-P-S represent shells K-L-M, shell numbers 1-2-3 in the periodic system, and orbitals 2-1, 1-0/00. Inversely we could regard these shells - from inside outwards in the atomic structure, as steps 5-4-3 in the chain of processes.
With debranched degrees meeting "the other way around, step 5 → 4 gets represented by the K-hell, step 4 → 3 by the L-chell; both views are possible.



The $2x^2$-chain behind the periodic system:

5	4	3	2	1	
50 —	32 —	18 —	8 —	2 —	0 *numbers for additions to whole shells*
	P	N	L	K	*whole shells*

O M
(x) f d p s *orbitals, intervals in numbers of electrons*

C-N-O-atoms belong to L-shell and the p-orbital in step 2 - 1, P and S to the M-shell of higher d-degree..

In the dimnsion model higher d-degrees are defined as binding forces in relation to lower ones and it could be observed that P and S in the 3rd shell appear as elements with binding properties on a higher, more complex level in DNA-RNA (P-atom) and among proteins (S in the amino acid Cys, creating S-S-bonds in the folding of proteins).

Covalent bonds:

The covalent kind of bonds give the structures in living organisms. These bonds of the elements imply "***shared shortage***" in relation to the "octette rule". Number 8 in the outmost shell represents a complete surface. Cf. number 8 in the $2x^2$-chain at x = 2; in the dimension model d-degree 2 for surfaces.

It's worth pointing out that it's not complementary poles (atom kinds) that bind to each other here but more or less similar ones, giving *counter-direction mutually* (→ ←) seen. (The degree of covalent bond beeing 60-100 %.)

About metal ions, see further below.

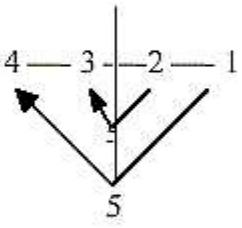
Some numbers:

a. P-atom, 31 A; Cf. DNA-bridges: N- H ---- O=
= 31 A

b. Number of electrons (e-) in the *p*-orbital for C-N-O: 2-3-4

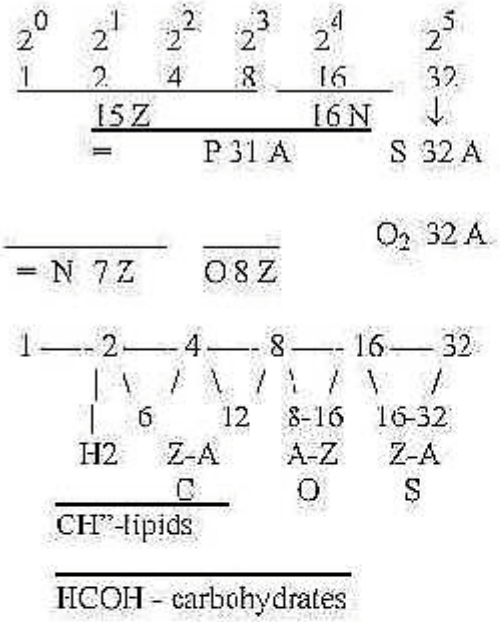
c. Z-numbers 1 - 6 - 7 - 8 - 15 for H - C - N - O - P:
14 23

Numbers 1-4 and 2-3 as read in the loop model:



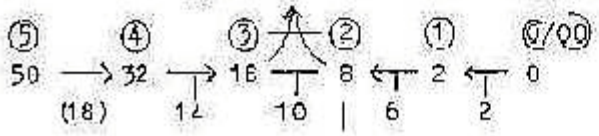
d. C - N - O P - S
42 A 63 A (See point *h*)
\ /
2/3 quotient

e. Z-A-numbers in the 2^x-series, sum 63 A:



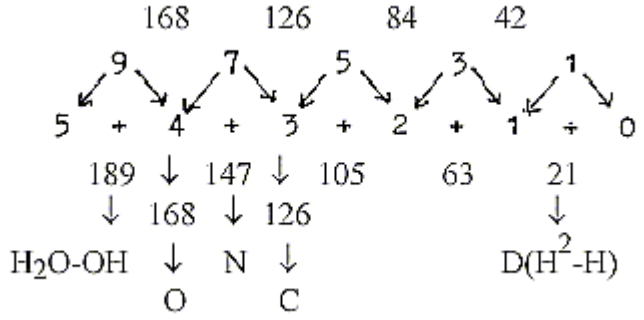
f. The figure sum 63 of series 2^x is about the mean value of side chains of amino acids in the genetic code. (62,67.), one half of the "magic number" 126.

g. Condensation = - H_2O dimensionally interpreted? As - 2, - 8 Z, (valences 1 and 2) in the $2x^2$-series for whole shells and orbitals in the periodic system, as combining molelcules through elimination of their charged lower d-degree steps:



H_2O: 10 Z, number 10 in step 3-2.
Condensation as depolarization ~ increase in d-degree for level development.

h. "A-Z"-numbers of elements:Number readings downwards with additions:
95 + 94 = 189, 94 + 74 = 168 etc.:



This "A-Z"-chain may illustrate the two main fusion processes: the right half the first elementary fusions from e.g. D to He to Li... (with steps between dismissed), the left half the carbon-nitrogen cycle in the sun. Here we have factor 21 in the steps and numbers 42 and 63 (*point d*)

Metal ions as "trace elements":

The function of metal ions is partly not understood (or hasn't been earlier (1976). Some general hypothetical aspects are given here departing from the dimension model:

1. At the level of elements in the periodic system metals may be interpreted as representing the "00-pole" in relation the non-metals as "0-poles" (i.e. C-N-O…). This polarity (complementarity) expressed in minus/ plus, lack versus surplus in relation to the octet rule.

According to first postulates in the model, metals then corresponds to "anticenter", inward direction and polarizing forces.

2. Metal ions represent "anticenter" as the surrounding of organic cells, in sea water or soil or clay of some kind. And charge is positive outside of the cell membranes (rest potential).

Metals are used to build skeletons, by unicellular organisms, and in multi-cellular animals the skeleton was from the beginning an exo-skeleton (as "surfaces"), which through immigration (direction inwards) became an endo-skeleton. This illustrates one general principle of life, the successive built-in of the 00-pole during evolution (as later in the evolution the built-in of the environments differentiates internal forces into a psyche).

With regard to the organs, the lighter metal ions Na^+ and K^+ gets the central function in nervous signals, Ca^{2+} role in skeletons and muscles. The nervous system and skeleton cells derive from the neural plate at the animal pole of an embryo and ectoderm, in embryos the 00-pole, outer cell layers (*Biology,* not yet translated files in this booklet series).

At the same time some metal ions as Fe, Mg, Cu become built-in to centres in coenzymes, as in porphyrines: centres as end points of inward directed vectors. (We could perhaps regard these heavier metal ions from a higher atom shell as stronger vectors, pointing deeper inwards.) There is also the feature in our model of a "pole exchange" in last step of the dimension chain, inward directed motions defining new centres.

(Such a pole exchange may possibly be expressed as the repeated changes in potential over the membranes of axons making up the nervous signals.?)

The 00-pole represents also manyfoldness and separation: as primarily isolated atoms in contrast to the structure building non-metals.

The "S-curve" which describes the gradual transition from dominating covalent bonds to ion bonds in electronegativity, may be regarded as an expression for the complementary relation between non-metals and metals in lower d-degrees: a polarity "concave/convex" as one of the assumed geometrical definitions in d-degree 2.

Geometrically the inflection points of such a curve (representing a polarized surface) make up a line, d-degree 1 (2b---1---2a in the model) and could eventually be though of as defining a first border for a cell. (Cf. lipids.).

It follows from the assumptions in the dimension model that metal ions as 00-poles should have a polarizing effect or function. The common expression that many enzymes are "activated" by Me-ions seems to imply just this fact. A few examples:

- Ca contributes to cell division.
- Fe divides the O2-molecule (in haemoglobin) through a step $Fe^{2+} \rightarrow Fe^{3+}$.
- Mn takes part in photolysis, the division of water.

(Very hypothetically one could wonder if for instance the richness of Zn in eyes - (and of Ca in the balance organ) has something to do with the "bifurcation" to 2 eyes or 3 semicircular canals?)

Metal ions, incorporated from the environment, go to and gather in different organs according to their indivual atomic kind. Hence, there is a connection between one or a few organs and a certain metal. It doesn't seem as only the electron configuration furthest out, the group in the periodic system, was determining this connection, even if this also may be the case. (Ca, Calcium, and Strontium in the same group go both to bone tissue).

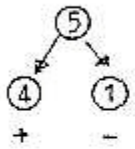
Cadmium, Cd, and Hg belong to the same group but Cd is said to gather in kidneys while Hg gathers in the nervous system and brain. Zn in the same period goes chiefly to the eyes.

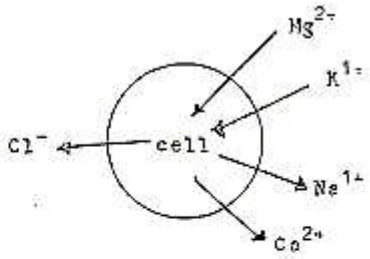
A general hypothesis here is that mass numbers like Z-numbers are derived from a dimensional evolution, and also on a higher level the embryonic development of different organs in organisms. Then it ought to be possible, at least theoretically, to trace a dimensional connection between the different Me-ions and the differentiation of organs?

Some small annotations about the 5 ions Na, Mg, Cl, K, Ca:

Na^{+} - K^{+} - Cl^{-} - Ca^{2+} - Mg^{2+}

5 ions divided into 4/1: 4 plus-ions,





Of the 4 plus-ions 2 are dominating inside the cell, 2 outside.

Mg + K : 12 + 19 = 31 Z, 24 + 39 = 63 A
Na + Ca: 11 + 20 = 31 Z, 23 + 40 = 63 A... sum 126 A (a "magic number")

$31 = \Sigma\, 2^0 + 2^1 + 2^2 + 2^3 + 2^4$. 63 = sum of the series $2^0 - 2^5$..

Mg + Na: 23 Z. 23 = A-number of Na, → e-shell ~ M
Ca + K : 39 Z. 39 = A-number of K, → e-shell ~ N

Mg^{2+}, Ca^{2+}: connected with ligh, Mg: in chlorofyll, Ca with D-vitamin.
Na^{1+}, K^{1+}, + Cl^{1-} : connected with the nervous system.

Zn-ions are said to manage the balance between the other ions,
a function possibly, as a suggestion, connected with the e-numbers:

In:	Mg^{2+}	Ca^{2+}	Out	= 28 e-: 10 + 18
Out:	Na^{1+}	K^{1+}	In	= 28 e-: 10 + 18
	Zn^{2+}			= 28 e-

Na^{1+}-Cl^{1-}

↓

28 Z

60 A with Cl 37 A

58 A with isotop Cl 35 A

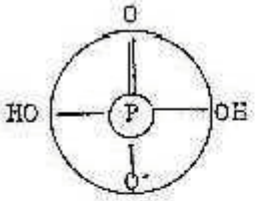
50 - 32 - 18 - 8 - 2 - 0

58

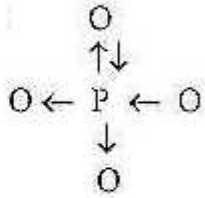
28

60

P-groups, various small annotations:

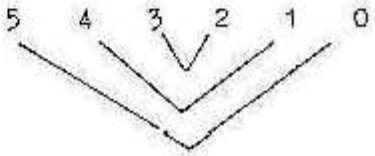


Valence 5 divided 4 outwards, 1 inwards:

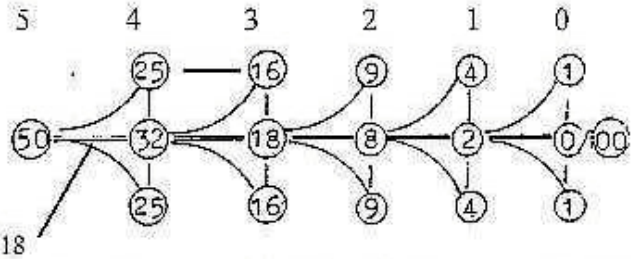


Z-number for P-groups as a dimension chain in loops:

H_3PO_4:	50	Z
H_2PO_3~:	41	Z
HPO_2~:	32	Z



Number readings in the $2x^2$-chain with poles as a dimension chain:



P - H_3 - O_4 (18 - 32) P - H - H - O_3 (16 - 25) P - H - O_2 (16 - 16)

The bond P-O in Z-numbers: a 15 to 8 relation:

Cf. The simple numbers = odd through even d-degrees in the dimension chain.

15 = 5 x 3 x 1

\ / \ /

8 = 4 x 2

The difference in A-numbers, 31 - 16 = 15 = Z-number of P.

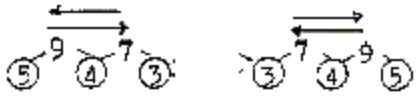
Sum 31 + 16 = 47, appearing as mass of side chain of amino acid Cys and factor in total sum of 20 + 4 double-coded amino acids (side-chains) = 47 x 32 = 1504

A.numbers inverted (Λ) = number series 2^x:

A-tal:	H_3PO_4	= 98 A, Λ	$= 2^x$ ($x10^{-x}$)	= 1 0 2 0 4 0 8 16 32 ...
	$H_2PO_4^-$	= 97 A, Λ	$= 3^x$ "	= 1 0 3 0 9 27 ...
	HPO_4^{2-}	= 96 A, Λ	$= 4^x$ "	= 1 0 4 16...
	PO_4^{3-}	= 95 A, Λ	$= 5^x$ "	= 1 0 52...'

97-79-numbers read in the superposed level of a dimension chain:

$H_2PO_4^-$ = 97
$PO_3^{2-}\sim$ = 79



P-groups in the co-enzymes of the codon bases. In ATP before condensation:

3 x H_3PO_4, à 98 A	Ribose	A-base	Triplet series
294	150	135	345 |
\	/		234 |...sum 579
444		135	123 | |-- 444
	579		012.|..sum 135

*

8. Molecular structures

Some elementary annotations:

1. 5-6- atoms in many molecules

It could be noted that the number of atoms (C-N-O-types) on a primary level in biochemistry is about 5-6, also the number of dimension degrees or steps in a dimension chain (transformed to d-degree 1 giving 5 x 1):

- Carbohydrates as essentially C5-C6 molecules
- A tetrahedron: 5 atoms as CH4..
- A central amino acid as Glu from α-ketoglutarate is a C5-molecule.
- Start of synthesis of fatty acids as C2 + C3.
- An isoprene molecule: a C5 molecule.
- Bases: A-base as 5 x HCN, pyrimidines U-C-T: C4 + N2, a molecule of 6 ring-forming atoms.

a "5-unit"
tetrahedron

a 5-ring
built of tetrahedrons

porphyrines
4-5 x 5-units

The PO4 molecule like the carbon tetrahedron with one central atom and 4 peripheral ones are fives, which may be regarded as still more elementary configurations.

(Why branching of chains after 3-5 glucose units in glycogen ?)

2. Forms of these small molecules, dimensionally interpreted

- Tetrahedrons in relation to ring structures: 3-dimensional.
- Ring structures in relation to their own R-groups: 2-dimensional.
- R-groups of the rings in relation to different kind of bonds: 1-dimensional, as for instance the H-bonds between R-groups of the bases in DNA.

It has been said that a condition for life is the development from sp^3-hybridizations in tetrahedrons to sp^2-hybridization in planes, dimensionally interpreted as a step $3 \rightarrow 2$. Such a step towards lower d-degrees implies increasing number of movements or kinetic energy according to the main hypotheses in the model.

3. Chair- and boat-forms of d-degree 2:

The ring forms as 2-dimensional illustrate both poles 2a/2b of d-degree 2 in the dimension model, in one expression described as convex/concave, this in the "chair" form.

4. Valence numbers and division in orientation of bonds:

The divisions in directions of bonds around atoms of different valences look like illustrations of d-degree steps:

- P-atom with valence 5 get 4 bonds "outwards", 1 inwards giving one double-bound oxygen atom. A division 4 + 1.

- C-atom, with valence 4, has its bond directions divided 4 →3 + 1 in amino acid tetrahedrons as examples. Number 1 represents here the most differentiated radical line.
(As a guess it's the empty place for an electron with outward directed spin in the p-orbital of the C-atom that corresponds to this direction for R-chains of amino acids.)
It's 3 directions is further divided 3 → 2 + 1, where 2 come to represent the division of directions in charge plus and minus (charge assumed as property in d-degree 2): the polarity $NH3^+$ <— —> COO^- leading to peptide bonds.

P-group and amino acid tetrahedrons:

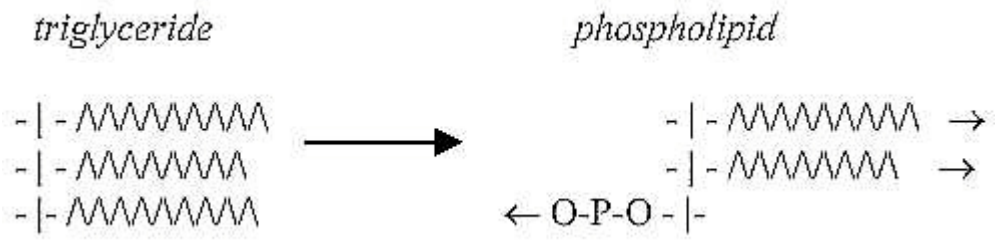
P: 5→ 4 + 1 (or 3 + 2, the double-bound Oxygen)
C: 4 → 3 + 1
3 → 2 + 1
N: (4)3 → 2 + 1, (NH^{3+} 2)
O: 2 → 2 or 1 + 1, (O^- 1 + 0 (2 in keto-oxygen, or 1 + 1, e.g. in carbohydrates)

In ring structures in the codon bases or carbohydrates and in fatty acids there is also the division of 4 →2 + 2 or 2 → 1 +1 for R-groups: 2 forming parts of the ring or in fatty acids wavy chain structures giving 2 or 2→1-dimensional forms. Compare generally waves as expressions for more motions, lower d-degrees.

- N-atom, when with valence 3, is in amino acids for instance or base rings divided 2 + 1 in directions and the O-atom with valence 2 has a still narrower angle between it's bond directions, 3 in double-bonds, or 1-1 in water.

5. Triglycerides divided 2 -1:

On a macromolecule level the triglycerides undergo a similar transformation step or division 3 → 2 +1, two hydrophobic fatty acids in one direction, the 3rd replaced by a hydrophilic P-group or (later) other more complex hydrophilic groups. (The fatty acids already in themselves, before binding to glycerine, polarized in hydrophobic and hydrophilic ends.)



Reevaluating the lipids:
Regarding the structure of phospholipids, they illustrate in fact most obviously the 4th d-degree of directions outwards/inwards in our model - and at the same time how the d-degree 3 appears through the polarization in poles 4a -- (3) --- 4b according to the model, creating the "circular" cell membrane (with "radial" canals). Enclosing / excluding, individualizing units as cells.

6. Chains and rings as 1-2-dimensional elements building forms of higher d-degrees

Life chemistry is processes, characterized by increasing motions, while structures of second order are of low d-degrees, chains and rings, principally d-degrees 2 and 1.

In the dimension model the dimension chain of structures becomes opposite in direction to the dimension chain of motions, with increasing d-degree in each step outwards in structure:

0/0 ← 1 ← 2 ← 3 ← 4 ← 5 D-degrees of motions
D-degree of structure: 5 → 4 → 3 → 2 → 1 → 0/00
| ↓chains (proteins, fatty acids...)
↓ rings (carbohydrates, nucleic acids...)

We could test to look at the relation the other way: motional patterns taking the form of structure d-degree in the opposite directed dimension chain:

- *protein chains* (1) moving "linearly" (1) in angular steps through 3 dimensions, when folding to "globular" proteins, partly also spiralling (α-helixes), a 2-3-dimensional motion;
- *carbohydrate chains* of rings spiralling, ~ rotation (2) + pathway motions (1), also crossed chains forming surface layers (2-3) as in cellulose coats of plant cells.

Higher d-degrees of structure are replaced by motional patterns as a substantiation of kinetic energy. 3-dimensional forms on this level are only created through motional patterns:

It could perhaps be one way to interpret the *folding* of proteins?

(Following internal bonds between different parts and the aggregation to dimers and tetramers possible to regard as expressions for the 4th d-degree, e. g. in histones and enzymes?)

7. Displacements in carbon chains at additions of other ones:

Displacement steps in the connection between "C-atom-lines" of the included units seem in many cases to be a factor in the formation towards units of higher d-degrees:

In such cases the added unit don't bind to a C-atom at the ends of the other but to the second one or the like:
- One obvious example is when two *δ-aminolevulinic acids* (C5 molecules) combine to *porphobilinogen*, where the 3rd C-atom in one of the molecules binds to the 4th in the other, leading to the creation of a 5-ring.
- Another example is the connection between *acetyl~ and dimethylallyl*(-P-P) molecules on the way to mevalonate and isoprenes.
- Also the coupling of acetyl~ to middle C in malonyl~ at the synthesis of fatty acids.
- The fact that it is the oxygen group of the second (an inner) C-atom that is replaced by an N-group at amination of α-ketoglutarate to amino acid Glu could illustrate the same principle?

Such features could eventually be interpreted as expression for primary versus secondary development within a dimension chain:

```
      5" — 4" — 3" — ...
      |
  5' — 4' — 3' — 2' ....
  |
5 — 4 — 3 — 2 — 1 — 0/00
```

8. Formation of rings in 5-6 types:

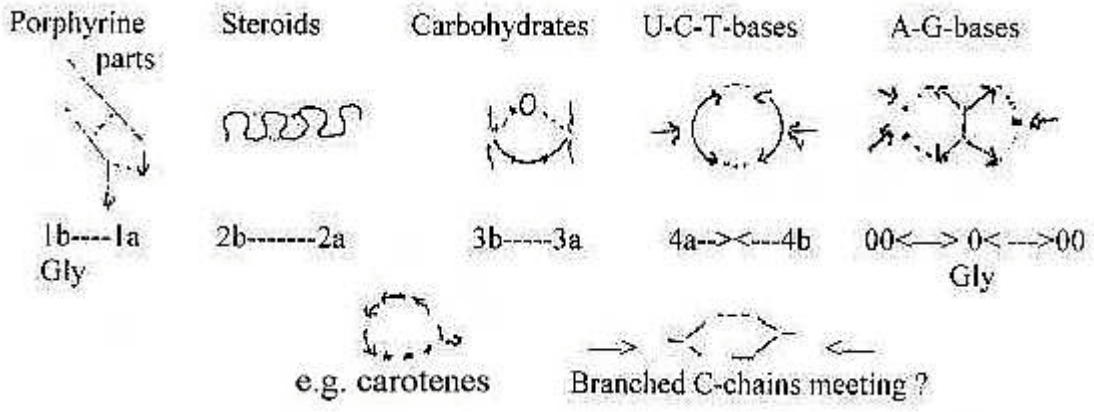
Forms of molecules "of second order", combined smallest molecules, are chains and rings, i.g. d-degree 1-2-(3). (Eventually connected with step 1-2 on the atomic level, the p-orbital, to which the C-, N-, O-atoms belong?)

There seems to be at least 5 quite different types of ring formations, as if "every tool" for the purpose of ring-closing were used. They are however more or less connected with the different main classes of substances and perhaps but not easily possible to interpret as formations in different d-degrees in the model, in a secondary dimension chain developed within step 2 →←1. ?

The step from tetrahedrons with central atoms to ring-formed molecules (cf. $sp^3 \rightarrow sp^2$) may be regarded as a projection of centre to anticentre, to a circumference, as of the 6 edges in the tetrahedron; a displacement to a new level, a level of lower d-degree.

According to general hypotheses here a whole dimension chain may also close stepwise towards a ring form through *angle steps* if in the same direction.

Figures below are only vaguely suggested associations with geometries of the different d-degrees, surely debatable.



a. ***Porphyrine*** synthesis with two nearly parallel or anti-parallel C-chains who through side bonds form 5-atom rings.

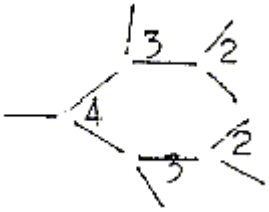
b. Synthesis of ***steroids*** where the wavy chains (of ***squalene***) give closed rings in both directions, convex/concave as poles 2a-2b of d-degree 2.

c. The simple bending of the C-chain (3a) in ***carbohydrates*** bound as through radii (3b) from an O-atom as centre, a loop formation.

d. The meeting (opposite *directions* as 4a--4b) of two bent C- and or C-N-chains forming "half circles" of a ring as in the creation of the ***pyrimidine rings***,U-C-T-bases.

e. Creation of double rings as in ***purines*** (A-G-bases) from a "radial" centre (0) (there the amino acid Gly, a tetrahedron) and a multitude of small individual molecules meeting from outside (00) supplementing and completing the ring forms.

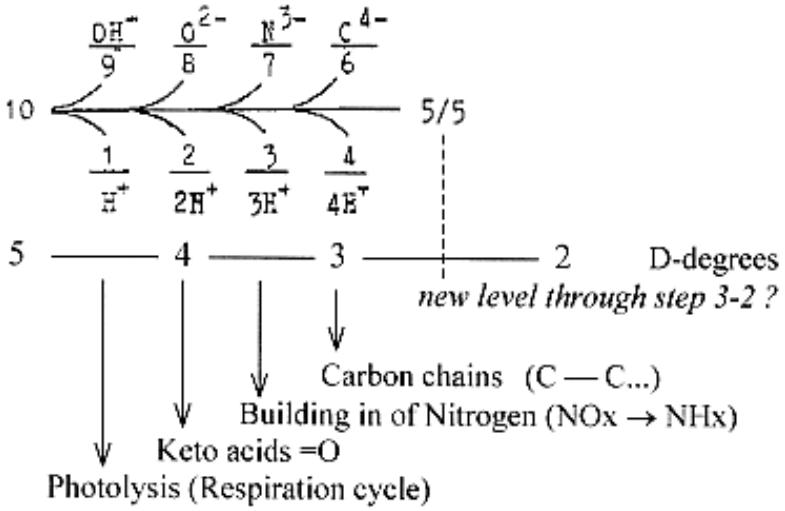
Theoretically 3 steps of bifurcations can give a 6-atom-ring.
To compare with 3 polarizations from d-degree 5 to 2.



(The interpretation of the ring forms belong to the many ambiguities in the dimension model. A molecular ring may be interpreted as a surface, d-degree 2, further as a circumference (pole 3a of d-degree 2) or as a secondary, complex centre on a superposed level as in the many ring-formed coenzymes in relation to the surrounding globular protein enzymes, Ep.)

9. Z-numbers of most elementary molecules in a "10-chain":

Number 10 stepwise polarized, giving OH-H, O-H2, N-H3, C-H4:



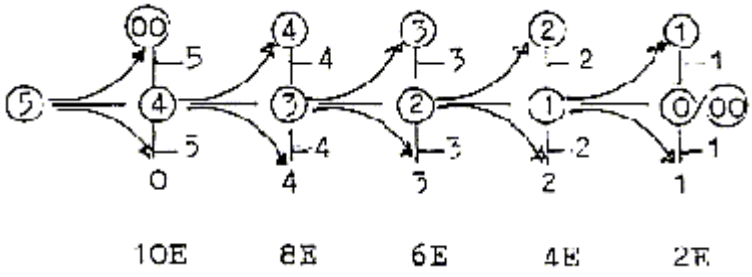
(Abiut the Citrate cycle: In reality there seems to be - 5 H from substances/molecules in the citrate cycle. If 8 H are gained to the respiration cycle, 3 of them ought to come from outside during the circle…?)

A level development within step 3-2 .

The "10-chain" may be regarded as a doubled elementary dimension chain with its two polarizations 5 → 4 + 1, 5 →3 + 2.
9-1, 7-3 in that case as partitions in the half steps 5 → 4, 4 →3.

H-atoms = the d-degrees which are lost during the stepwise process towards lower d-degrees, translated into movements. Compare H+ as an essential "force" or "carrier of force" in biochemistry.

2 H = "2 E", E for the sum of poles in respective d-degree, a kind of energy value in this model. Total sum of a dimension chain give sum of poles = 30 "E".


5
4
3
2
1
0
00
5
4
3
2
1
0
4
3
2
1
0
10E
8E
6E
4E
2E

*

9. Classes of substances

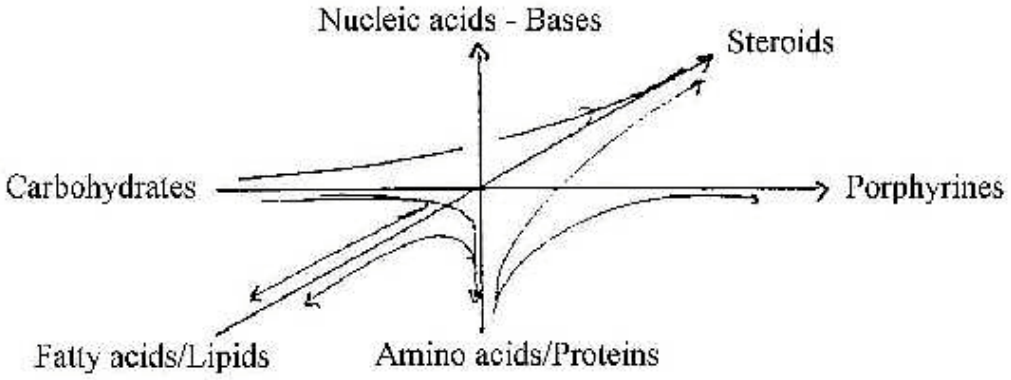
Some tested aspects from the viewpoint of the dimension model.

1. How many main classes of substances to count on? 3-6 ?

- Carbohydrates — Porphyrines
- Proteins — Nucleic acids, bases of the genetic code
- Lipids — Steroids (isoprenes)

We can try regarding the left and right classes as complementry pairs:

The classes as "poles" in a 3-dimensional co-ordinate system?



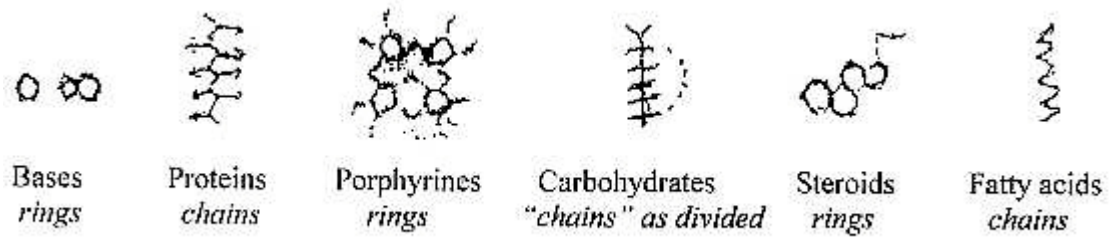
Connection between the classes in pairs:

Carbohydrates - via keto acids →to Succinyl~(CoA) → to Porphyrines,
Porphyrines → chlorophyll→ photosynthesis → synthesis of carbohydrates...

Proteins, amino acids - via Asp and Gly → to synthesis of pyrimidines and purines, the nucleic acids, U-C-T and A-G. (Asp ~ ½ of U-C-bases. Gly starting centre in A-G-bases) → to protein synthesis...

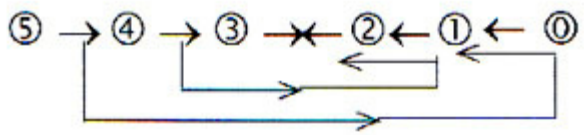
Lipids, fatty acids one branch from Acetyl~ , the other branch to isoprenes, steroids, carotenoids, uinones.

The polarity between open ("radial") chains and closed ("circular") rings may be observed, as one feature of complementary poles in the dimension model:
(Condition: carbohydrates divided and transformed to keto acids.)



Interpretation of the 3 "coordinate axes" in a dimension chain as 3 levels **?**

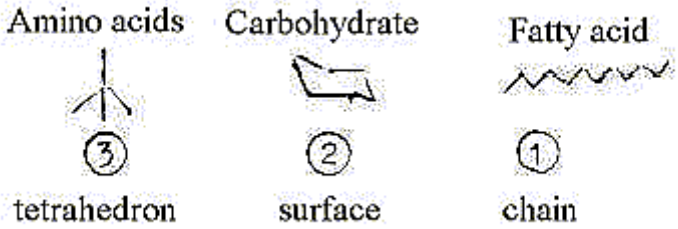
Level III	Lipids	Steroids
Level II	Amino acids	Bases (nucleic acids)
Level I	Carbohydrates	Porphyrines



Here we see the closing to ring forms as following from steps in lower d-degrees. (The order here of levels I-II-II corresponds to characteristic atom kinds O - N - C and their "A-Z-numbers".) From other aspects, the order of level I and II should be the opposite.

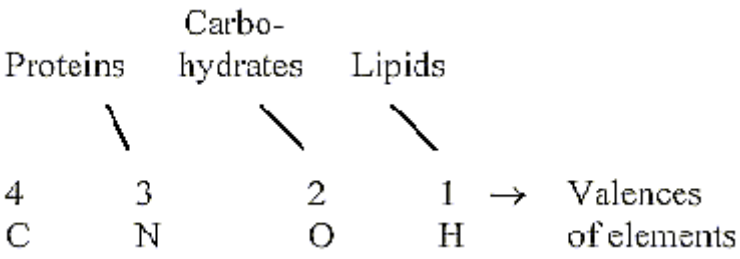
2. Classifications from aspects on elementary molecules:

2.1. D-degree of main form character:



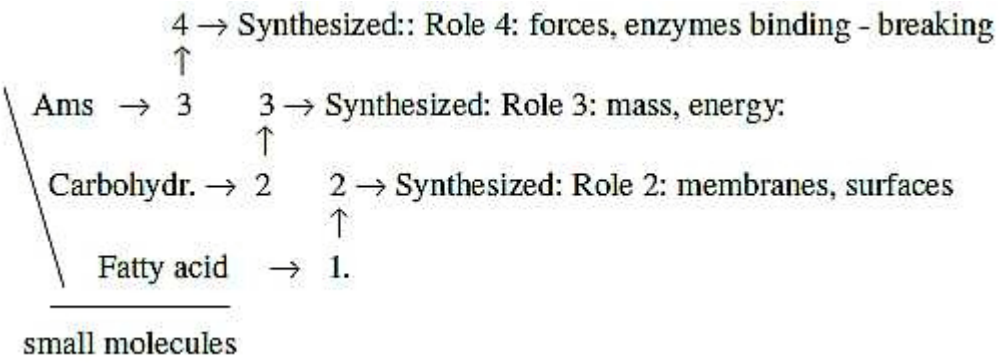
Inward direction: fatty acids - *hydrophobic*
Outward direction: carbohydrates - *hydrophilic*
Secondarily polarized: amino acids of both kinds: *hydrophilic/hydrophobic*

2.2 Characterizing elements - valences:



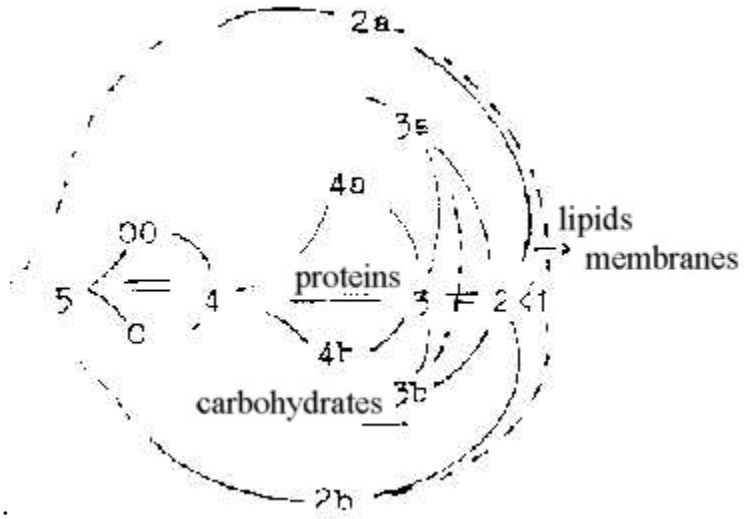
Forms of the molecular parts: 3-2-1-dimensional;
Roles when bound together in macromolecules: 4-3-2-dimensional.

Thus, the synthesis of the small molecular parts implies an increase of the dimension degree with 1 step :



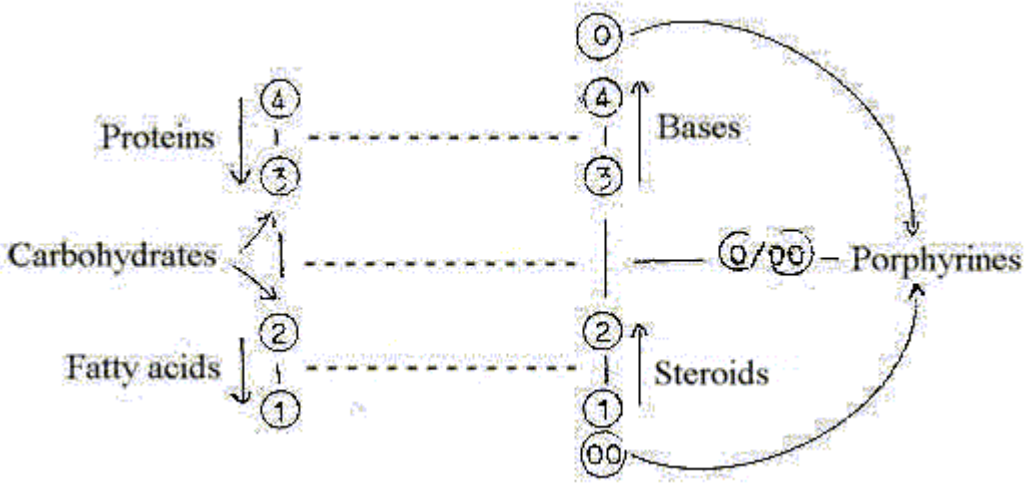
(This aspect is of course a simplification. Amino acids for instance make up also structural part of d-degree 3, the radial 3b-pole in the model here. And lipids may be seen as characterized by the C-atom and have a more high degree role than usually are attributed to them?...)

2.3 Genes - proteins - carbohydrates - lipids in the cell as a "fruit":
Growing and increasingly circular potentials towards lower d-degrees as one hypothetical aspect on a dimension chain:



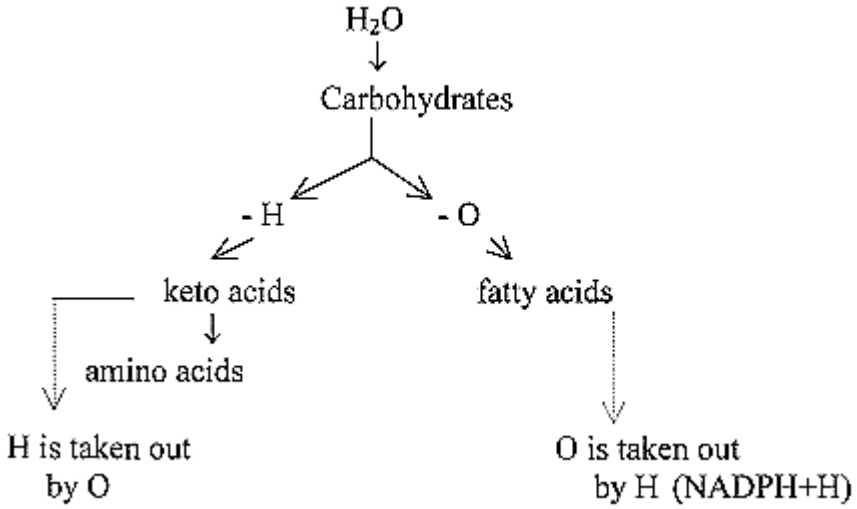
Core - pulp - peel:

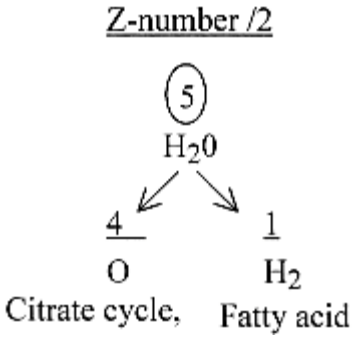
2.4 Ring forms as through inward direction in d-degree steps,
chains as outward direction in the pair of classes respectively?



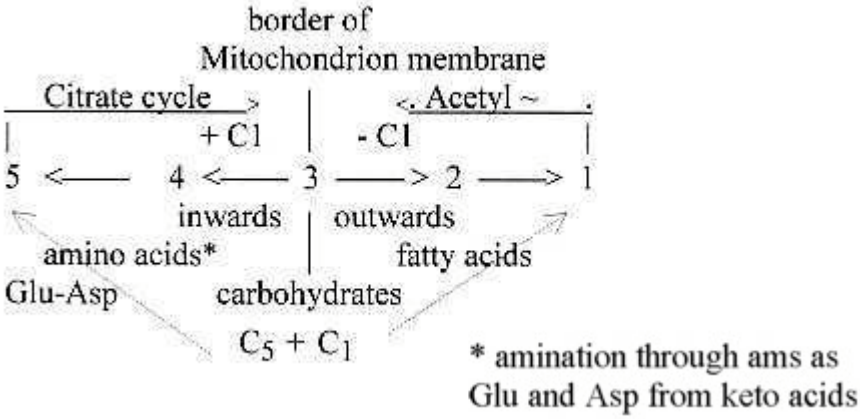
4-3- and 2-1-steps: chains in outward direction, ring-forms in inward direction?
3-2 step: as double directed: *carbohydrates*.
0/00: outer poles meeting as 5', porphyrines.

2.5 The treatment of water:



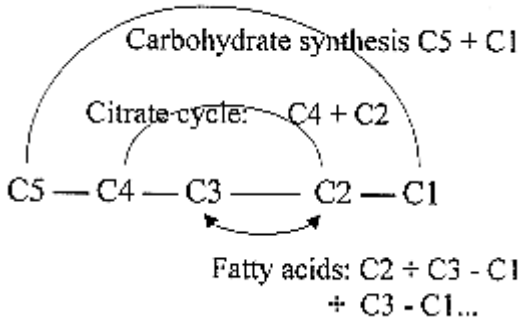


Inside/outside mitochondria:



2.6. Synthesis in number of C-atoms as an aspect:

O: Carbohydrates C5 + C1 → C3 + C3 (Pentosephosphate cycle: 3 C5 →5 C3)
N: Amino acids C4 + C2 → - C1 → C5 Glu (from citrate cycle); also ams from C3 molecules in glycolysis...
C: Fatty acids C3 - C1 + C2 x n.



Fatty acids: inverted direction in middle-step 3← 2.
- Pentosephosphate cycle 3C5→ 5C3: compare sum 15 of the elementary number series.

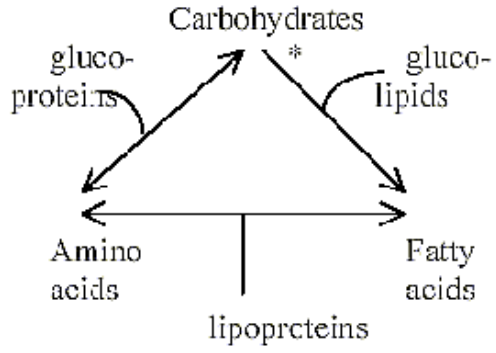
Middle level C4 + C2 → Citrate cycle - keto acids
↓
Succinyl~ + Gly = C4 + C2,
↓ - C1
Porphyrines → Chlorophyll

A note about porphyrines and their "side-chains" or "rope ends" at the rings:
- Rings: C5 x 4

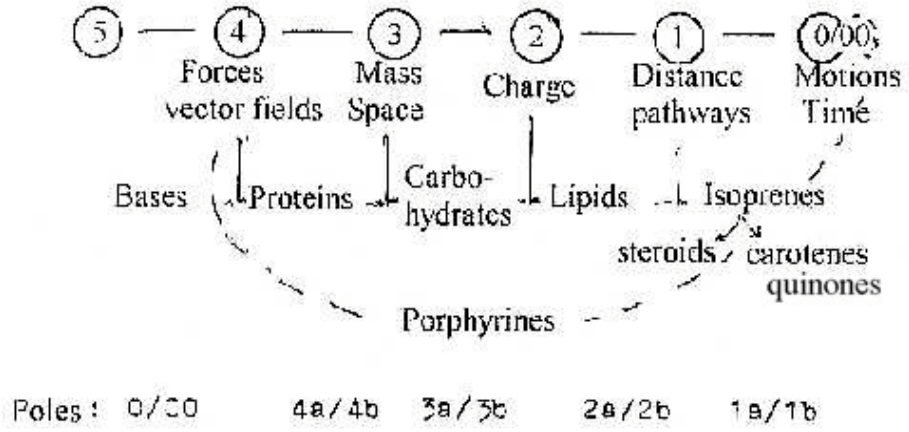
Chain ends 4 x (C3 + C2) before turning
becomes 1 x (C3 + C3), 2 x (C3 + C2), concerns Uroporphyrinogen III),
becomes 1 x (C3 + C3), 2 x (C2 + Cl), 1 x (Cl+CI),
this a principal in Haeme and Chlorophyll.
Reduction/cut/diminution of chain ends as a kind of step displacements ?
Cytochrome a: addition of an isoprene chain (isopentenyl~).

2.7 More complex molecules, the combinations:

*(certain organisms are able to transform lipids into carbohydrates)



3. A dimension chain with elementary physical concepts as suggested in files about *Physic*s, connected tentatively with classes of substances:



The figure refer to a mix of aspects: connections agree approximately with forms and functions in the cell. (Lipids as responsible for potentials +/- over cell membranes.)

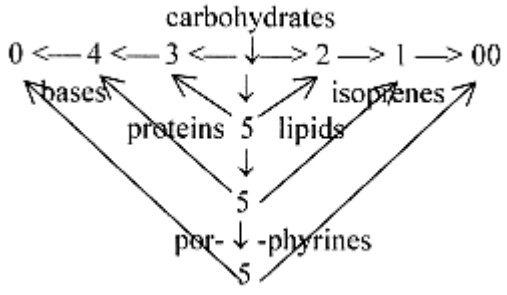
However, connections don't agree with the view of polarization steps outwards in the chain: Bases don't "polarize" into proteins even if they guide the differentiation of amino acids. And proteins assuredly don't polarize into carbohydrates but individual amino acids "break down" to different stations in glycolysis and citrate cycle and most steps in these are double-directed. Hence, proteins may this way be transformed to carbohydrates. With the aspect of synthesis, this appears double-directed inwards and outwards respectively.

Most obvious example of a polarization giving complementary "poles" as partial structures in accordance with the dimension model is naturally the division of carbohydrates (hexose Glucose → Fructose) leading to amino acids (proteins) and fatty acids (lipids) respectively: Two forms making up radial versus circular parts in the cell as poles 3b versus 3a.

(We may regard the radial 3b-pole as derived from the 0-pole in a haploid chain, the "circular" 3a-pole as derived from the 00-pole:

```
                3a <— <— <—- 00
                 |
0 —> —> —> 3b                    )
```

To get this polarization - regarding direction of *synthesis* - in some correspondence with the figure above, a version of the loop model seems needed, the three polarization steps 5→ 3/2, 5 →4/1, 5 → 0/00:



.

[Cf. in the figure vertically 5-5-5 and Pentosephosphate cycle 3 x C5 → 5 x C3.]

Proteins: step 4-3, poles 4a/4b:
- Amino acids which in synthesis (~ inward direction) give parts of the codon bases.
- Enzymes as forces, polarizing / binding as 4a/4b-poles,
(- L/D-forms of amino acids (example of secondary double-direction), where one direction has been selected as dominating in higher species.)

Carbohydrates; step 3-2, poles 3a/3b;
- Number of C in pentoses 3 + 2, in glucose 3+1+2: The 6th C-atom gets bound in the middle of the C-chain. Hexoses divided C3/C3 as poles 3a/3b.
- 3a as the part transformed to glycerine, building "circular" backbone form of lipids, 3b developing to Pyruvate and Acetyl~ C2, starting synthesis of fatty acids.
- Also another polarity on macro-scale: 3a as cellulose type, with role as "spherical" coating, 3b amylos or glycogen as stored substrate in the cells, a complementarity similar to the type space / mass in the model.

Lipids, 2:
- Synthesis from the parts of carbohydrates, the poles 3b/3a.
- Number of C-atoms in syntheses: 2 + (3 -1), x n, Plus C3 for the backbone to triglycerides."Linear" chains coupled to glycerine into 2-dimensional forms.
- Roles in membranes as demarcation, "shell", surfaces, d-degree 2.
- *Charge* (assumed as property defined as such at d-degree 2) across the membrane: negative inside, positive outside, inversely to the distribution of charge of atoms.(! Life as antimatter on a higher level! Cf. life as processes, the dimension chain in opposite directions to structure degrees.)
- The 2/1-division of triglycerides in directions from binding backbone (glycerine) to P-lipids and more complex .molecules as glycolipides.

Ring structures:

Isoprenes
→ (squalene) → steroids → carotenoids → quinones: 2 → 1 → (0/00):
This class with the derivatives of isoprenes illustrate in many ways the d-degree steps 2 →1 → (0/00, the porphyrines).

- Synthesis of an isoprene as of fatty acids from Acetyl~, C2 but from 2 x C2 plus a third branch C2:(as a step 2 →2a/2b)

C2 + C2
|
+ C2

- Lipids versus isoprenoids: two different ways to form 2-dimensional macromolecules: in lipids: 2 crossing coordinate axes, in steroids: wavy forms of chains closing to rings in opposite directions. This opposite use of C2-molecules seems to reflect a polarity of the kind radial versus circular in the synthesis itself.

- The wavy form of squalene as oscillation forms of max/min, convex/concave: equivalent with (~) poles 2a/2b, closed to steroids: flat planes (2).
- **Steroids** among other things parts of membranes, hence closely related lipids.
- Functions: among other things as hormones, the chemical signal system. Connected with light, electromagnetic waves, as in D-vitamin. In these functions also representing less of structure building, more of motions as in the polarity particles/waves in physics.

- Further ***carotenoids***, ***xanthophylls*** connected with organelles for photolysis and a derivative as visual purple (rhodopsin) for light absorption in eyes. Long "linear" chains with ring-closed ends as in d-degree 1 with poles: 2a----1-----2b. Note the complementary directions of ring bows at the ends.

- **Quinones:** 1b ----- (0/00): Only "1-dimensional" isoprene chains, here connected to a ring from the amino acid Tyr (side chain 107 A), as from a 4-1-loop from proteins to last step.
- Function: Ubiquinone for instance: directly part of the "pathways" (cf. Distance), "elevator ropes", for photon energy and H2-transportation in the respiration cycle.

Porphyrines, 0/00:
- The synthesis giving a picture of inward directed vectors, pole 4a (Gly and Succinyl~) under rotation pointing to location for the metal ion. In some sense similar to "black holes" in macrocosm, "catching" light energy. (Outer poles of d-degree 4 = 0 and 00, from polarized d-degree 5.)
- As chlorophylls key substances in the big loop photolysis - respiration cycle (vegetative/animal worlds).
- In type of form c/ac-figures, centre - anticentre, 0 and 00-poles.

The polarity on the more fundamental, underlying level of chemical elements, appears here inverted: Non metals as representing outward directions from 0-pole form here anticenter (from 00-pole), while metals representing inward direction from 00-pole become centres. (Such a pole exchange has been assumed in he background model. Also in agreement with the general principle of stepwise building-in of the environment as anticenter.)

Codon bases in nucleic acids, the building stones for the genes:

- Responsible for integration of the "whole" (d-degree 5) , the unity of a cell.
- In the figure above proposed as representing a step 5 ← 4.
- Constructed by amino acids and some other molecules, as in synthesizing, inward direction, associated here with ring forms.
- Are 5-4 in number.
- Represent the most typical complementarity in a pair relation as poles of a dimension degree in our model.
- Synthesis characterized by centre — anticentre respectively, the partial structures out of polarized d-degree 5.
- In one sense it's the polarization of base pairs to one-way direction which leads to the proteins, the class associated with d-degree 4-3: the separation of the double helix of DNA for copying of mRNA.
- The "haploid" role becomes a condition for the function of bases as "forces"in their role as coenzymes. Cf. that one-way direction is a condition for a force to be acting. Balanced, opposite forces cancel each other.)

- The "outer poles" (or partial structures) of d-degree 4 meet in the last step, in "d-degree 0/00" (of motions) to which the class of porphyrines has been attached here. DNA is also present in chloroplastes with chlorophyll for photolysis as in mitochondria with cytochromes for the respiration cycle. And in both Gly contributes at the synthesis, the simplest amino acid. (Gly as outward vector from 0-pole, centre, in G- and A-bases, as anticentre (?) vector inwards in porphyrines when combined with Succinyl~ chains).

8. Application of other aspects on a dimension chain:

a. Increasing one-way direction toward lower d-degrees:
One possible aspect is the number of bond directions of the macro-molecules:
- Proteins, folding or not, with bonds in at least 3 directions, surely often 4 as coenzymes. - Carbohydrates with bonds in 2-3 directions (3 for instance in glycogen with branched chains).
- Lipids with bonds in 1-2-directions (2 with glycerine).

b. Motional moments as Vibration - Rotation - Translation in 3 dimensions:
The aspect in the dimension model that d-degree of motions increases when d-degree of structure decreases in steps towards lower degrees have been dealt with in files about physics, applied to the atomic level. Surely it seems silly trying to apply this elementary hypothesis about motions, built on 1-2-atomic molecules, on the very complex biochemical level. Yet, here some views on the molecules from a similar aspect.

- Protein chains in the muscle fibres (actine/myosine) and their motion in/out may be regarded as a *vibration* (through pacing by hooks on the chains), an **1-dimensional** motion as assumed in d-degree 4. (Muscles the organ for motions.)
Perhaps the function of protein microtubules in cilia, elementary "linear" organs for motions, could be regarded as a substantiated form of linear vibration? (The motions of *kinesin* and *dynein* as "motor proteins", "walking" on tubules, see *Wikipedia*.)
The first *folding* of protein chains on the underlying, elementary level could possibly be interpreted as a stepwise 1-dimensional motion through the 3-dimensional space.
Surely however, a lot of other aspects on protein motions could multiply the degrees of motional patterns.

- Motional pattern of carbohydrates?
Do the macromolcules of amylos, glycogen or starch rotate, a 2-dimensional motion?!
(The spirals of amylos implies rotation in the structure, the branching of glycogen may be regarded as "*translation in 3 dimensions*", but these are examples of patterns in the synthesis. They don't correspond to motional patterns for the macromolecules, the aspect here.)

- With lipids associated in structure with d-degree step 2 (then 2-1 in elementary form))the motional patterns should be **3-4-dimensional**. The *amoeba-like motions of membranes, in- and out invaginations,* could be identified as an expression for such a 3-4-dimensional motion. Cf. in structure poles 4a/4b defined as outward/inward direction.

- About steroids as 2 ← 1-dimensional in structure and often attached and integrated in lipids, they assuredly move around **3-dimensionally** in inner space - as sex hormones for instance, but also take part in the regulating of gene activity. Cf. the connection 4 - 1 in the loop model which should give a connection between genes/bases or repressors of proteins and steroids in the figure above. If this latter function could be interpreted as an expression for a **4-dimensional** motional pattern is debatable. Originally "pumping" has been proposed as the form of 4-dimensional motion. Maybe also a typical vector character (with address) of a motion could be regarded as 4-dimensional?
Long chains of isoprenes (polyprenoles) t**ransport** carbohydratepeptides through the cell wall in bacteria.

- A "**5-dimensional**" motion, when structure d-degree is zero (in d-degree 0/00) is in the model presumed as only the "*pole exchange*", the "germ" to Motions in itself. It could perhaps be identified as just the mentioned positioning of metal ions in the centre of porphyrines? And/or only with an internal change in charge, in electronic energy. In

other aspects the porphyrines interpreted as principally 5-dimensional structures seem to be characterized of great immobility.

c. Higher d-degrees defined as binding forces in relation to lower d-degrees as structures:

Is this postulated definition in the model in any sense applicable to the classes of substances? "Binding" (sign <) - in which sense? And which molecule binds which in an addition?

Generally it may be said that bases in the form of coenzymes with their P-groups (valence 5) binds many other substances and that proteins as enzymes act as both binding and polarizing forces.

Regarding the classes in the suggested order, application of the aspect seems very debatable, even if some examples may be found illustrating it.

Bases <Proteins < Carbohydrates < Lipids < Isoprenes< kinones < porphyrines

- Bases< Proteins? (The inverse in histones !) How in rRNA, in repressors?
- Proteins < Carbohydrates ? Examples could be *Glycoproteins* (nearly all proteins in plasma are said to be of this kind, and often proteins extending through cell membranes).
- Carbohydrates < Lipids ? Glycerine < fatty aids, okay**.** The inverse in membranes? In *glycolipids* and *gangliosides** (much of these in grey areas of brains), the complex combination of carbohydrates and fatty acids (including a transformation of amino acid Serin), it may really be discussed which part binds which.
- Lipids < Isoprenes as polyprenoles, okay, but
- Isoprenes < karotenes (fat-soluble) or quinones ?
- Quinones < porphyrines ?

* A ganglioside looks like an outline of an insect larva (fatty acid part) eating leaves (the carbohydrate hexoses).

In short, the more complicated molecules seem integrating several steps along the suggested chain for classes.

d. The different classes of substances may be seen as undergoing different number of steps from chains towards higher d-degrees on superposed levels:

(5)-4-3-2-1:	4-5 levels of storage for DNA.
(4)-3-2-1:	3-4 for proteins as fibres, folded surfaces, globular forms to enzymes with coenzymes as 4-dimensional.
3-2-1	2-3 for carbohydrates (C6), chains to rings to macro-chains, branched or folded or spiralled to volumes.
2-1:	1-2 for steroids from isoprene chains.

9. Can the codon bases be connected with different classes of substances?

Only to a certain extent as it seems. Here bases as nucleotides - coenzymes. According to limited data:

- TTP - cellulose synthesis
- UTP - *carbohydrates*, glucose synthesis, (also cellulose)

- CTP - *lipids*: connection between the amino acid Ser and fatty acids
- GTP - participation at *protein* synthesis on rRNA (and in the citrate cycle)
- ATP - *general energy storing and transportations*.

Most obvious is the connection UTP/TTP with carbohydrates. T/U-bases represent directions inwards (T) towards DNA and outward direction (U) towards active RNA, an essential opposition. (We could see the similar opposition expressed in cellulose as inward" enclosing cover in plant cells and the other carbohydrates inside the cells or parts of them outward directed from lipid membranes of the cells.)

There is also the fact that most of the essential amino acids which human beings cannot synthesize are U-base-coded.

All amino acids with U in 1st and/or 2nd position in their codons derive from stations in the glycolysis of carbohydrates (glucose →fructose), a fact that presumably is connected with the role of UTP.

GTP-GDP keeps citrate cycle going around, by transforming Succinyl~ to Succinate. (Keto-acids in the cycle closely related amination.)

GTP-GDP is also a factor in the protein synthesis at rRNA.

"G proteins" act as "molecular switches", in transport of signals.

These data may give reason for connecting G-base more specifically to proteins?

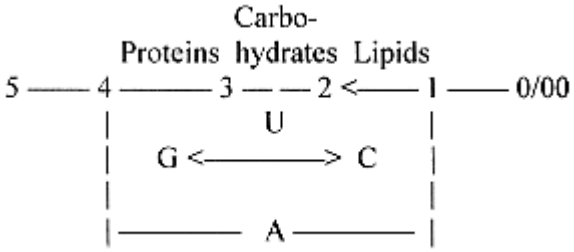
CTP is said to be more specific: taking part as a coenzyme in the synthesis of glycerophospholipids and glycosylation of proteins (*Wikipedia.*) It is involved in adding the amino acid Serin to phospholipids.

ATP (with the A-base part in NADP, NAD and FAD) is obviously the least specified, a main energy storing molecule and engaged in a lot of processes.

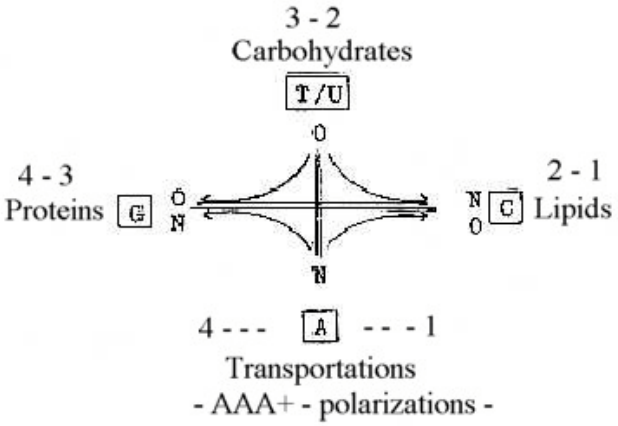
AAA+ proteins: - many polarizing functions - (as "protein degradation") and "intracellular transportations" and motions in cilia...

As NAD the A-base is also involved in the respiration cycle with ubiquinone (located to d-degree 1-- 0/00).

A summary could look like this:



With the view on carbohydrates as fructose polarized a) towards keto- and amino acids in synthesizing direction inwards and b) toward fatty acids and lipids outwards, we get following picture, with d-degree steps marked:



Three number operations - without sense?
Mass sums of bases with +1 for bond to ribose:
G 151, A 135, T 126, U 112, C 111.

Wiith U/T-bases regarded as representing the division of directions of d-degree 4 (inwards: T/outwards: U), as in the views on protein synthesis:

a) T/4 + A/1 + G/3 + C/2 = 1/2 x **544**,666. 544 an essential number in the mass analysis of the genetic code.

b) 4 x U +3 x G + 2 x C + 1 x A = 1258, = sum of side-chains of the 20 amino acids in the genetic code, + 1 C + 1 A = + 246 = 1504 = 20 + 4 double-coded ams R.

c. Dimension loops 4-1, 3-2 with similar numbers 141, 232, sum 373 =
mass numbers of T+U+A (126 + 112 + 135) and C+G+C (111 + 151 + 111).
373 in number-base system (nb-x) 8 = 251 in nb-10 =1/3 of 753, sum of triplets in the elementary number series 5 - 0, 543 + 210 or 432 + 321.

*

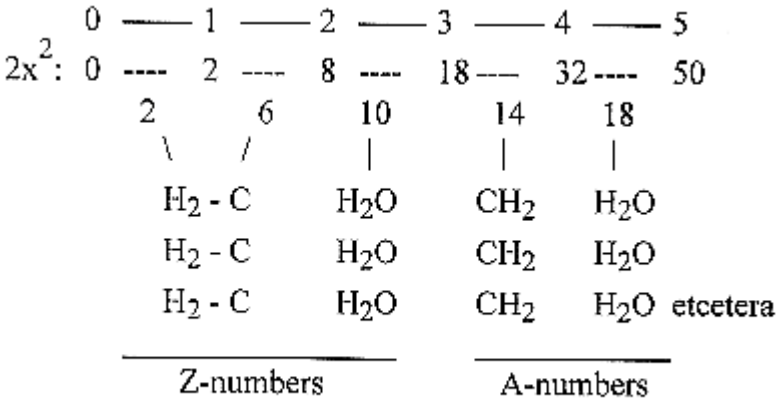
10. Fatty acids and lipids

Some general aspects:

1. Main feature of the process from carbohydrates to fatty acids implies the excluding of oxygen while storing H2. One suggestion below is to think of this process, the creation of enclosing barriers, as a result of steps toward lower degrees in a a dimension chain.

The aspect on elementary atomic masses gives the order O-N-C from higher to lower mass (cf. the opposite direction in the carbon-nitrogen cycle in the sun, carbon → nitrogen → oxygen , minus alpha, back to carbon, and "A-Z-numbers").

The excluding of water, A- and Z-numbers in the process: numbers in the $2x^2$-series:



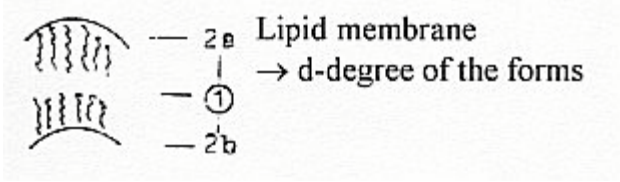
Synthesis of a fatty acid as -H2O, + H2.

(Mass a property in d-degree 3 in relation to Charge as a property assumed in the model as defined in d-degree 2.)

2. Fatty acids, bound to Glycerine (Glycerol), lipids:

Lipids
, build the cell membranes,
(together with **P-groups**, P for phosphorus). The macrostructure of a membrane may illustrate d-degree 2 and 1.

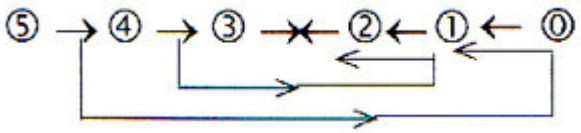
Glycerine as "the backs",
- binding 2-3 fatty acids as 1-dimensional zigzag chains turned toward one another, inside-outside as opposite poles:



Fatty acids with glycerine build the barriers to a water environment, that's surfaces and as such 2-dimensional on a macro-scale. The same character is reflected in the synthesis of the fatty acids, if we may regard the number of C-atoms as expressions for d-degrees,

roughly an addition of C2-pieces.

In the loop model of our dimension chain



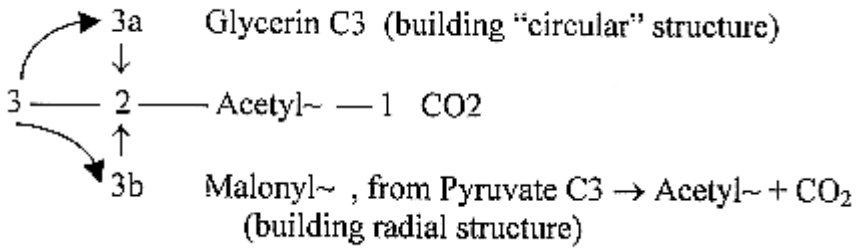
the debranched degrees from steps 5 - 4 - 3 are meeting the other way around; the d-degree step 4→ 3 correspond to d-degree step 2 ←1 and 3→2 to a kind of half step back 3 ← 2.

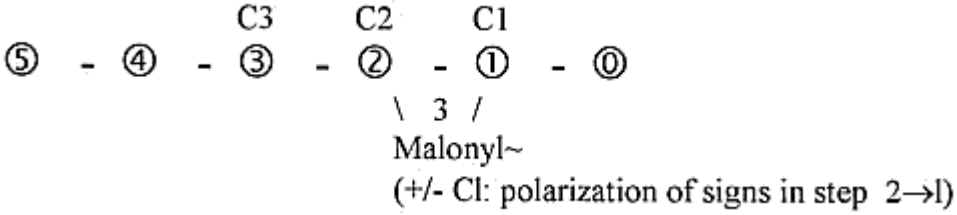
At the same time (compare step 4 → 3 in the figure) the fatty acids as "linear" have the character of 4-dimensional vectors in opposite directions. The membranes with glycerine, illustrate also the geometrical poles 3b versus 3a of d-degree 3, radial versus circular form.

The division of C6 into to halves C3 reflect the polarization of the complementary character: one half, Glycerine C3, as forming part of the circular structure, with feature from the 00-pole (ac) and inward direction, and one half further transformed outwards during glycolysis to Pyruvate C3, from which one branch leads to Acetyl~, C2, and the synthesis of fatty acids, the radial part of membranes, with feature from the 0-pole (c) and outward direction.

In number of C-atoms:

Glycerine versus Malonyl~ (from Pyruvate) as 3a---3b-poles in d-degree 2:



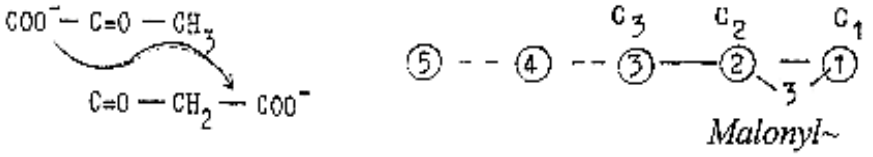


It could be noted that Pyruvate represent the border to the citrate cycle, and the glycolysis in relation to this cycle as whole processes have also the geometrical character of radial versus circular.

The bifurcation of the way for Pyruvate, into the citrate cycle with + C1 in direction of synthesis to keto acids and amino acids, and outwards to Acetyl~, C2, to fatty acids, represent a main division in classes of substances and their role in cells, with similar geometrical complementarity on that level.

The fact that Acetyl~ also enters the citrate cycle (with an OH-group) after a couple of steps (forming isocitrate) seems as an obvious example of the views in the loop model above.

The transformation from Pyruvate to Malonyl~ implies that the COO-group is moved to the other end of the C3-chain:



Mass quotients: : Pyruvste 45 - 28 - 15 ≈ 3 - 2 - 1-quotient
Malonyl~ 28 - 14 - 45 ≈ 2 - 1 - 3-quotient

Pyruvate and Malonyl~ uncharged.

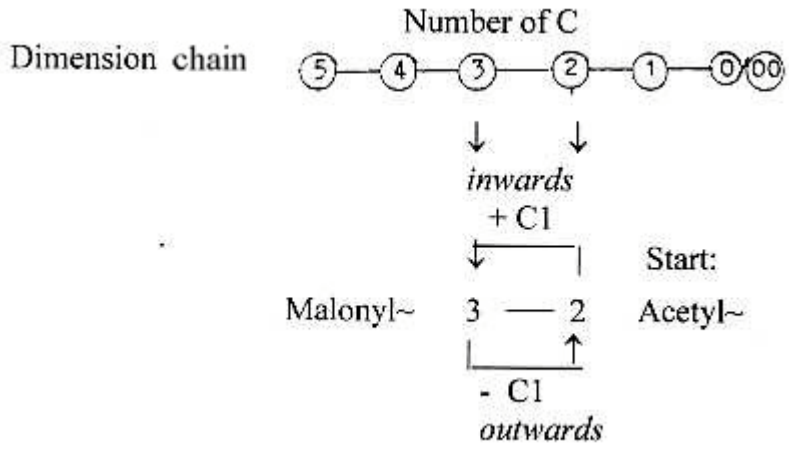
This displacement may be regarded as an essential expression for the change of direction in the loop model above, here from outward fragmentation direction toward the synthesizing inward one

.

3. The synthesis of fatty acids in detail:

It starts with C2, Acetyl~ (CH3-C=O ~).

Another Acetyl~ C2, +C1 forms Malonyl~, C3 (COO-CH"-C=O ¨) , which is attached to another site and the first C2 (Acetyl~) moves to bind with this, debranching the C1-(COO-group) of Malonyl~. Compare the dimension chain:



Since the "outer poles" (or partial structures) of d-degree 2 and 1 is 3a/3b and 2a/2b, the illustration of the process could be imagined as moved to step 2-1 and connected with the a-poles for instance.

(+/- Cl: polarization of signs +/- in step 2-1 as a parallel to
the polarization of charges in p/e on the atomic level?).

In the dimension model d-degree 3 have the "outer poles" 4a --- 4b, d-degree 2 the poles 3a -- 3b.

We may note - as a coincidence? - the mass numbers of Acetyl~ and Malonyl~ :

	4a 3a	**43** as number = mass of Acetyl~
	| |	
Poles in dimension degrees:	3 — 2	
	| |	
	4b 3b	
Sum of poles	8 6	**86**, mass of Malonyl~

*86 = Malonyl~ charged: C=O — CH2 — COO^-~

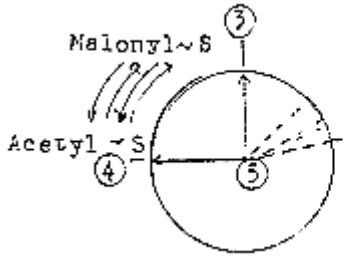
4. The synthesis as a process of repetitions:

The synthesis of the fatty acid chains: /\/\/\/\/\/^{COOH}
is a process between Acetyl~ (C2) and Malonyl~ (C3) with removal of C1.

Keeping to the vector character of d-degree 4 in fatty acids, the multi-enzyme complex with two S-binding sites where the synthesis takes place could illustrate an oscillation between poles 4a and 3a.

Connecting the dimension chain with angle steps in a circle, the division to d-degree 4 implies a division to 180°, in next polarization a division to 90° - according to our first assumptions in the model. Positions at 180° and 90° seem possible to connect to the S-binding sites.

The multi-enzyme complex as structure giving a picture of angle steps through a circle:



D-degree 3: 90°

D-degree 4: 180°

a. Acetyl~ , (C2), gets bound to site 4, S in the R-chain of Cys (47-1 A).

b. Malonyl~, (C3), gets bound to site 3, S in Pantetheine, (358 -1 A), part of HS-CoA

c. Acetyl~ connects to C number 2 in Malonyl~ at site 3, and the COO-group of Malonyl~ is debranched.

This combination C2 + C3-piece gives virtually a C5 piece, immediately divided **C5 →C4 - C1**: cf. first step in the dimension model with 1 d-degree debranched.

d. The C4-molecule gets moved back to site 4 (3 → 4) and

e. A new Malonyl~ gets bound to site 3. Etceteras.

It's Acetyl~ that moves "outwards" to site "3" and as 2 x C2 inwards again to site "4"; cf. the vector character of directions, while Malonyl~ (from C2 + C1) always takes position at site 3. The "vector" growing through substrate from lower d-degrees ("anticentre").

The COO-group of last Malonyl~ becomes the "head" of the fatty acid.
(It seems logical then that the coupling with glycerine follows.)

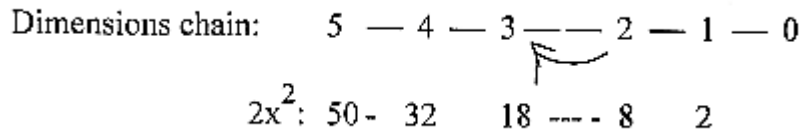
Hence, the synthesis starts from the end of the fatty acids, which become double directed towards one another in membranes, and this agrees with the interpretation of sites in d-degree terms, d-degree 4 within membranes in the double membranes.

Outer poles in step 3 - 2 = 4a/b - 3a/b. In the $2x^2$-chain (50 - 32 - 18 - 8 - 2 - 0) the step 4 - 3 corresponds to interval number 14, the CH2-pieces, and 2 + 8 + 18 = 28, the CH2-CH2-pieces.

5. Why are C18 and C16 most common fatty acids, 8 or 9 C2-pieces?

Most common fatty acids in animal life:

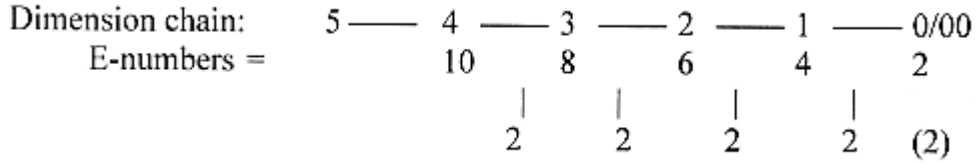
33 % palmitic acid, **C16**, saturated: C15H31COOH = 256 A
17 % stearic acid, saturated, **C18**: C17H35COOH = 284 A
35 % oleic acid, unsaturated, **C18:1**: C17H33COOH = 282 A



One aspect: The process towards C18 implies C2 + 8 x C3 (Malonyl) = 26 C = 18 + 8, minus debranched 8 C1, rest C18. (?)

Or: one pole of d-degree 4, represented by number 32 in this chain, = 16. (?)

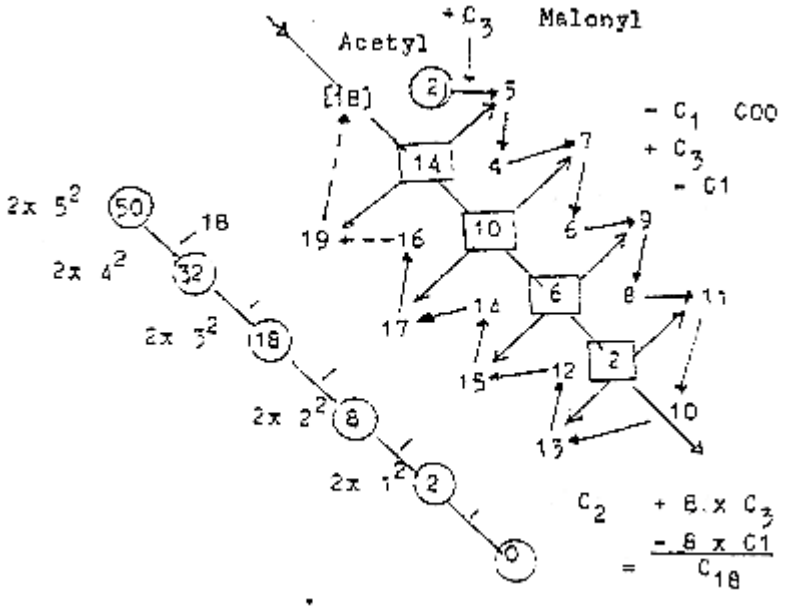
Another answer to the question could eventually be connected with the "E-numbers", the sum of poles in the dimension chain - if the difference of 2 in the steps here may represent C2-pieces. The process as occurring in step 4 - 3, including all lower degrees, as double-directed to and fro (0 → 1 →2 →3 → 4 →3 →2 →1 → 00), gives 2-4-6-8-10-12-14-16-(18), counting from d-degree 0/00 with E-number 2.



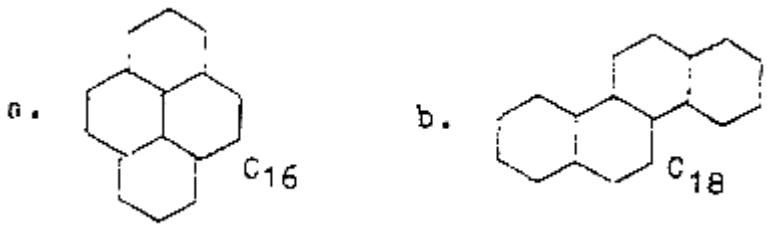
The fact that double-bonds as in C18:1 appear in the middle of the CH2-chain could in that case depend on the d-degree 4 representing double-direction.

An alternative could be departing from the intervals in the $2x^2$-chain, reading Cn-numbers to and fro as with these intervals: Also here double bonds appear in the middle:

Number of C in the phases:
2---5---4---7---6---9---8---11---10--13--12--15--14--17-16--19--18:



In steroid figurations C16 and C18 = C24, minus C8 or C6 respectively, one gets following structures:

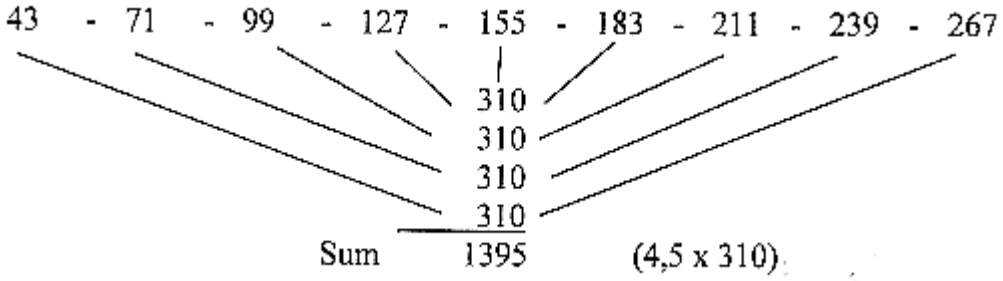


6. Some numbers:

<u>The process in detail</u> with mass numbers, addition of one C2-piece (CH2-CH2) = 5 steps:

43 + 86 - 44 + 2 -18 +2 = 71
Acetyl~ Malonyl~ -CO2 + 2H -H2O +2H

<u>Mass sum of 9 stages</u> of synthesis to a fatty acid C18, (bound, without end-group OH)*:*

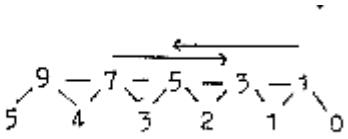


<u>Z-number</u> for 9 stages, with +1 for bond to S:
24 - 40 - 56 - 72 - 88 - 104 - 120 - 136 - 152 = **4,5 x 176 = 792**; numbera paired and added in the same way. (Cf. number 176, ½ x 352, middle 3-figure number in the chain below.)

Sum 792 = 18 x 44 is interval between the triplet series outwards and inwards of the elementary chain 5 - 0: (543 + 432 + 321 + 210) - (012 + 123 + 234 + 345) = 792.

π-number involved?
π connected with the geometry of "spherical" membranes?

The superposed chain to the elementary one:



753 / π = 239,7. 239 = C18 without the COOH-group
135 / π = 42,97. 43 = Acetyl~, (Sum 282 = C18:1, unbound.).
975 in the superposed chain: 975 / π ≈ 310. the sum of stages paired as above.

Some mass numbers of triglycerides:

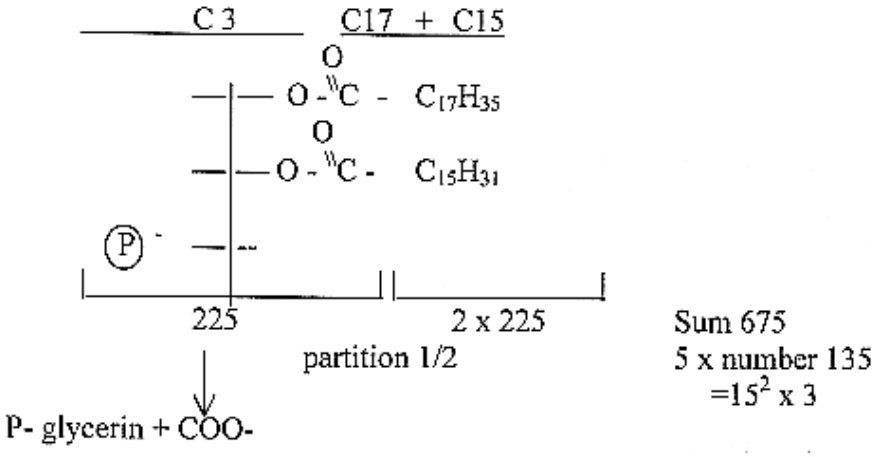
Maximum with 3 C18: 890 A
Minimum with 3 C16: 806 A
2 C18, 1 C18:1: 888 A
1 C18:1, 2 C16; 832 A

With P-group (uncharged) and only 2 fatty acids:

2 C18: 704 A
1 C18, 1 C16: 676 A $(18+8)^2$, middle numbers 18 + 8 in the $2x^2$-chain

P-lipids:

A P-lipid charged, 675 = 3 x 225 (≈ 2/3 x the sum of the exponent series 1011 (see about amino acids.)



Number 273:
Mean value for the 3 fatty acids, C16, C18, C18:1 if charged = 273 A.
Compare mean value for 2 unbound amino acids = 273 A.

Transformations between number-base systems (nb-x):

256 in nb-10 = 1104 in nb-6 = 3 x 368.
284 in nb-10 = 1152 in nb-6 = 3 x 386

2(368-1) = 734 and 2(384 +1) = 770: this is the sum of the two codon type groups of amino acids (side-chains). (Amino acids)

Z-sums for fatty acids = mass of G- and A-bases in the genetic code:

Z-number for stearic acid C18 = 151, the mass number of the G-base in codons.
Z-number for palmitic acid C16 = 135, the mass number of the A-base in codons.

Tha's when the fatty acids are bound, i. g. minus OH in the COOH-groups.

Numbers from a dimension chain, similar to the Z-A-numbers of Uranium:

Glycerine and a fatty acid C16:

C16 - OH = 256 - 17 A = 239 A
Glycerine - H = 91 A

Cf. triplets in the elementary number chain inverted:

92 x 2 /\ = **543**,47 x 10^{-5}
238 x 2 /\ = **210**,08 x $10^{-5.}$

238 and 92 the A- and Z-numbers of Uranium.

*

1/7

11. The inversion of number 7, a periodic number — a mathematical principle behind the synthesis of fatty acids - and collagen?

It is a fundamental assumption in this model that physics and chemistry has a mathematical underground - a geometrical and arithmetic one.

We can presume too that dimension degrees not only represent and form the geometries but also generate numbers.

The cell-membrane could be seen as one of the most essential conditions for life, an individualizing border. And its most elementary structure as a border is made up of fatty acids and glycogen.

Atoms as units has a parallel in cells as units on the biological level, and cell-membranes could be interpreted as an expression for the nuclear force in life chemistry.

What about 1/7 ?

7 /\ = 0, 14-28-57-14-28-57... etc.

- The synthesis of fatty acids is a periodic one as the periodic number of 1/7.

- The elementary molecules of the acids are CH2: 14 A, CH2-CH2: 28 A...

- According to the views of the String Theory we should have 11 dimensions, with 7 of these dimensions "not developed", interpretable as inwards, and curved - to compare with the function of a cell- membrane ?

- Compare number 7 as 4 + 3 in the superposed chain of a dimension chain, see general aspects on fatty acids.

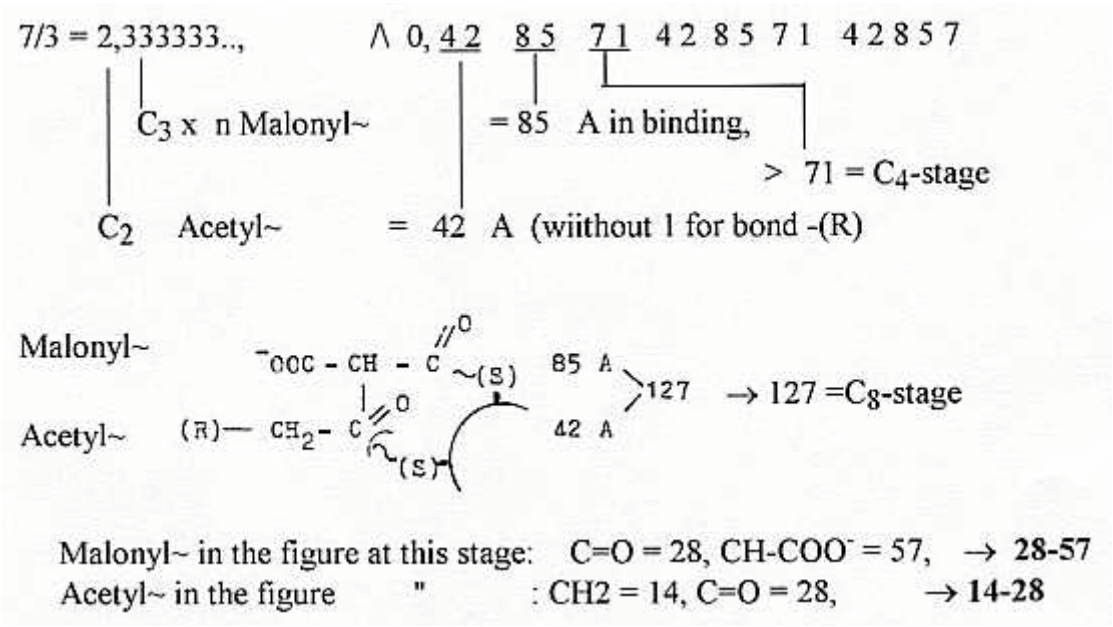
(22 / 7 ~ π. (Cf. 22: d-degree 2: 2a------1------2b, the form structure of lipids.)

A fatty acid and the process of synthesis and mass numbers (A):

First step: An Acetyl-group (C2) at one binding site binds to the middle C-atom of a Malonyl-group (C3) at another site.

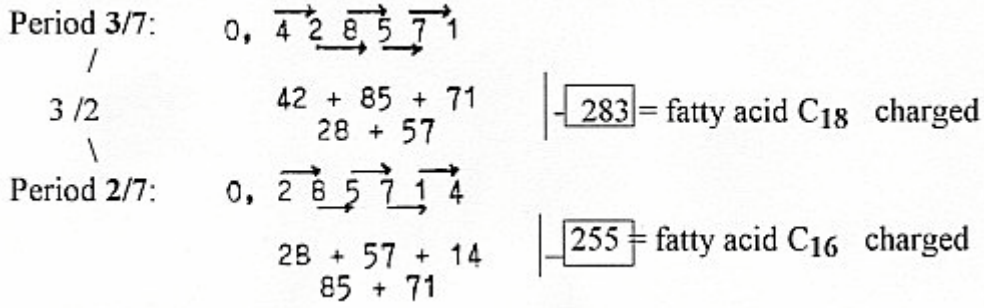
Following illustration is not correct. It should imply that one H in the CH2-group of Malonyl~ virtually during the moment of bond creation should be replaced by the Acetyl-group (giving Malonyl~ number 85), before the Acetyl-group replaces the bond to the COO^--group of Malonyl~ , which gets detached.

Instead: the rest of Malonyl~ without the COO-group = 42. Added Acetyl~ 43 gives stage 85 A. After +2H, - H2O, + 2 H (= - 14) the sum gets 71, the C4-stage. Hence stages 42 - 85 - 71.

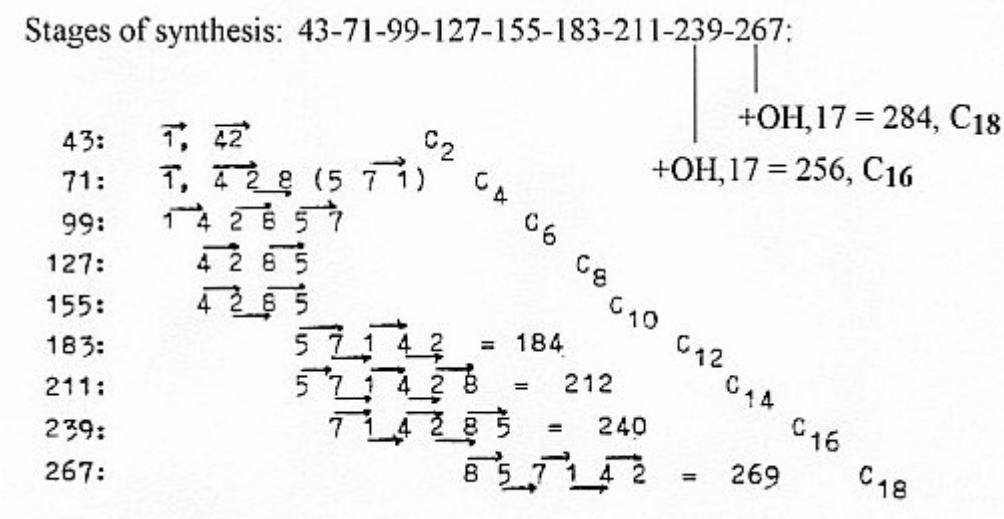


[Cf. **the quotient proton/electron**:
$(0{,}428571..)^2 = \underline{1836,7346\ 9387} \times 10^{-4}$
$= 4 \times 1836{,}7346$ ... etc.
$42{,}85^2 = 1836{,}12\ 25$ = p/e.]

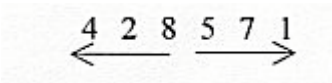
Mass numbers of two of the most common fatty acids in animals:



Observe: The CH2-CH2-groups (28 A) can also be derived not from Acetyl¨but from the amino acid **Ileu: side chain 57 A**.



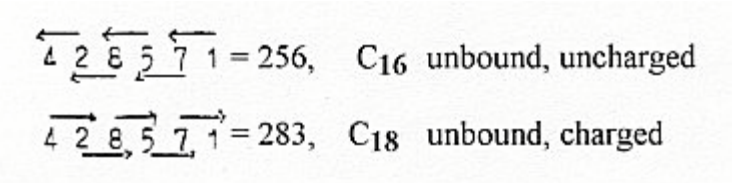
Triplet numbers:



824 + 571 = 1395 = sum of 9 stages in the synthsis to C18 bound.

And what should it imply, reading the periodic number backwards (!)
- and parts of it too ? Mirror resonance in the underlying dimensional patterns of vibrations in the complex rooms of the 7 hidden dimensions of the String theory??

We can note that mirroring the 2-figure-readings in the period 3/7 gives a relation between the two fatty acids C16 and C18, uncharged and charged respectively:

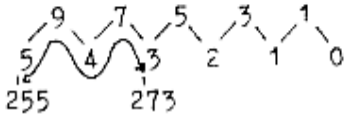


Mean value of C16, C18 and C18:1 if charged = 819 / 3 = 273.
The period 28 57 14 mirrored:

273 = 4 1 7 5 8 2 → reading direction = 41+75+82, +17+58 = 273

255 = 4 1 7 5 8 2 ← reading direction = 14+57+28, +71+85 = 255

The same sums are given from the "2-figure-chain":



273 = 59+94+47+73

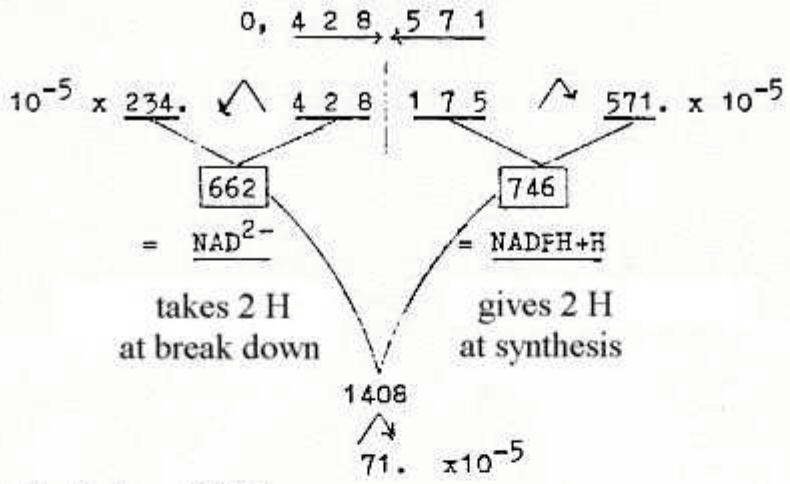
Note: 273 = the mass number of the π+-meson in e^-, actor in the strong nuclear force.
Cf. nuclear force appearing in hydrophobic bonds of lipids creating closed units as cells.
It's also the mean value of 2 amino acids unbound.

Coenzymes, some of them, in the synthesis and breakdown of fatty acids:

Reading numbers backwards in endless periodic series may of course be judged as mad. Only possible motive for it is the assumption that numbers at bottom are connected with geometries and opposite directions are essential geometrical features.

In the operation below this counterdirected reading is combined with another "invention": the eventuality that mass of molecules could be a combination of numbers which are inversions of one another:

NAD(P):



71, the beginning of 5 / 7.

ATP^- = 506, Λ = 198. .x 10^{-5}

704. = 1/2 x 1408. [704 = P-lipide with 2 C_{18}.]

$FMNH_2$:

4 2 8 5 7 1 4 : 714 Λ = 140. x 10^{-5}

854

= 458 = $FMNH_2$

Biotin:

4 2 8 5 7 1 4

41 Λ = 244. x 10^{-4}

285

COO^- ~Biotin-NH~ (bound) (Biotin-transported COO^- -group at synthesis)

= **285** A

One lipid:

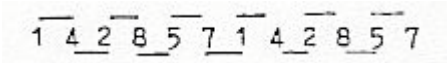
Phosphatidylserine = 763 A - if with two fatty acids: one C_{18}., one C_{16}. = 240+523. (Yet, mostly one of the fatty acids is said to be unsaturated.)

240:

283 > = 1 4 2 8 5 7 1 4 2 8 5 7 1 4 2 8 5

523:

1/7 and Collagen:



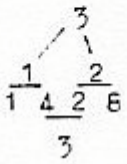
The collagen fibres are made up of series of the amino acids **Gly - Pro - Pro**: (Sometimes Lys or Leu instead of a Pro.)

Why just these amino acids, in this order? Is there any chemical explanation?

Their side chains (here called R-chains) has the mass-(A-)-numbers
1 - 42 - 42, sum 85:

Collagen: periods of	Gly	- Pro	- Pro
	↓	↓	↓
A-number, R-chains	1	42	28+14: → Sum 85

0,1 4 2 8 5 7 .



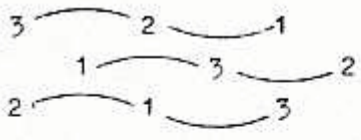
1/7 = start 0,14 ...
2/7 = start 0,28 ...
3/7 = start 0,42 ...

The "B-chains" of the amino acids, the similar parts which combine through condensation in the peptide bonds, have the mass number 74-18 = 56 = 14+42.

Strangely enough we also find such figures as from 1/7 in measures of length and breadth of collagen in the entity Å (10^{-10} m):

1 4 2 8 5 7	:	14 Å = the breadth of the spiral with 3 chains
——	:	2,86 Å (2,857 ?) = the rising of the steep helix of the peptide chain per amino acid
——	:	8,58 Å (8,571?) = the identity period of 3 amino acids in the spiral
	:	2800 Å = the length of each individual collagen fibre.

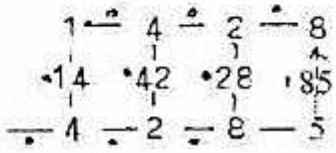
The fibres line up alongside each other with 1/4 of a period length of displacement between them. (Numbers in the figure below from the source *PK*):



By aassociation:

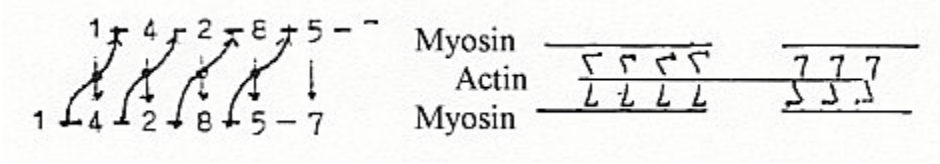
Chains of the periodic number 1 / 7 lined up alongside each other with displaceements

give "vertically" the same period:

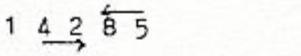


In muscle fibres of parallelly arranged Myosin and Actin filaments cross-links between actin and myosin are formed when the muscles contract - as if actin was "climbing" stepwise on the myosin filaments.

Could there eventually be a related mathematical pattern of periodic numbers underlying this biochemically expressed action?

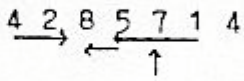


After synthesis of the collagen chains, some side chains of Proline get oxygen as additions: **hydroxi-Pro**. Mass number 42 + 16 = 58 A.

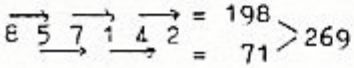


Could this eventually express changes of direcions in the chains?
(Compare that this addition needs Ascorbic acid which has the mass-number

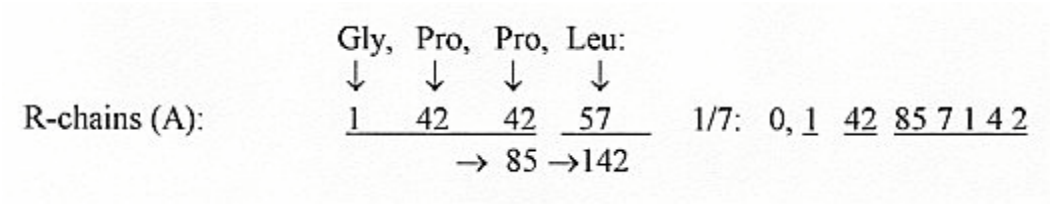
176 ---> 175 --->174 (A)



Period: Gly--Pro--Hydroxi-Prolin = 269 (R- plus B-chains bound)
= 75+115+131, -18, -17, -17: [Gly (R+B) = 57, hydroxi-Prolin = 2 x 57 = 114.]



Elastin, another fibrous protein, is said to contain much of the amino acids Gly, Pro and Leu: The side chain of **Leu** has the mass number = 57 A
Suppose we just add Leu to the series of collagen; we get:



4 R-chains of Lys 73 A (14+42+17) get ordered in cross or ring formation: the group 14+17 are replaced by 1+28-group (aldehyde group) in 3 of the 4 chains. The Lys rests get the mass value 71. Of these Lys rests following parts are included in the ring formation: 42+29+42 = 113 = 14 + 28 + 57 + 14. To this comes the 4th Lys rest NH3 = 17.]

Other molecules appearing added to collagen:

$Ca_{10}(OH)_2(PO4)_6$ - crystals attached to collagen in bone tissue:

Mass-number = 1004 A = 4 x 251 = 4/3 x a collagen period if with 3 chains
- Gly - Pro - Pro- = **251** A,

Gly and Pro, mass numbers with R- aand B-chains in bonds:

Gly, R+B, unbound	=	75 A,- H_20 (18)	= 57	- 251
Pro " "	=	115 A, "	= 97	
Pro " "	=	115 A, "	= 97	

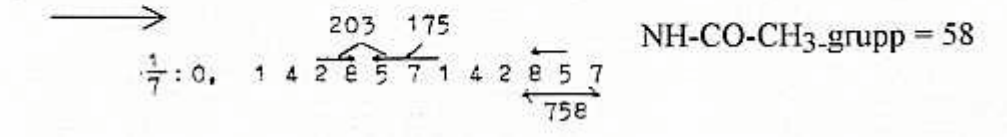
Triplet numbers of a dimension chain: **3 x 251 = 753 = 543 + 210**.
1004 = = 2/3 x 1506: 543 + 432 + 321 + 210. Cf. sum of 24 amino acids.

In connective tissue, cartilage and bone appears

Hyaluronic acid, a disaccharide x n with a COO^--group at one of the hexoses, a group NH-CO-CH3 at the other.
(It is for instance found in the synovial fluid, among other locations.)

Chondroitin sulphate, a disaccharide x n, with a COO^-group at one of the hexoses, and a SO3-group + NH-CO-CH3-group at the other.
(Much in cartilage.)

A-numbers:
378: Hyaluronic acid: 175 + 203 (bound, charged groups)
457: Chondroitin sulfate: 175 + 282



Hyaluronic acid, two disaccharides bound = 2 x 379 = 7 5 8 , uncharged.
Chondroitin sulphate: (if with uncharged SO3- group) = 175 + 283 = 458:
283 = 42+28+85+57+71.

With periods 7 / 13 and 13 / 7:

Chondroitin sulfate: 175 + 283 (uncharged SO_3- group) = 458

283 = 4 2 8 5 7 1

As unbound disaccharide: 175 + 283 +18= 476, x 3 = 1 4 2 8

7/13 = 0, 5 3 8 4 6 1 5 3 8 4 6 1

53+38+84 = 175, + 46 + 61= 282 Sum 457.

The period of n/13 ?!

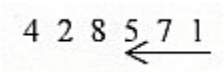
13/7 = 1, 8 5 7 1 4 2 8 5 7 → 2 8 3 → 1 7 4 > Sum 457

Histamine and **Serotonin**, in connective tissue:

- Histamine from the amino acid **His, 155** A, -COO = 111 A:

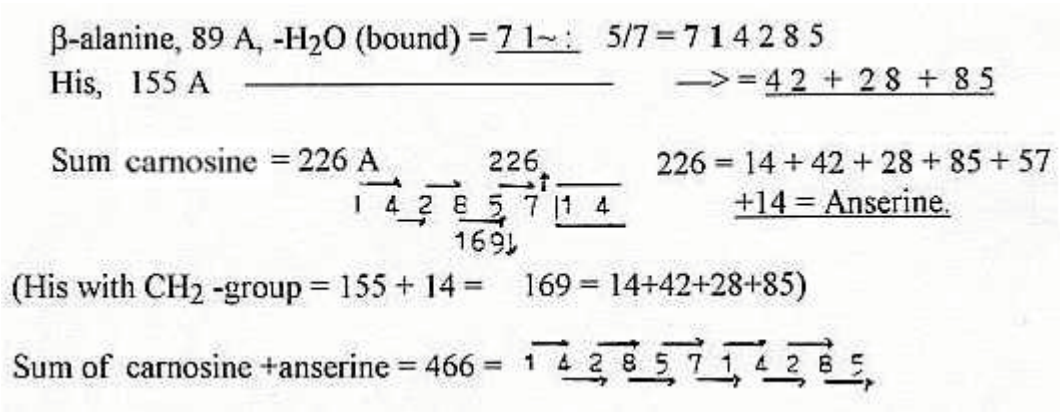
4 2 8 5...: 42 + 28 + 85 = 155 = His (Histamine = 111 = factor in the period 1/7)

- Serotonin from the amino acid Trp, 204 A, + 16, -44 = 176 A, 175 charged.



In muscle fibres:

Carnosine and **Anserine**,
two peptides made up of β-alanine and the amino acid His:



An energy storing substance:

Creatine phosphate, uncharged = 212 = 42 + 28 + 85 + 57

*

n/7-periods with factor 11 x 11 (1221) were also investigated in relation to amino acids of the genetic code. 7 pages, still more extravagant or insane operations:
Amino acids and the period n/7, pdf

12. Carbohydrates

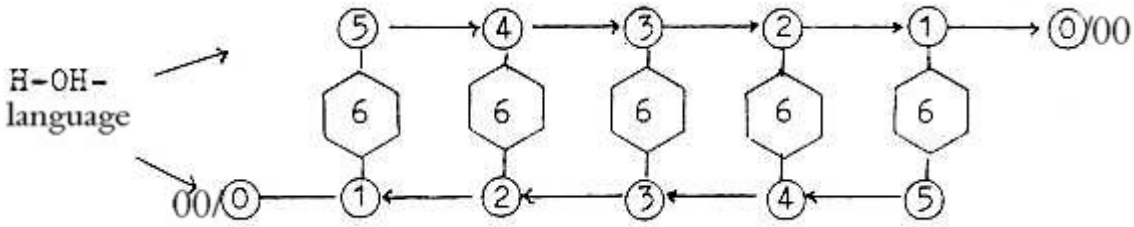
A very first note: The ring-closing of sugar molecules could reflect the last step of the carbon-nitrogen cycle of fusion in the sun: after synthesis of protons from C via N to **O** back to C with emittence of an α-partic1e**.**
Cf. "A-Z"-figure here.

1. The OH-language?

The carbohydrates (cbh) have their own language - the OH-language. They are individualized not only in number of HCOH-groups but in different directions of OH-groups from the individual C-atoms. What does this imply?
It obviously indicates a differentiation in the configuration of electrons around the separate C-atoms. (Cf. the sp^3- to sp^2-hybridization.)

An illustration of two opposite directed dimension chains could illustrate such a differentiation between electron shells of C-atoms, in the figure below with one step of displacement. Of the opposite chains one could be regarded as corresponding to the d-degrees of structure, the other the d-degrees of motion, or alternatively just a- and b-poles, as in our primary model.

Mass of the group HCOH is 30 A. That's the sum of poles in a dimension chain. The number of such groups seem primarily to be 5. as dimension degreex in our model. (Including 0/00, the "d-degree of motion", as substantiated, gives number 6.)



An elementary script of Nature? On the Z-level writing a series of sexes for the C-atom.
Cf. perhaps that inversion of 15, sum of series 5 - 0, = 0,666...

The C-atoms become here individualized in different relations between the chains. We could attach the numbers 5-4-3-2-1-(0/00) to the C-atoms in the chain not just as a convention in biochemistry but as "5/1, 4/2, 3/3, 2/4, 1/5. (Eventually the intervals as "+4" — "+2" —0 — "-2" — "-4" as differentiating?)

If the script would be so simple, it implies that the electron shells of C-atoms is dividable in several ways and may be composed in several ways. *s*-electrons of both K- and L-shell should be included — and engaged in the bonds arround the C-atom.
The varying directions of OH-groups on the surface of cell membranes function as a language.

2. The incorporation of a 6th C-atom:

What about the *hexoses* in this imagination?

It should be noted that never more than 5 C-atoms are included in the ordinary structure-building *ring formations* of carbohydrates. It seems that the only way for 6C-atom rings to get formed is through sharing C-atoms with other rings as in steroids or with open C-chains as in carotenoides.

The 6th HCOH-group is built in by plants by absorption of the molecule H2CO3 (or HCO^-). (Minus O2 giives H-COH.).

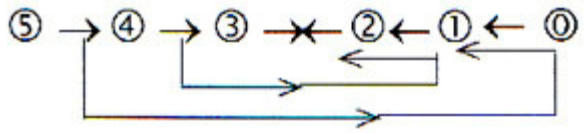
It starts from ribulose, a pentose, in P-P-bonds. (The P-groups as connected with 0- and 00-poles in the figure above.)

We may note that the 2 P-groups charged à 39 Z exactly balance the Z-number of this bound ribulose, 78 Z.

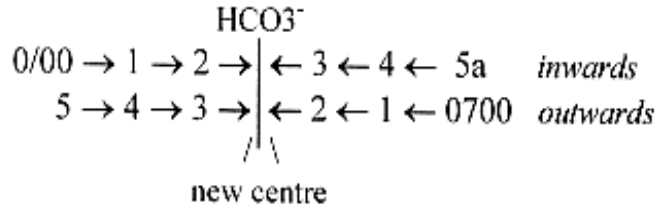
The 6th HCOH molecule gets built-in in the *middle* of the ribulose chain, more or less at the same time that this chain gets halved into two C3-pieces (treoses with COO-groups at at ends in the middle. Through +2 H - H2O the two C3-pieces unite again to an hexose.

Why in the middle?

Even if we adopt the view on the process as a substantiation of last d-degree 0/00 in the chain, we have to regard it from the perpendicular aspect on the chain: the double direction from higher d-degrees and from lower degrees meeting in step 3-2.



Or with two opposite chains:



Sums vertically here 5: Only 5 electrons involved in hexoses ! ?

This is underlined by the 2 P-groups. The central role of these P-groups, (here as well as in the partition of fructose at start of glycolysis), can be regarded as polarizing force from outside as anticentres, initiating the polarization steps - and also the driving force towards development of a new level through step 3-2.

The built-in of the 6th C-atom group implies a displacement of the middle in the chain half a step, a decrease half a d-degree, as from 3 to step **3 - 2**, (from "border to interval", the elementary illustration of a quantum jump proposed in files about *Physics*).

We could compare with transformations between number base systems (nb-x), from 10 to 6:

nb-10: 12 = C, 18 = H2O (Mass numbers A)
↓ ↓
nb-6: **20** **30** = HCOH A quotient and a relation in step 3 - 2.

The A-numbers 12 and 18 as intervals:

nb-16 —— nb 10 —— nb 8:
32 —|→ 50 —|→ 62 (= H2CO3, - O2, 32)
18 12

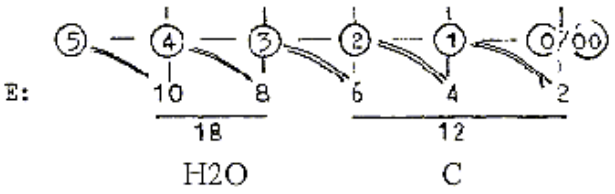
In the Pentosephosphate cycle, where 5 C3 get tranaformed into 3 C5.molecules, one C3 gets a C2 from C4, giving C5, another C3 gets C2 from C7, giving 2 C5.
(There are also in intermediate steps, C6 - C4 and C7 - C3 molecules, reminding of the number *10 division chain.*)

3. Elementary numbers of carbohydrates:

Some simple associations with the dimension chain in alternative forms.

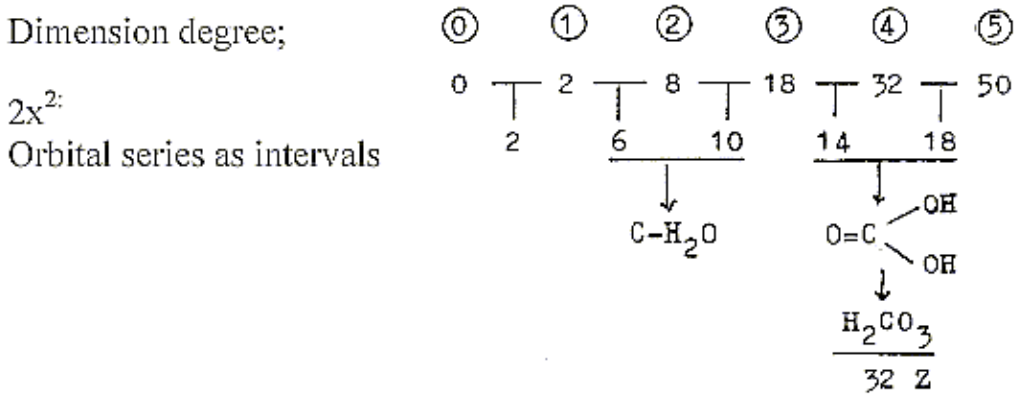
- Numbers O = 8 Z, H2 = 2 Z, a relation 4 — 1.

- Why primarily pentoses as a condition for synthesis of carbohydrates?
150 A is 5 times 30, the sum of poles of the dimension chain.
E-numbers = value as sum of outer poles in the different d-degrees.

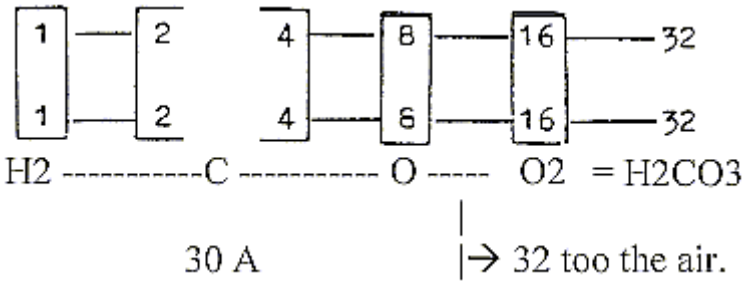


Numbers of the carbohydrates in the $2x^2$-chain:
All numbers Z.

H2CO3, the molecule which (minus O2) is built-in as the 6th HCOH-molecule.



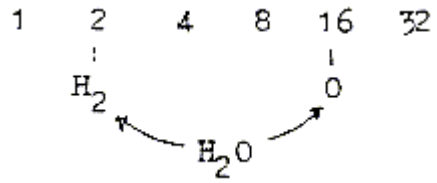
Mass numbers with 2 chains 2^x:
Hypothetically the 2^x-series is assumed as valid in polarizing direction inwards in a dimension chain.



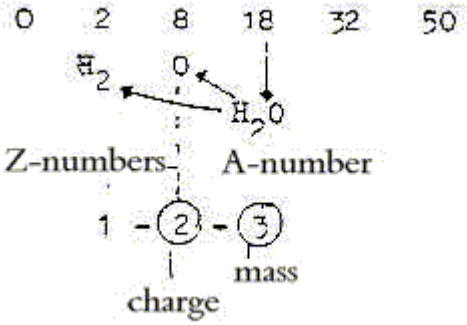
The division of H2O:

a. Elementary dimension chain: Z/2:

b. 2^x-chain, A-numbers:



c. $2x^2$-chain:



4. The ring-closing of carbohydrates:

A first question: Why do the ends differ in open, unclosed carbohydrate chains? One end is the aldehyde group H-C=O and the other end H2-C-OH.

It could be read (-/+), minus H at one end (aldehyde group) and plus H at the other. It's suggested here that this reflects the polarization in last step of the dimension chain from d-degree 1 to d-degree 0/00,

1a — 0/00 — 1b,

Sum of poles = "E-number" = 2 for 2 H, poles which define a (new) 0-pole and 00-pole respectively, here identified with minus/plus one H.

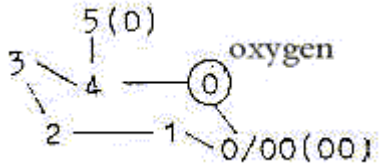
With C-atoms regarded as representing different d-degrees, the closing to rings of pentoses or hexoses may be interpreted as illustrating the connection between these outer poles 0 and 00 (also together representing 5').

Conventionally the numbering of C-atoms begin with C of aldehyde group as number 1. Accepting this order but decreasing the number series one step, relating it to the dimension model gives in an hexose:

H2COH — HCOH — OHCH — HCOH — HCOH — **O=**CH
5 4 3 2 1 0/00 (~5')

Then, in terms of the dimension model, the ring-closing implies a connection from d-degree 4, outer poles of which are 0 and 00, with the C-atom at the end representing d-degree 0/00 where these poles are met again.

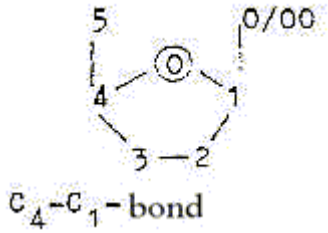
00
|
4 — ——— 0/00
|
0



Perhaps the oxygen atom of the aldehyde group could be identified as expression for the 00-pole "meeting the other way around".

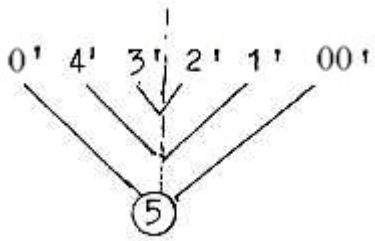
Within P-P-bonds, as for instance when C6 glucose is transformed to C6 fructose at start of the glycolysis, the oxygen bond changes to a relation 4 — 1:

C4 —Oxygen — C1:

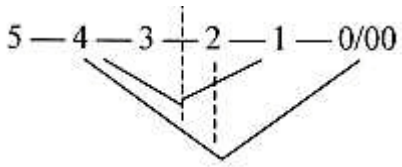


The same figure can illustrate pentoses with only an OH-group at position 0/00.

The C4-C1-connection implies an angle change, similar to the turn from a more linear aspect on the dimension chain, formally 180°, to the loop model, 90°, a vertical aspect on polarizations:
5 → 0/00, 5 → 4/1, 5 → 3/2:



The transformation of glucose to fructose implies that the middle of the rings is increased half a degree, as it was decreased a half degree when the 6th HCOH-group were built in, here from 2 in glucose to step 3-2 (C3 — C2) in fructose (as in pentoses).

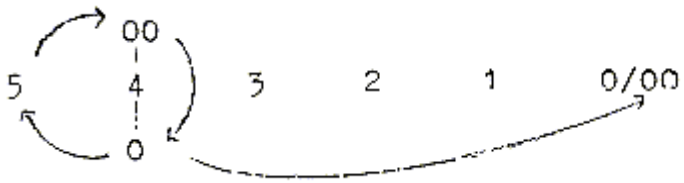


(We may here remind of the two classes of *amino acyl tRNA-synthetases* related to C3 and C2 in ribose of nucleotides at the protein synthesis, dividing the attributed amino acids into 2 groups, as the opposite directions of the chain meet in this step 3-><--2.)

In the dimension model d-degree 3 gets polarized in poles 3a—3b (defining d-degree 2). We suggest to compare with the more or less immediate division of a hexose when the 6th C-group has been built-in, into 2 C3-pieces - and the same division in this 3-2-step when glucose has been transformed to fructose at start of glycolysis.

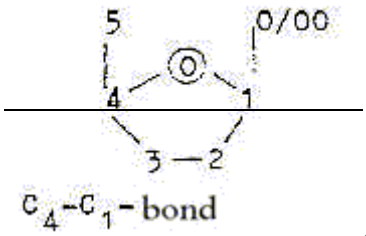
Closing of the carbohydrates into rings is geometrically, in the macro-structure, expressions for the steps from d-degree 4 →3 →3a in our dimension model. The model implies also that rotation as a 2-dimensional motion appears in step 4 →3. Also assumed as an angle step as 180° to 90°.

Such a rotation appears also here at closing of the ring around C4: H turns 180°, OH-group 90°, which also leads to the turn of C5 90°. The OH-group is turned towards C "0/00". Hence, ring-closing and rotation seem connected as geometry and d-degree of motion in the dimension model.



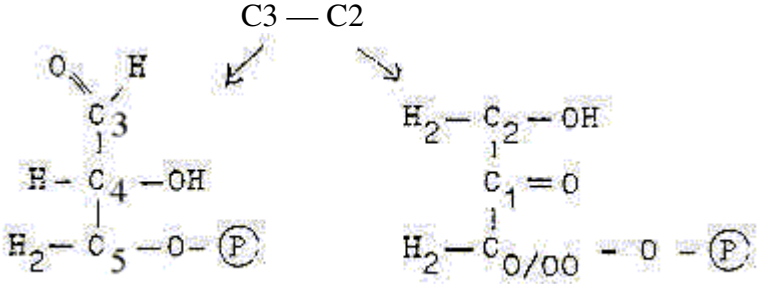
5. Aldehyde - Keto parts:

When hexoses as fructose are split into two C3-parts, one gets an aldehyde end, the other a keto-bond in the middle: we have an aldehyde and a keto-part.



conventional numbering

Original aldehyde end to the right at C0/00.



- Original ends COH and H2COH now appears at C3 and C2. (Equivalent with minus 1 H at C3, +1 H at C2). The part with original aldehyde end becomes the keto-part. A change in direction of numbering seems needed if the keto-group C=O should represent d-degree 4 in the C-chain.

- The main features in the process of glycolysis and citrate cycle may in some respects be regarded as an illustration of the double direction in a dimension chain:

$$5 \rightarrow 4 \rightarrow \underset{3C}{3 \rightarrow\!\!<\!\!-} + \underset{3\,C}{2 <\!\!-\!\!- 1} \leftarrow 0/00$$

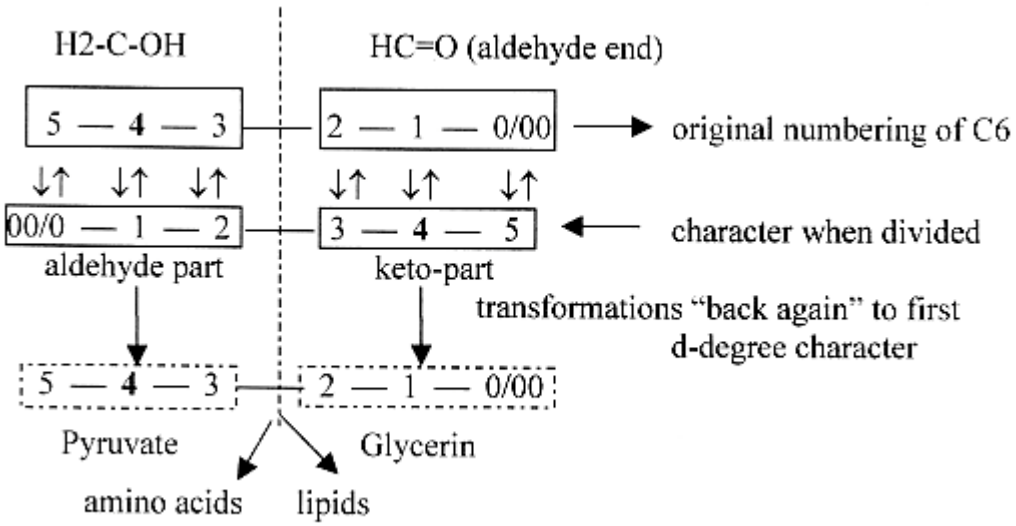
The halving of the fructose molecule as a polarization outwards, one half in d-degree 3 meeting +1 C + 2 C (CO2 and Acetyl~) as from the other half, representing the complementary pole to isocitrate 6 C.

- It's the aldehyde part C3, here numbered 5 - 4 - 3, which develops through up to ten steps to C3 **Pyruvate** through glycolysis, and further in synthesizing direction into citrate cycle, + C1 and + C2 to C6, isocitrate, that's to the higher d-degrees of C-atoms.
The way is connected with generation of amino acids and proteins.

- It's the Keto- part, here numbered 2 - 1 - 0, with the double-bound oxygen at C1, which develops to C3 **Glycerine**, the "circular" backbone part of membranes.

- The separate ways of transformations for the C3-pieces underscores the differentiation of C-atoms in glucose as well as the geometrical polarity "radial" versus "circular" (3b-/3a-poles) as amino acids (proteins) versus cell membranes on a macro-scale.
From Pyruvate the way leads also to C2, Acetyl~, which starts the synthesis of the radial parts of membranes, the fatty acids.

If we want to associate higher C-numbers 3-4-5 as C-numbers with the way to amino acids, the lower ones with the way to glycerine, according to dimensional aspects, and further double-bound oxygen with d-degree 4 as C4, the figure below could illustrate the ambiguousness in numbering and transformations (as "pole exchanges") between the two opposite number series.
A division vertically of the horizontal chains shows that both C3-parts "virtually" contain whole dimension chains. Cf. in the model debranched d-degrees 1 --- 2 from higher steps meeting the other way around.

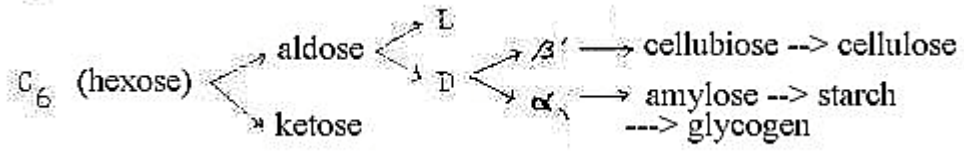


Identifying C4 with d-degree 4 (in the model double-direction) may give an aspect on why transformations always have the direction from keto-form to aldehyde form (possible to read as outwards?) and why the keto-form form is the actual one when carbohydrates transform into one another.

The association of C-atoms with different d-degrees seems supported by the change in mass distribution during glycolysis: The transformation of the aldehyde part as 3-P-glycerate to Pyruvate in several steps implies that a nearly equal mass 30 - 30 - 30 transforms to 45 - 28- 15 in Pyruvate, CH3— C=O—COO(H), that's quotients circa 3 - 2 - 1. as if an underlying differentiating process between the C-atoms manifested itself. (In reality expressed as plus / minus 16, oxygen, between first and third C-atoms.)

6. Polarizations of the OH-language:

Different directions of the OH-groups around the C-atoms seem possible to regard as a way through polarization steps, different paths at bifurcations leading to different roles and positions in the cell:



The figure shows three such polarizations where the 3rd leads to the opposition between cellulose <—> amylose and starch: it implies one kind of **2-3-**relation in d-degrees regarding the forms on a macro-scale: cellulose for cell coats, surfaces, amylose as substrate in the cell, volumes. (Cf. different coenzymes connected with different carbohydrates: UTP with glucose, TTP with cellulose.)

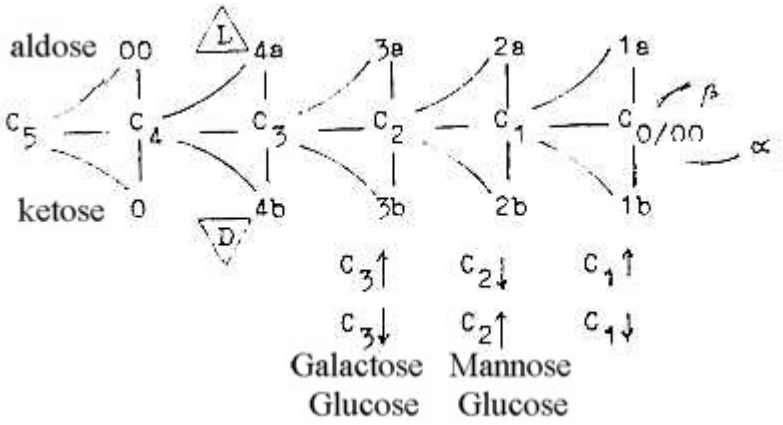
This 3rd polarization, α, β, refers to the orientation of the OH-group at what here has been regarded as C-atom "0/00" in original hexose.

A 4th polarization in hexoses in direction "up/down" at C3 (conventionally C4) gives the difference galactose/glucose: united in the disaccharide lactose.

We have hypothezised that the 2^x series may reign, from the end of a dimension chain and (formally) there are 2^5 isomers in a hexose, C6, 2^4 in a pentose, 2^3in a C4 piece, 2^2 in a C3-piece:

Carbohydrates:	C3	C4	C5	C6
Number of isomers:	4	8	16	32

Following figure may not illustrate the real way of derivations but could perhaps give a hint of the way of thinking here, with associations to the dimension model:



- Arrows for the direction of OH-groups.
- The β-form should be associated with the 0-pole and pole 4b (D), (outward direction).

- The up/down polarity of OH-groups could perhaps be expression for the polarization at C1, represented in each step.

7. Forms of macro-molecules of the carbohydrates:

Another aspect on the different carbohydrates gives the behaviour of the polymerized macro-molecules if we regard them in terms of motions of different dimension degrees:

- Cellulose gets folded, which may be seen as an 1-dimensional motion to and fro, a kind of vibration.
- Amylose gets spiralled, a kind of 2-dimensional rotation, connected with pathway motion giving a 2- to 3-dimensional motional structure.
- Amylopectin and glycogen get branched, as illustrating "translation in 3 dimensions".

In this respect there is no opposition between d-degree of form (structure) and d-degree of motions; the motions if we regard the formations of the macromolecules as such, are and give the macro-forms.

8. Some number operations;

a. Quotient A/Z in hexose = 180/96 = 1,875 = w: [5x3x1] / [4 x 2]
pentos: 150/80 = " "
(0,1875 also a number in Balmer series for wavelength of hydrogen.)

b. Hexoses - Pentoses: numbers 180 - 150 as "triplets"?

180 = 3 x 60 (5,454545 x 33)
150 = 3 x 50 (4,545454 x 33)

$2x^2$-chain: 50 - 32 - 18 - 8 - 2 - 0
→ ←
50 60

c. Disaccharides, bound with help of coenzyme UTP (UMP - UDP):

P-glucose = 260 A (uncharged)
UTP = 484 A Sum 744 = 2 x **372**

372 = the sum of both terms in the formula for synthesis of carbohydrates:
6 H_2CO_3 = 372
6 H_2O + 6 CO_2 = 6 HCOH + 6 O_2
108 + 264 = 180 + 192 A

744 also A-number for NADP.

Glucose + UTP = 180 + 484 = 664, Λ (inverse) = 1506. x 10^{-6},
1506 the sum of the triplet series = (543 + 210) x 2.
Cf. The Genetic Code, sum of side chains of coded amino acids.)

664 also the A-sum of NAD.

Inorganic phosphoric acid binds glucose: H_3PO_4 = 98 A.
(Cf- number-base transformaations in files about The genetic code.)

98 in nb-16 = **372** in nb 6 or 412.)

Quotient Glucose/H_3PO_4 = 180/98 = 1836,7346... x10^{-3}, about
p/e quotient, apart from 10-powers, decimals 4 times the same integer...

Glucose + H_2PO_3 = 180 + 81 = 261, mirror number 162 = glucose
in chain binding: 180 - 18.
2 glucose within a chain = 2 x 162 = 324 = 18^2 = watwe 18 squard, =
= A-number for UMP.

END

To Appendix:
Amino acids and the period *n*/7

APPENDIX

Amino acids and the period *n*/7

The reader should be prepared for some really insane operations but also for some perhaps less mad ones.

1. Factors 111 x 11 in one period *n*/7:

1/7	142857 =	111 x 11 x 117	117 = the amino acid (ams) Val
2/7	285714 =	111 x 11 x 234	
3/7	428571 =	111 x 11 x 351	
4/7	571428 =	111 x 11 x 468	21 x 117 = 2457
5/7	714285 =	111 x 11 x 585	
6/7	857142 =	111 x 11 x 702	

2457 = 3/4 x 3276, sum of 24 ams, R+B
468 + 351 = 819, x 4 = 3276.
351 + 702 + 585 = ½ x 3276.

Factor 111 x 11 in the period = 1221, /\ (inverted), x 4 = 3276,00 3276... x 10^{-6}
24 ams R+B, unbound

(R = side-chains of ams, B = backbone chains)

Cf. 1221 x 1,234 = **1506,714**:, numbers as sums of the triplet series, outwards 1506, inwards - as decimals! - 714:

.

1221 x 1,234 =	1506,		714	1506 = A-number of 24 ams if + 2H
	543		345	
	432		234	
=	321	=	123	
	210		012	

$1{,}11^2$ = 1,2321, x 1221 = 1504,4.
C:\26-u5d\booklets\ams_roots6figurenumbers.htm

2. Number 1221 as sum (abbreviated) appearing among square roots out of 6-figure numbers **read in an elementary chain with superposed odd-figure series:**

√594735 + √537495 = 1504. = 24 ams R-chains
√947352 + √253749 = 1477. = 20 ams B-chains
√473523 + √325374 = 1258. = 20 ams R-chains

√735231 + √132537 = 1221.

Observe: this factor in n/7 starts from number 7 in the chain.

The "2-figure chain" and number n/7:

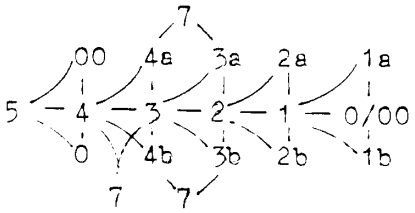
59 + 94 = 153
95 + 49 = 144

(117 = 52+23+31+11)

117 x 1221 = 1 4 2 8 5 7.
144 + 207 = 351, x 1221 = 4 2 8 5 7 1 (number 153 read backwards)
144 x 1221 = 1 7 5 8 2 4 = the mirror number to period 3/7 !

3. If 1/7 (x 1,2,3,4,…) should have some reality in the underground of the biochemical world - why?

- Numbers in the dimension chain?

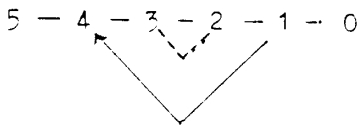


Acccording to elementary hypotheses in the model here mass is created through d-degree step 4→ 3.

Number 7 is the sum of poles in step 3-2 and the second figure in the superposed chain 9-7-5-3-1.

According to other suggestions mass could eventually be defined or created through inversion of inward directed vector fields.

Possibly as inversion of number 1-4 read as d-degrees?



The String theory counts on 11 dimensions, 7 "not developed", interpretable as inward directed.

- 4 - 7 as a divided number 11 connected with outward / inward direction. Compare numbers 444 for G1+C1 in coded numbers, 777 for U1 + A1. See parapgraph 6 below.

Splitted number 11 —> 4 / 7

4 and 7 are also = "loop numbers"* in d-degree steps 1-->0 resp. 0-->1 .
A number for dimension steps *ab* + 2 x opposite number *ba*, divided by 3, with the same operation repeated, returns to a number earlier in the series or to a point number:
10 + 2 x 01, through 3 = **4**. 01 + 2 x 10 through 3 = **7**

* [Loop number for step number 54 = 36. (36 + 2 x 63) / 3 = 54
" " " " 43 = 91 (91 + 2 x 19) / 3 = 43
36 x 91 = 3276, sum of the 24 amino acids.
Loop numbers for steps "inwards", 45 and 34 = 63 and 52
52 x 63 also = 3276 .]

Number 11 is the difference between steps in the elementary version of the number chain: 54 → 43 → 32…

- $\sqrt{1/49} = 1/7$. 1/49 = the number series 2^x: 2 0 4 0 8 16 32 ...
Perhaps this number chain 2^x is the primary start?
We have suggested that this partition in bits could be valid for polarizations in inward direction, 2 as the log number. Cf. biological reproduction, cell divisions…

Should we eventually look for periodic numbers as 1/7 in molecular cyclic processes?

4. Fatty acid 283 = C18 charged, x 1221 = 345 543.

4 / 3276 = 1221-period: 122100122100... (3276 = 24 unbound ams, A-number)

3276 / 4 = 819 283 / 819 = 0,345 543 345 543 ... -

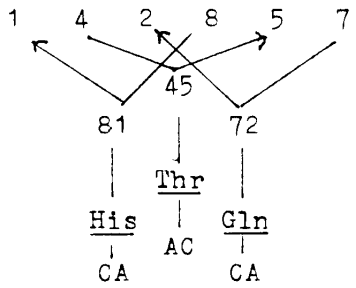
Cf. fructose within P- -P- bonds = 178:

178 / 3276 = 0,543 345 543 345...-

543 + 345 = 888 = 12 B-chains à 74 A.

5. Some individual mass numbers of amino acids, R-chains, from the period 1/7;

The CA+AC-group:



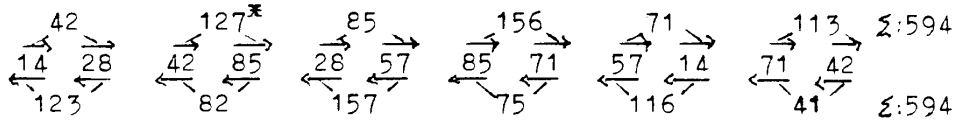
R-chains, mass numbers

Sum: 198
= 2 x (14 + 28 + 57)

Two periods with a displacement of three steps:

81 72
↑ ↑
1 4 2 8 5 7 → 1/7
| | |
8 5 7 1 4 2 → 6/7.
↓
45

Displacements in the period: Differences between forward and backward readings:



123 -42 82-127 157-85 75-156 116-71 41-113
↓ ↓ ↓ ↓ ↓ ↓
81 - 45 72 - 81 45 - 72

= His	Thr	Gln	His	Thr	Gln
CAY	AC	CAR	CAY	AC	CAR

6. "Coding" the amino acids - mass of R-chains - in number of 7th.

n in the expression *n*/7 as starting figure:

1 3 2 6 4 5 → starting figure *n* in *n*/7
| | | | | |
0, 1 4 2 8 5 7

Number 14 becomes 13 coded, number 57 becomes 45 etc., reading numbers of *n*.

Transforming the mass numbers of side chains of the amino acids to these "coding" numbers 1.3.2.6.4.5, really very arbitrary, is surely an unsain behaviour.

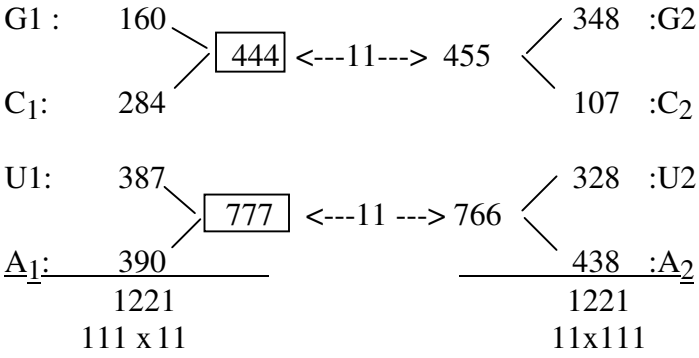
The table shows clearly this mad experiment.
Some numbers inply backward reading: 17, 58, 75, 107.

Ams	R, A-number	In number of the period n/7	"Coded" in number of n/7	Codons
Gly	1	1	1	GG
Ala	15	57 - 42	45 - 32 = 13	GC
Ser 1	31	17 + 14	15 + 13 = 28	UC
Ser 2	31	14 + 17	13 + 15 = 28	AG
Pro	42	42	32	CC
Val	43	57 - 14	45 - 13 = 32	GU
Thr	45	45*	34	AC
Cys	47	47*	35	UG
Ile 1	57	57	45	AUA
Ile 2	57	57	45	AUU/C
Leu 1	57	71 - 14	51 - 13 = 38	CU
Leu 2	57	1 + 14 + 42	1 + 13 + 52 = 46	UU
Asn	58	58	46	AA
Asp	59	17 + 14 + 28	15 + 13 + 26 = 54	GA
Gln	72	72*	52	CA
Glu	73	17 + 14 + 42	15 + 13 + 32 = 60	GA
Lys	73	14 + 17 + 42	13 + 15 + 32 = 60	AA
Meth	75	75	54	AUG
His	81	81*	61	CA
Phe	91	17 + 75 - 1	15 + 54 - 1 = 68	UU
Arg 2	101	58 + 57 - 14	46 + 45 - 13 = 78	AG
Arg 1	101	142 - 41	132 - 31 = 101	CG
Tyr	107	107*	105	UA
Trp	130	57 + 17 + 14 + 42	45 + 15 +13+ 32 = 105	UGG
			Sum 1221	

* Not figures in series.
Tyr 107 as a backward read figure including 0, as a figure closing the period to a circle.

Hence, it was curious that the sum became the number 1221, the factor in the period, reasonably a pure chance.

Yet, adding the code numbers we get:



7. The factor 1,234 x 1221 = 1506,714:

G1 + C1 = 444, x 1,234 = 547,9. Real sum of R-chains = 544.
U1 + A1 = 777, x 1,234 = 958,8. " " " = 960.

$G_1 + G_2 + U_1 + U_2 = \underline{1223}$
$> \underline{1221 +/-2}$
$A_1 + A_2 + C_1 + C_2 = \underline{1219}$

Cf. real mass sums, same groups: 1502
> 1504 -/+2
1506

(Difference 1504 - 1221 = 283, a fatty acid C18 charged.)

Individual codon groups "coded" and real sums, a comparison:

	"Coded" sums ↓			Real sums ↓
G1:	160,	x 1,234	= 197.	191
C1:	284,	"	= 350. ...547	353...544
U1:	387	"	= 478.	463
A1:	390	"	= 481. ...959	497...960
G2:	348,	x 1,234	= 429.	411
C2:	107,	"	= 132. ...561	133...544
U2:	328,	"	= 405.	437
A2:	438	"	= 540. ...945.	523...960

8. The amino acids in weight order:

Gly ----------> Asp * Gln ----------> Trp
|
477 Mass number middle 744

14 ams 10 ams

9. The amino acids ordered in accordance with their derivation from stations in glycolysis and the citrate cycle:

Glycolysis - citrate cycle: stations			Coded mass numbers R	
	3-P-glycerate :	Ser1, Gly, Cys, Meth	118	
753 A	P-enolpyruvate	Trp, Phe, Tyr	278	
	Pyruvate-Acetyl~	Val, Ile1, Ile2, Leul,Leu2	206	- 777
751 A	Oxaloacetate	Ala, Asp, Asn,Thr, Ser2	175	
	α-ketoglutarate	Glu, Gln, Lys	172	
		Arg1, Arg2, Pro, His	272	- 444

No explanation here of why the division 777 - 444 occurs between Oxaloacetate and α-ketoglutarate.

10. Codon type order gave without exceptions numbers with factor 11:

	GG + CC	= 33	= 11 x 3		
Pair-<				> 253	
	AA + UU	= 220	= 11 x 20		33
	UC + CU	= 66	= 11 x 6		
Form-<				> 286	
	GA + AG	= 220	= 11 x 20		33
	AC + GU	= 66	= 11 x 6		
Cross-<				> 319	
	CA + UG	= 253	= 11 x 23		44
	AUG+ AUA	= 99	= 11 x 9		
RNA-<				> 363	
	UA+AU-U/C + GC + CG	= 264	= 11 x 24		
			11 x 111		

Nothing of these results were naturally expected when the code.numbers were derived.
In spite of such and other results it seems impossible to believe that the transformations to the "code numbers" have any reasonable sense. (?)

11. The coded mass numbers grouped in codon types related to "factor chains":

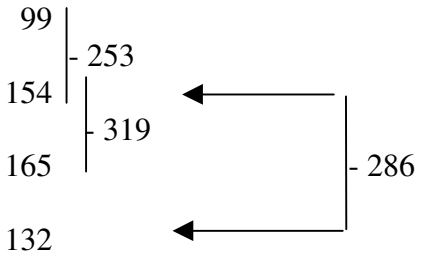
"Factor chains"		
1 x 54 = 54 ---- 45 = 45 x 1	99	
2 x 43 = 86 ---- 68 = 34 x 2	154	- 418 = Cross-coded, real sum
3 x 32 = 96 ---- 69 = 23 x 3	165	
4 x 21 = 84 ---- 48 = 12 x 4	132	- 352 = Form-coded, real sum.

5 x 10 = 50 ---- 05 = 01 x 5 55
370 235 (→ 5 x 74, B-chains of ams, and 5 x 47, R-chain of Cys)

Column sums outwrds inwards of the factor chains = 370 + 235 = 605, 5 x 11^2 -/+ 84 = 286 + 319 = Form- plus Cross coded ams in "coded" numbers n/7..

The "coded" codon grouped sums of R-chains: 253 - 286 - 319 - 363:

Factor chains "outwards + inwards":



55 RNA 363: 2 x 99 + 165 or 253 + 2 x 55...

*