COMPLEMENTATION TO THE ''BASIC HYPOTHESIS'':
REGRESSION TO THE INORGANIC VERSUS SELF - REPRODUCTION

András Balázs

Department of Biological Physics, Eötvös Lóránd University

1117 Budapest, Pázmány s. 1/A, HUNGARY

Phone: +36 23 381 377

E- mail: balazsandras2002@yahoo.com

Abstract

We show in this study that the living organism, after its birth, had two routes of time evolution, which is represented at also multicellulars, due to our internal „backwards" time process (introduced originally by Gunji), namely, direct disintegration or a tedious space - mapped, metabolism – based growth and ''self'' – reproduction. We investigate in some details the physical conditions which made (and makes) possible the second route, chosen by Nature, evidenced by organic evolution. We will find that the crucial internal components are informational, *classical, additional* degrees of freedom, which lead to a matrix structure of the system's phase space and forming our leading principle of internal ''self – measurement'' chains, the overall process termed by us ''endogenous exophysics''. We also examine the build – up of these crucial informational, ruling (controlling, constraining) biopolymers. We will find that their structure can be described by well – known technics of molecular physics (the SLMO picture), however, our *logical* monomeric factorizations, contrary to these technics, is not only unitary but also projective and is *unique*. We maintain that the life process could come about only in a mesoscopic structure, allowing for a natural quasiclassical internal dynamics, and also allow for the joint introduction of both underlying quantal, also informational classical observables *internally.* We conclude that chosing the more difficult and involved life process, as opposed by disintegration, (cell division), had to be a choice of Nature, which we must accept as a *natural fact.*

Keywords*:* classicality; overdetermination; drives; SLMO picture; metabolism; self – measurements; difference from quantum automaton.

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1. INTRODUCTION

In two previous papers [1,2], we introduced the concept of an internal ''backwards'' time process in biological organisms, emerging as a post – effect of a primordeal amino acid – codon quantum mechanical primeval molecular (in fact, macromolecular) *measurement event*. Thus we arrived at an internal ''time reversal'', with the ultimate ''goal'' of attaining internal/external time symmetry. By the internal actions of *natural symbol* (in the simple terms of Post [3]: time process mapped onto space) the internal backwards time process, in its progression towards symmetry, is thus *mapped onto space*, in the well – known internal space – like processes of metabolism, where the enzymatic lock – and - key (space complementing) phenomena play the central role.

It must be admitted, that the existence of an internal ''backwards'' time process was first introduced by Gunji [4], considering, in its focus, the external ''unprogrammability'' nature of (biological) systems, together with the observation that if time is irreversible (fall of ''detailed balance''), time and space are *inseparable*. This is foreign to Newtonian mechanics, and only can be discussed in quantum mechanics, where the two unitary opposite time evolutions are also correspond to adjoint operators. In our case, the total Hamiltonian, in the gradual internal progression towards adjointness (symmetry), is itself permanently *not* self – adjoint [1,2].

Our analysis, we think, is a continuation of the many – decades old conceptually founding studies of Pattee, e. g. [5-9], Matsuno, e. g. [10], Liberman et al., e. g. [11,12], Conrad, e. g. [13,14] Igamberdiev, e. g. [15], and others, all emphasizing the importance, in protobiology, some kind of internal/external *molecular quantum measurement*. Our quoted studies differ first of all in that we tried to deduce the DNA/Protein *assignment phenomenon* from such an elementary, unique *endophysical* (see below) quantum measurement process.

Here we try to show that the internal time process (and hence ''natural symbol'') has two competing ''goals'': regression back to the inorganic (the endophysical state) or the successful conversion to the internal space – like (''asynchronous'') (space) interactions [4], with the ultimate result of space – mapped (quasi -) symmetry, ''self'' – reproduction (arriving at the ultimate evolutional emergence of *observing entities*, so ''exophysics''), (here we concentrate on the most elementary forms of the latter, the coming about of daughter cells, of which the very diversing forms of ''self'' – reproduction, arised).The evidence of *partial* success (not forgetting extinct species) of the ''self'' – reproductional ''drive'', is evolution itself.

These two ''drives'', to borrow here this ethological expression, both are of a two – levels one: a molecular one, and one which penetrates into the phenotype, *representing the molecular one*, to guide the phenotype through its life – cycle. Both have a destructive and a counteracting vital component: direct physical molecular disintegration/the space – mapped ''self'' – reproductional molecular processes; and the destructive regressive/self – maintaining, focusing – ordering ''orientation reflex'',''drives'') [16]. The formers correspond to *direct* (''strong'') self – reference, the latters to *indirect* (''weak'') ones [17] in relation to the basic regressive time evolution (the internal space - mapped ''backwards'' time process).

Note that in what follows, space – time, space – like and similar terms do *not* have any relation to relativity theory, they belong to Gunji's terminology, cited above.

2. DISCUSSION

2. 1. Endo – and exophysics

Endophysics is a description of a system (or Nature in general) with the *exclusion of an observer* (''God's panorama'' in Primas' words, as the ''system in itself'' is, by EPR correlations, part of the totality of the Universe), wheras exophysics is a description with the *inclusion of an observer*. It must be stressed that the rigorous mathematical formalisms of the two descriptions is widely different. The concept was introduced by Rössler [18], and worked out by Primas, e. g. [19-21]. It is natural that, as observing humans emerged much later in evolution, the supposed primordeal molecular quantum measurement (i. e., a many – to – one process) must have been an *endophysical* one. If we use the Copenhagen interpretation of quantum mechanics (so quantum measurement), which we also suppose here, we seemingly run into trouble there. In ref. [2], however, we put forth an argument of how quantum *dynamics* (a many – to many or, in an other aspect, one – to – one) phenomenon can have evolved into a successive many – to – one event – chain (quantum *measurements*) in connection with protobiological polymers (and thus protobiology *alone*). *This might have led to exophysics: the arisal of (quantal) measuring humans.*

It belongs here that as self – reference, in a loose way, can be interpreted as nonlinearity, it follows that the internal quantum dynamics of biological systems are dynamically *en gross* nonlinear. This essentially nonlinear process, when placed into a linear frame, clearly shows the *basically energy – driven, yet autonomous, active measurement dynamics.*

2. 2. One – to – many and many - to - one behavior

One of Gunji's main argument concerning unprogrammability of certain (thus biological) systems stems from the observation that they function in an one – to – many way *externally.* This leads to unpredictability and unfollowability of behavior. We know from Bohr that to change the situation is to destroy the living state of matter [22]. Though he later withdrew his conclusions, we would like to stick to this idea, which is very original and, according to us, holds true (we are considering here individual living organisms, not an ensemble of quasi – identical individuals, where the (human - involved) situation evidently changes, as is shown by genetic engineering, for example).

Living organisms *are* programmed by their *internal DNA ''program''*, so they follow a many – to – one behavior *of internal origin. This does not mean that externally they do not appear to be one – to – many behaviorial systems.* On the contrary, it is exactly their hidden internal ''program'' which is the very reason of an external Gunji – type one – to – many behavior (unprogrammability). The ultimate reason of the internal ''program'' is different inherited, but in essence of the same origin, primordeally emerged time inversion process, which is flexible enough to trying different space – mapped strategies (interaction with the external world), i. e., different *metabolisms*. With the Cambrian Explosion, we have then also multicellular phenotypes, and the ''mental phenotype'', i. e., *real drives, representing the molecular process*, i. e., destruction/self – maintenance, becomes much more visible and effective with the evolving (also coded!), originally interface (of ectodermal origin) nervous systems.

2. 3. Quantum mechanical system theory: the competing space mapped processes – molecular identity

Organic metabolism has two components: anabolism, composition, upbuilding, i. e., making external material (molecules) identical to its body (growth) and catabolism, its opponent: the decomposition, degradation of the organism's body. After division, anabolism far exceeds catabolism, till ariving at the height of the life – cycle, where division occurs. If we think it over, this is quasi – true for multicellulars: only after ''divisions'' does catabolism takes over. For instance, for *Articulata* we have a special word for the individuals having reached the state for zoogamy: imago. This line of thought is *not* quite true for unicellulars, as they, at the height of the life cycle, divide over and over again. However, even in this case, there can be observed a certain *ageing* of the descendant line, which can be observed for example in cell cultures, too, experimentally. The question arises, what is the biological function of this two opponent metabolic processes, and which is the ultimate ''winning'' one. In fact, in theory, we could conceive a triumphant marsh of growing and division without declination. *Note that we consider here individual biological systems, not a population*.

This problem touches upon the general topics of ageing in general. One popular line of thought brings into the debate the many destructive effects which influence the cell during its cycle, particularly its DNA (oxidative radicals, etc.). The result is misformed enzymes, having their destructive effects (at multicellulars: dehydratation as a general consequence). An other one (with which we sympathize) states a programmed process, a kind of ''fate'' of every organism.

We would not enter this debate, as our general aim is, if related, different and somewhat deeper: is it possible that the general goal of the living state of matter is to ultimately defeat self – destruction by prolifiration, i. e., that the *internal backwards time evolution (antiunitary) process successfully reach time (thus space – mapped, space – like) quasi – symmetry*, even if *individual identity ceases* (even at unicellulars). If taken seriously, down to the component polymeric structures, this raises the question of (biomacromolecular) *molecular identity:* are they pure physical entities, composed of constituent physical atoms, or the *internal information*, upon which the ''backwards'' antiunitary time evolution is based (as involving space - mappings), they are something more than their pure physical entity *within the living cell*? (Compare here [23].)

We think this question can be theoretically discussed most appropriately in the frame of what Primas and Müller – Harold termed ''Quantum Mechanical System Theory'' [24]. This needs some elaboration on the fundamentals of quantum theory.

However, first we must discuss at some length the quantum mechanical ''subjectivity'' theory of Stapp (and its similar related quantal ''mind'' models) which underly the identity of living matter, even if they deal with *only* the human mind (see however Balázs [25]).

2. 3. 1. The ''subjective'' aspect of the living state and Stapp's quantum mechanical proposal

Psychophysiology, behavioral genetics, ethology (the biological sciences) do not deal with the problem of *what* the *subjective* process is. They *describe* it, i. e., describe what can be *observed* in this respect.

1) In psychophysiology, the mind/brain problem is approached, i. e., the mental response to various physical influences is investigated (founder: Fechner [26]).

2) In behavioral genetics (see originally e. g. [27]) the correlative functions between different genetic loci and different *behavioral patterns, strategies*, etc. can be observed.

3) In ethology (e. g. [28,29], [30,31]) it is described what behavioral patterns are ''*fit to survival*'' and what is their general place in evolution, including individual differences, e. g. in appetitive functions and the latters' general various possible faiths, etc.

Here we adopt Stapp's quantal (human!) mind model [32] to expound our own general standpoint.

Stapp's original central idea is that the human (conscious) subjective process is a (*measurement*) quantum transition between the potential superposition of *possibilities* (of an ontologically existing vaguely defined ''unconscious'') → brain state ''conscious'', *which is the conscious thought*, facilitated by the external world or by body stimuli. (Stapp's ''facililitation'' is generally regarded to be a version of the well – known ''stochastic collapse'' concept of the wavefunction, upheld by some researchers investigating the problem of quantum measurement (see e. g. [33]).

''Subject'', in Stapp's and related models [32,34-36] the leading idea is (*quantum*) *measurement*, the many – to – one quantal process. In these models, ''Self'' is unimportant; it is doomed to a reflectional, recording function, internal ''self – measurement'', in the sense of Stapp's own introductory chapter, is dropped later, and the overall process, proposed so ingeniously *in physical terms*, later degrades to a Pavlovian ''conditioned reflex'' ''Self''.

Generally speaking, the split between the unconscious/conscious process is not a general biological characteristics of the subjective process. It is the *feeling of Self* as *''Self – measurement''* which is of universal importance and it is definitely an *internal process*, excluding, rather than introducing, the external world. ''Ego is first of all a body – Ego'', says Freud [37]. ''Self'' is a central feel; the whole nervous system being both onto – and phylogenetically of an interface (dividing) origin, reflects its origin in the excitable membrane of unicellulars, splitting the world into two parts: the body of the organism and the external world. (It is by no chance that nerve pulses propagate along the neuron (generally: the cell) *membrane*, with selective inclusion and exclusion of originally sea - water constituting chemical substances, such as Na^+, K^+, Ca^{2+}, and Cl^- ions under excitement, and that there is a *resting potential hill* across the living cell's membrane, i. e., the organism's *own* body and the external world.

It has been shown (e. g. [16, 37]) that conscious thought is only that part of the unconscious which evolutionarily became accomodated to the external world. Hence we should, in fact, place the emphasis on modeling, in physical terms, the basis of drives (''instincts'') if we want to get closer to the concept of subjectivity (the identity) phenomenon (process). As it has been pointed out, in humans, it is the Ego which is the battlefield of the competing pulses of destruction/survival (self – maintenance) [16, 37], and a similar *integrative* ''mental'' structure should be present in *all* biological organisms (compare e. g. [38]]) as discussed above, and both stem from the internal basic regressive, molecularly originated, ''drive'', with its two opposite sides (disintegration/attaining space - mapped time symmetry, see [25]). These drives thus must have been born together with the chemistry of life, the endophysical primordeal *assignment quantum measurement* [1,2]. They are as ''actual'' (in the quantum measurement sense) as is the conscious thought (in humans even more), corresponding to permanent internal ''self – measurement''.

A note is in order here of the concept of ''*identity*''. While the idea behind it is valid, the expression itself is misleading, at least in our interpretation. Every real identity needs a reference point, in relation to which it is selfidentical. The nonlinear reference (in fact ''dis – identity'') of the human mind is the body – world schema [32].

We will see that a similar interpretation gives sense to the concept of *molecular identity*.

2. 3. 2. *Quantal structure and classical information of biopolymers: vital mesoscopicity*

It was Primas who most sharply raised his voice against what he has called the ''molecular myth'' [39]. He proposed that ''*physical first principles*'', such as the fundamental laws of quantum mechanics, refer to the endophysical description, with a quantum algebraic C* representation. (We have characterized endophysics above.)

Exophysical descriptions, on the other hand, refer basically to an *open* quantum system, with interactions by the observational device, where this endophysical *holistic nature* is *broken*. It is argued that endophysics requires an ontologically *existing*, so *stochastic* interpretation, while exophysics that of the usual *statistical* one. This latter description, according to the argument, is only a *projection onto a partial Boolean reference frame* (the experiment) of the holistic first principles, yielding only a *phenomenological description*, and belongs to a richer, W* representation.

As a W* algebraic observable (physical quantity) does admit many unitarily nonequivalent representations of the Heisenberg canonical commutation relations of quantum physics, also certain *classical observables*, such as molecular shapes, thermodynamic temperatures, etc. can be deduced in the several *partial* exodescriptions. It is very important, however, that these classical observables thus deduced *depend on* Planck's constant *h,* and classicality means that they belong to the non – trivial center Z of a W* algebra, i. e., they commute with *all* other observables.

What is important from the present point of view is that according to the theory, the symmetries of the underlying kinematical group (the Galilei – group) of nonrelativistic quantum theory *may be spontaneously broken* when proceeding from physics to chemistry and from chemistry to biology, due to these *emergent classical observables*, characteristic of exophysics.

In this light, we will call our biological model system justly ''*endogenous exophysical*'' with *internal* classical observables (macromolecular *information*) ruling internal space - mapped dynamics (metabolism), a leading principle of the internal dynamics, in connection with a *time asymmetric evolution*, the latter also discussed at some length by Primas in relation to biology [19]. He pointed out that time inversion symmetry breaking (also required by our regressive time evolution) is *possible* only but *can not be excluded* in an exophysical description, leading to ''*teleological*'' behavior; this is *not* included in, but *neither excluded by*, endophysical first principles of quantum mechanics.

The basic difference from Primas' spontaneous symmetry breakings and our ''endogenous exophysics'' is that our ''exophysics'' stemmed from endophysics, it is *internal* as a generally ''self – measurement'' lock – and – key one in space, e. g. enzeme action, requiring originally, as an endophysical system, a true *two – parameter* (forwards/backwards time) representation of time evolution of a (bidirectionally deterministic) system (the informationless chemical evolutional vesicle with a certain degree of spontaneous metabolism, compare e. g. [40]). By ''spontaneous'' symmetry breaking, we have a natural one – parameter *semigroup* as symmetry of the gradually progressing space mapped *internal time evolution*.

Our description calls for a *special* W* system, in which the tensor product factorization of ''environment'' and „object" are both essentially *internal*. EPR correlations with the rest of the Universe, however, are excluded by the above discussed *self – distinctioning* aspect of the living state (a typical *internal exophysical* effect).

Thus the central idea of ours is a permanent, internal space – like self – measurement series of a *mesoscopic system*, whose characteristic feature is the *internal* coexistence and nonlinearly interacting quantal/classical observables, with a certain well – defined *molecular/phenotypic identity* and molecularly emerged, and phenotypically *represented*, competing *drives*.

First we must deal with (original, unicellular) *mesoscopicity* and in connection with it*, the *quantum mechanical/classical nature of the primordeal mesoscopic biological system (contemporarily: the individual cell, from bacteria to eucaryotes).*

It is possible to introduce an internal dynamics by a ''coupled state'' representation and by Primas' statistical description, with a discrete (grained) time evolution in the quantum theory for biological systems, which leads to an internally programmed (quantum -) ''automaton''. The living state, in the light of what has been discussed above, could be described as the coexistence of the two nonlinearly interacting descriptional modes: the quantum dynamical and *classical symbolical*. Thus, a classical symbol concept and quantum dynamics is introduced as a natural self – constrained dynamics with a noninvertible Boolean function as underlying structure. The formalism is based on a biological Mesoscopicity Postulate, which joins the symbolic and dynamic aspects. We show that this formalism is based on a Neumannian projection operator algorithm, supplemented by our Mesoscopicity Postulate. This formalism naturally gives space to the symbolic (controlling) side of the quantal system, as space - mapped internal time reversal. Though we use computational (and formal languages) concepts, it is not because they are essential for the understanding the basic argument, but because of their widespread nature. Occasionally we call the controlled quantum dynamics ''hardware'' or ''syntax'', while the symbolic side ''software'' or ''semantics'' of the evolutively (internally programmed) ''natural computers''.

In fact, besides Primas' quantum algebraic view [20], there are several other ways to describe ''mesoscopicity''. In the Copenhagen interpretation, it is a $h \rightarrow 0$ intermediate process, while in the dynamical ''decoherence'' view, a partial washing out the system's quantum correlations with the environment (so the ''measurement device'', which can be internally a large polymer, too, consisting of an ordered ensemble of *quantal* monomeric units).

We thus think that besides analogies, there are deep differences of the biological organisms (primarily the DNA – Protein system) and conventional computers, which has a bearing on the biophysical notion of internal classicality. Computation needs an *externally* prepared program in the Turing machine theory, whose core is the IF – THEN conditioned branchings (the *rewriting sequence*), called by Pattee the *switching rules* [41]. We wish to maintain here classiciality in the meaning of (internal exophysical) dispersion – free observable values, i. e., by a quasi – Boolean one – to – one function (computational description) of the organism's software. In doing so, we must consider a certain true mesoscopic dynamics, in fact a quasiclassical one (in the Copenhagen interpretation), in which the dynamics, the {**Q**, **P**} observables, but not the wavefunction itself, is *classical* (here **Q** represents the spatial coordinates, while **P** the conjugated momenta of RNA, DNA, proteins, also those of the mesoscopic cellular organelles). While Primas' quantum algebraic concept of mesoscopicity might be correct, we would stick here to the Copenhagen, much more simple, interpretation.

It is then well – known, that *meaning* is only assigned, for instance, to a DNA chain in a ''linguistic mode'' only in connection with the successive *classical* dynamic control function of it [42]. However, the central question in this respect is how do function dynamically these controlling structures, i. e., what is the (nonlinear) relation between these classically functioning internal structures and the controlled quantum dynamics, how do they dynamically control (*constrain*) the quantum system in strict physical terms?

We think that this question touches upon the physical existence and characteristics of *natural symbols*, as the *classicality of the spatial coordinates of the corresponding informational biopolymers*, lending to the system its *classical aspects.* The concept of nonholonomic constraint in physics of a special, measuremental origin [43], which, in turn, constrain the dynamics, is useful only if only its certain elements, not the whole theory, is considered. However, Pattee's pioneering work in the field on the subject hardly can be overemphasised, and we follow his line of work wherever possible to find an acceptable answer. In fact, it follows from the above notes, that in the case of fundamental informational nucleic acids, the software is a function of the hardware (the macromolecular quantum mechanical structure), in turn *nonlinearly constraining* the biological system's space - mapped underlying micro – (quantum) dynamics as *classical constraints*. As has been shown in [1,2], once a code vocabulary came about, it stands conceptually *above* the given base sequence. We will point out here that this is not a self – evident relation, possibly not even a *dynamical* relation.

A note is in order here concerning the exact (mathematical) description of ''natural symbol''. It is a law – like iconic ''sign'' [44], and its primary function (i. e., the space - mapping of the internal backwards time evolution) can be studied by a special mathematical function of a Symbolic Tensor Calculus [45], but this is not our concern here due to its rather involved nature.

We propose an alternative description of *classical* nonholonomic constraints: (''self'' -) projection (control) may originate from an irreducible *overdetermination* of the system's dynamics, by adding, as a direct sum, to the quantal degrees of freedom {**q**, **p**} also the classical degrees of freedom set {**Q**, **P**} with interaction (mutual linear interdependence) of them in the *same system.* This causes a *linear dependence* of the system of phase space coordinates, and allows for the spontaneous arisal of *both* quantum dynamics *and* the measuremental classical records, out of which natural symbol emerged, *in the very same system*. Thus a certain conceptual ''matrix'' of the phase space will not be diagonal, it will have off – diagonal elements, too (mutually interdependent degrees of freedom).

The IF – THEN branchings in living matter in the quasi – Boolean computational frame then is realized as an evolutively emerged, underlying dynamics – dependent projection operator time series of the density operator class of the ''program'', acting on its own Hilbert space, *chosing between existing possibilities by the very same possibilities.* Noteworthy in this

respect, that proteins have also ''codes'': their active three dimensional mesoscopic structures, determined by the so – called ''amino acid code'' [46]. In this respect, ''computing'' in living organisms does appear as a digital, algorithmical, nonlinearly constrained quantal dynamics, *formally* describable in automata and formal languages concepts. In fact, summarising of what has been said above, the classicality we propose for the living state refers to this special constraining nonlinear interaction of (spatial) classical and quantal states, together forming a special ''mesoscopic'' object.

Only living systems are able to perform (quantum) measurements; on the other hand, it is precisely measuring which underlies natural (overdeterminated) projection algorithms. Matsuno proposed internal (molecular) successive fuzzy boundary conditions in his emergent local ''internal measurement'' frame [10]; we add that in his ''quantum update'' in our internal projection algorithm (one molecule is once a measuring, once a measured entity), the measuring one successively determines the *initial conditions* of the object, too, and this fact might be even more important than boundary conditions, it has evolved even to a phenotypic phenomenon, too: to determine the system's own initial conditions [1] (acting on the surroundings, setting the general basic initial coditions of its metabolism).

Note that Conrad, in his notes on different scales study of systems, pointed out that mesoscopicity plays a central role as a point of departure of studying biological systems, similarly to us [47]. It is noteworthy, though, that the cited authors evidently uphold a decoherence view of quantum measurement, which is neither compulsory, nor necessary. The point is that for an (in a way constrained) historically *open* quantum system one can not in general guarantee conservation of energy (unless we consider the whole Universe as ''the system'').

The externally observable one – to – many, and internally ''programmed'' many – to – one dynamical modes are distinctly different in the usual exophysical quantum description, as there is a discrete quantum jump between them. If we retain exophysical quantum measurement as we know it, then if we insisted on describing the internal process exophysically, either the uncertainty relations must be modified, or we accept that the internal ''program'' is fully autonomous. Quantum mechanics can not be modified on its *own* grounds. This is the basis of Gunji's observations on ''unprogrammability'' of biological systems, and lends the autonomous character to the living state. This is also the point of departure of ''molecular identity'' (see below). Sticking to the Copenhagen interpretation, the transition, then, from quantum mechanics to the classical element needed a discrete step in endophysical time evolution: the splitting within the system into (altered) microscopical states *and* the *classical measuremental records* (the genetic *codes* [1,2]).

We maintain the view that internal measuremental records (natural symbols) behave also classically among each other [48], so the resulting overdeterminated dynamics will be quasiclassical, essentially a Boolean ''computation'', the internal overall dynamics will then be a classical one – to – one process, even if it is externally uncomputable.

The projection operator algorithm is then a realization of an ''internal measurement'' chain, adapted according to our conceptual approach. In fact, the genetic code is understood in *classical terms* [48]. It is self – evident, that when we state that ''GCU'' is the *code* of the alanin residue, we mean a time invariant [1] *classical entity*, with a classical symbolic function, i. e., a one – to – one classical automata transition function, dynamics. Furthermore, when we point out the existence of incredibly efficient enzymatic catalysts, we mean also that their crucial steric structure is a *classical object*, whose physics does not obey quantum dynamics *acting as catalysts.*

Considering the problem in some more detail, ''internal measurement'' in fact calls for such an *informational* projection operator formalism, where mesoscopicity is postulated as a synonym for an ''irreversible Loss of Optimum (dynamical) Details'' [49], and the *individuality* of larger part systems, such as atoms or groups of atoms of the coding (informational) biopolymers provide allowance for *coupled* purely classical (spatial coordinates) and purely quantal (the wave*function*) within the same system in a quasiclassical dynamics. In other words, the (spatially founded) information is *classical*, but the wavefunction is *quantal,* forming a general ''symbol – constrained'' ''special mesoscopic'', quasiclassical (quantum) dynamics in the *overall, systemic, $h \to 0$ sense in our description.*

Tentatively, we introduce the symbol – controlled projection time series,

$$\hat{P}_{ij} [\Psi_i(\mathbf{q}_i) \Psi_j(\mathbf{Q}_j)] \; \hat{P}_{i+1, j+1} [\Psi_{i+1}(\mathbf{q}_{i+1}) \Psi_{j+1}(\mathbf{Q}_{j+1})] \to c_{j, i+1} \hat{P}_{i, j+1} [\Psi_i(\mathbf{q}_i) \Psi_{j+1}(\mathbf{Q}_{j+1})] \qquad (1)$$

in which a naturally evolved hierarchycal way the already existing structure – dependent symbols constrain the underlying dynamics, *while themselves depending on the same dynamics* (nonlinearity, weak self – reference, overdetermination). (Here subscripts i, j refer to the state of the ith, jth mesoscopic particle, with $\mathbf{Q}_i$, $\mathbf{q}_j$ denoting classical and quantal space coordinates.) This, at the same time, defines the steps of the internal quasi – Boolean process. $c_{j, i+1}$ here is a real number in the (0, 1) interval, the ''overlap matrix element'' between states (wavefunctions) $\Psi_j(\mathbf{Q}_j)$ and $\Psi_{i+1}(\mathbf{q}_{i+1})$. This is but syntax dependent semantics and semantics dependent syntax, resembling Montague grammar [50], corresponding to Pattee's Semantic Closure Principle [49] and defines a nonlinear projection operator algorithm. It is *natural symbol* which projects out dynamically what is space - mappingly symbolised.

Note that subsequent recursional steps express the unique space - mapped time evolution of the system, and *constraint essentially means here constraining the other projector's quantum dynamical part,* mapping the dynamical wavefunction formally to a scalar quantity times the next symbolic state function. Natural symbol thus projects out the i + 1th two – indexed projector state from the ith state in a tree – like fashion *via* $\{\Psi_j(\mathbf{Q}_j)\}$.

The individual states of the projectors are composed of quantum states and (quasi -) classical symbolic states and, as composite projector states, the individual projectors correspond to our *special* quantum automata theoretical states. Our off – diagonal projectors thus express coupled quantal and classical , i. e., ''object'' and ''record'' states when acting on each other in a converging algorithm, yielding thus the time series $(i \to j) \to (k \to l)$ (t'_i, t'_j, t'_k, t'_l) with the central

arrow equalling the discrete step $\Delta t'_{jk}$. It should be pointed out, accordigly, that the "off – diagonal" (two – indexed) projection operator does *not* describe quantum correlations, rather, *subsequency* (temporal) or *string – processing* relations [48]. It follows that the dynamics will not admit canonical (diagonal) Schmidt forms of correlations, rather, non – diagonal correlations of (space – like) "apparatus + object" correlations emerge, *in fact comprising the dynamics.*

Our Mesoscopicity Postulate states that the living organism is such a mesoscopic system originally, in which there are controlling classical observables, which harness the underlying quantum dynamics in Pattee's original sense, and which is possible only by an overdetermination of the mesoscopic system, and that, as a consequence, there is a nonlinear interaction between these two sides of originally alternative descriptions.Thus the system 1) had to reach a critical size, 2) many quantal degrees of freedom should correspond to a few quasiclassical states with purely classical degrees of freedom, represented *in the same system*, and 3) there must be a one – to – one correspondence between the phase space coordinates of these classical "self" – measurement objects and records (the latters also defining an integrated amino acid residue, for example, as a "holistic", classical entity, *originally also a joint measuremental record* [1,2]).

2. 3. 3. The quantum mechanical building – up of additional classical degrees of freedom

We define in the informational biopolymers for the nuclei the collective coordinate

$$\mathbf{Q'}_m = \sum\nolimits^{Am}_{i,j=1} \mathbf{L}_{j,i}\, \mathbf{q'}_i = \sum\nolimits^{Am}_{i,j} \mathbf{L}_{j,i}\, \mathbf{B}_{ij}\, \mathbf{q}_j \tag{2}$$

and for electrons the gross mesoscopic wavefunction

$$\Psi(\mathbf{r};\mathbf{R}) > \sim \Psi(\mathbf{r}_m;\mathbf{Q'}_m) > \sim \int \Psi \sum\nolimits^n_i \delta(\mathbf{r}-\mathbf{r}_i)\, \Psi\, dv_i \tag{3}$$

In terms of molecular orbitals in the LCAO expansion, with orbitals confined to logical (symbolic) unit m of a large (mesoscopic) polymer, we obtain

$$\sum\nolimits^n_i < \varphi_i \mid \delta(\mathbf{r}-\mathbf{r}_i) \mid \varphi_i > = \sum\nolimits_i \mid \varphi(\mathbf{r}_i) \mid^2 = \rho(\mathbf{r}), \tag{4}$$

which, in the basis of real Strictly Localised Molecular Orbitals, becomes $\rho(\mathbf{r};\mathbf{Q'}) = \Pi_m^N \rho_m$, so we have

$$\Psi(\mathbf{r};\mathbf{Q}) > \sim \Pi_m^N \rho(\mathbf{r}_m;\mathbf{Q'}_m), \text{ denoted by } \Psi(\mathbf{Q}) >. \tag{5}$$

Here $\mathbf{r}_i$ is the Cartesian coordinate of the ith electron of the Ath atom in the mth logical (monomeric) unit (triplets or ancient mononucleotides/doublets/quartets in RNA/DNA [51,52] and amino acid residues, in the dipeptide approximation, in proteins), N is the number of logical units; A_m is the number of atoms in the mth logical unit, n is the number of occupied spinorbitals, $\mathbf{q}_j$ is the Cartesian coordinate of atom j in unit m, respectively. $\mathbf{q'}_i$ is the ith internal coordinate of unit m, $\mathbf{Q'}_m$ is the collective ("normal") coordinate set of the mth logical unit, $\mathbf{B}$ and $\mathbf{L}$ are transformational matrices of *classical couplings* of individual atomic nuclei coordinates, $\rho(\mathbf{r})$ is the electron density function, Π denotes "product".

In this way, we obtain in the Born – Oppenheimer approximation and the Ising model

$$\Psi_i(\mathbf{Q}_i) > = \Pi_{m=1}^N \Phi_m(\mathbf{Q}_m) >, \quad \text{with} \tag{6}$$

$$\mathbf{Q}_i = \sum\nolimits_m^N \mathbf{Q}_m. \tag{7}$$

Thus $\Psi_i(\mathbf{Q}_i) >$ is built up from the prefixed, rigid, quasiclassical wavefunctions Φ_m, depending on the collective nuclear coordinates $\{\mathbf{Q'}_m\}$ and the collective electron variable $\mathbf{r}_m$.Note that we retain global center of mass coordinates, to account for the global movement in space of the local mesoscopic structure, and that the number of electronic coordinates are reduced by some two orders of magnitudes considering a few hundred logical monomeric units long polymer. This latter homomorphic map image corresponds to the classical building – block concept of conventional biochemistry. The closest concept to the present approximation is the above noted Strictly Localised Molecular Orbital concept of molecular physics. Note, however, that our approach is also projective rather only unitary, resembling the Density Functional Theory of molecules (e. g. [53]). In fact, we propose that due to an internal pre – constrained, "self – measuremental" teleonomic dynamics, the microscopic wavefunction is ill defined externally (see above) during the interactions, only the one - particle density function is well – defined (deducible by small angle X – ray diffraction). The former is given by the symbolic wavefunction, which is, then, defined *only with reference to the dynamics* (the proper space - mapping self – measurement step). It must be added that our procedure is permissible due to the well – known relatively rigid σ – electron frame of nucleic acids and proteins. These electrons are described collectively for the logical units, as the expectation functions of their variables *concerning the symbolic wavefunctions. Note that the symbolic (quasiclassical) wavefunctions are additional to the usual quantum mechanical ones*, the latters having been studied for a long time by quantum biochemistry, which, however, does not consider factorizations according to their *logical meaning.* Hence our factorization according to their meaning is *not arbitrary* as it is the SLMO picture but, is dictated by experiment, and is thus *unique.*

Noteworthy in this respect, that Primas called the LMO picture (minimal exchange interactions, maximal Coulomb repulsions or, maximal spatial separation) a *classical electron theory* in his quantum algebra, *in which molecular shape is a classical observable* [54].

The above deduction was done keeping in mind the DNA(/RNA) – protein system. The argumentation is also valid for enzyme – catalysed processes, but the argumentation is significantly more involved there, because we would have to consider the case also where the primary "object" is a smaller molecule, and the primary "symbol" is the "amino acid code", and classicality hence is that of the three dimensional buid – up of the enzyme molecule with its *active center.*

Internal metabolism, in particular anabolism, thus, *en gross*, is then possibly based on these physical principles. (*Catabolism*, as the reverse process, *destroys* classicality (in the above sense), coupling back to endophysics.)

Denoting the overall (external – internal) time evolution by *t '*,

$$t' = |+t| - |-\tau|$$

comprised of – τ (internal ''backwards'' time evolution) and + *t* (in the external frame of reference), as we noted, terminates when the life cycle corresponds to the dilation to the irreducible representation **l** (*t*) = **l** $_1$ (+ *t*) **+ l** $_2$ (− τ), with | + *t* | = | − τ |, this being the fixed point of the converging projection operator algorithm. It is important to note, that as time is predominantly internal during the life process, there are, as shown above, selective and coupled quantum transitions, thus *combination rules are generally not obeyed by the dynamics.*

The diagonal matrix of ordinary commutation relations are also peculiar: it is substituted, as noted above, by a non – diagonal one, between microdynamical (quantum mechanical) and the collective (symbolical) phase coordinates. Thus, it is not the *value* of ħ $_{ii}$ what is important, but its finite existence in the resultant quasiclassical dynamics. On the other hand, the basic property of ħ $_{ij}$ is then

$$lim_{\Delta Q i \to 0, \Delta p j \to \infty} \Delta Q_i {}^* \Delta p_j = 0. \qquad (8)$$

This follows from a more localised, more particle – like *actual existence* of the internal self – measurement structures (*so classical behavior*) as compared with inanimate matter. Putting it in a qualitative way, the *stochastic (probability) freedom in the event field gained by the system at the expense of quantal indeterminedness is turned into the very self – constraints over itself, expressed by the global relation* $\sum_{i,j} h_{ij} = h$.

2. 3. 4. Quasiclassical information controlled dynamics and molecular identity

Tentatively, we may put that by a general Δ E ''excitation'' *of* the biological system, there arises an *active search* (''expectation'') for the proper steps of its internal algorithmical behavior (the metabolic processes).

It should be stressed again, that the arisal of the ħ $_{ij}$ off – diagonal action quantities of overdetermination are *reducing* the dispersion domains of the respective observables and are fundamental in the possibility of ''drive for unity'', i. e., the conditioned information of *choice* may come about, as the subsequent off – diagonal projectors, exerting *control* in the system. As was pointed out in [1,2], it is essential that, being ''cast out'' of natural history is a natural driving force of life. In our frame [1,2], this is tentatively described as the *original primordeal self – measurement of matter (an endophysical event)*, with the splitting up of a measuremental record (RNA) and the ''object'' system (RNA oligomers), with the primordeal ''interface'' proto – proteins as ''measurement devices'' in reference to a chemical evolutional mesoscopic system.

The resultant internal time inversion was detailed in [1,2]. In fact, the the results of the original splitting – up (records and objects) becoming *internal*, the measurement records (the genetic codes) govern the protobiological system as an internal space - mapped time inversion process (- τ), the autonomous time evolution towards time symmetry with the external time process, above the (space – like) internal quantum dynamics.

Thus informational or ''*dis*'' – *identity* relations are in fact *time relations.*

The main problem is the general faith of the internal ''backwards'' time process. *Driving for symmetry,* it has two alternatives: direct return to the endophysical state (disintegration) or striving towards the (space - mapped) *special space – like symmetry of doubling – up in an indirect way.*

At a point, then, the system either disintegrate to the inorganic (the endophysical route) or, with a vital maintenance of its internal ''dis – identity'', divide and save in the two newly arising structure *the classical components* as two new organisms, subject to the original classical constraints with a primordeal origin, as two new time cycles, as *mesuring (''endogenous'') exophysics, with the loss of vital individual selfidentity. Evolution (or simply: Nature) evidently decided in favor of the second possibility, ariving at humans, performing true exophysical quantum measurements externally, ruling its own external initial conditions (of his metabolism). This can be regarded as a heuristic experiment of Nature, which we must accept ultimately as a natural fact.*

3. CONCLUDING REMARKS

It has been shown, that following its origin (in our ''basic hypothesis'' [2]) the living system had two alternative ways of time evolution: either direct disintegration according to the internal ''backwards'' time process to reach symmetry (''identity'') with the rest of the Universe, which we termed the ''endophysical'' route. Or, by its internal space - mapping controlling classical informational polymers, it choses a more hard and tedious route of reaching (time) symmetry by reaching the symmetry in a space - mapped growing, metabolizing, and finally space – like dividing way (the ''endogenous exophysical'' route,''identity'' *with reference to its metabolic object molecules*). Both routes were equally open for the proto – system. Nature decided according to the second possibility, evidenced by natural organic evolution.

During investigating the problem, we had to examine exactly which physical properties/processes made possible this second route. During this, we examined the origin of classicality in the system, revealing the latter's overdetermining nature, and the physical content of its space - mapped metabolism. Everywhere we found the central process of (internal) quantum measurement as leading internal characteristics. We have pointed out that at even multicellulars, the destructive/constructive ''forces'', in the form of representational ''drives'', are present. We have shown, that the presence

of additional classicality in an originally mesoscopic system, is crucial, as it forms the basis of constraining internal natural *information*, underlying the life cycle.

As a basic ''choice'' between the two aforementioned routes, we could not propose a better explanation than this was a ''choice'' of Nature, which we must accept, as we accept, for instance, the fundamental laws of quantum theory.

REFERENCES

[1] Balázs, A. 2013. The biological ''invariant of motion'' *vs.* ''struggle for life''? On the possible quantum mechanical origin and evolution of semiotic controls in biology. Information 4 (Oct. 2013), 367 – 397.

[2] Balázs, A. 2014. On the origin and invariance of the genetic assignments as elementary semiotic controls: A basic hypothesis. Eur. J. of Biophys 2(3) (Aug. 2014), 17 – 28.

[3] Post, E. L. 1965. Undecidable problems in logics. In The Undecidable, Davis, M. (ed.) Rowen Press, 240 – 333.

[4] Gunji, Y. – P. 1992. Form of life I. It is possible but not necessary. Appl. Math. Comp. 47, 267 – 288.

[5] Pattee, H. H. 1970. How does a molecule become a message? Developm. Biol. Suppl. 3, 1 – 16.

[6] Pattee, H. H. 1971. Can life explain quantum mechanics? In Quantum Theory and Beyond, Bastin, T. (ed.), Cambridge Univ. Press, 307 – 320.

[7] Pattee, H. H. 1972. Laws, constraints, symbols and languages. In Towards a Theoretical Biology Vol 4. Waddington, C. H. (ed.), Alding Publishing Company, pp. 248 – 258.

[8] Pattee, H. H. 1982. Cell psychology: An evolutional approach to the symbol – matter problem. Cognition and Brain Th. 5(4), 325 – 341.

[9] Pattee, H. H. 1989. The measurement problem in artificial world models. BioSystems 23, 281 – 290.

[10] Matsuno, K. 1989. Protobiology: Physical Basis of Biology, CRC Press.

[11] Liberman, E. A. 1989. Molecular quantum computers. Biofizika 34, 183 – 225.

[12] Liberman, E. A., Minina, S. V. and Shklovsky – Kordi, N. E. 1989. Quantum molecular computer model of the neuron and a pathway to the union of sciences. BioSystems 22, 135 – 154.

[13] Conrad, M. 1989. Physics and biology: towards a unified model. *BioSystems* 32 (2-3), 75 – 102.

[14] Conrad, M. 1993. The fluctuon model of force, life and computation: A constructive analysis. Appl. Math. Comp. 56, 208 – 259.

[15] Igamberdiev, A. U. 1993. Quantum mechanical properties of biosystems – a framework for complexity, structural stability and transformations. BioSystems 31(1), 65 – 73.

[16] Freud, S. (1953 – 1974). The Standard Edition of the Complete Psychological Works. Translated from the German under the General Editorship of James Strachey in Collaboration of Anna Freud, Vol. I. – XXIV. The Hogarth Press and the Institute of Psycho – Analysis. 1955. Vol XVIII. Beyond the Pleasure Principle, pp. 7 –64.

[17] Gunji, Y. P. 1994. Autonomic life as the proof of incompleteness and Lawvere's Theorem of Fixed Point. *Appl. Math. Comp.* 61, 231 – 267.

[18] Rössler, O. E. 1987. Endophysics. In Real Brains, Artificial Minds, Casti, J. L. , Karlquist, A. (eds.), North – Holland, pp. 25 – 46.

[19] Primas, H. Time asymmetric phenomena in biology. 1992. Open Systems and Information Dynamics 1(1), 3 – 34.

[20] Primas, H. 1993. Mesoscopic quantum mechanics. In Symposium on the Foundations of Modern Physics 1993. Measurement, Irreversibility and the Physics of Information, Lahti, P. J. et al. (eds.), World Scientific, pp. 324 – 337.

[21] Primas, H. 1994. Endo – and exo – theories of matter. In Springer Series in Synergetics, Atmanspacher, H. , Dalenoort, G. J. (eds.), Springer Verlag, pp. 163 – 193.

[22] Bohr, N. 1934. Atomic Theory and the Description of Nature, Cambridge Univ. Press

[23] Balázs, A. 2004. Is there a ''molecular Nirvana Principle''? Towards a unified resolutional model of the biological symbol – matter dichotomy.

[24] Primas, H. and Müller – Harold, U. 1978. Quantum mechanical system theory. Advances in Chemical Physics 38(1), 1 – 107.

[25] Balázs, A. 2015. On some evolutionary aspects of the mind – matter problem. Mind and Matter, to appear.

[26] Fechner, G. T. 1860. Elemente der Psychophisik, 2 Vol., Breitkopf and Härtel.

[27] Ewing, A. W. and Manning, A. 1967. The evolution and genetics of instinct behavior. Ann. Rev. Entomology 12, 471 – 494.

[28] Lorenz, K. 1978. Vergleichende Verhaltenforschung. Grundlagen der Ethologie, Springer Verlag.

[29] Lorenz, K. 1992. Das ''Russische Manuskript''. Pipper.

[30] Tinbergen, N. 1951. The Study of Instinct, Oxford Univ. Press.

[31] Tinbergen, N. Das Tier in seiner Welt. Pipper.

[32] Stapp, H. P. 1993. Mind, Matter and Quantum Mechanics. Springer Verlag.

[33] Zeh, H. D. 1996. In Decoherence and the Appearance of a Classical World in Quantum Theory, Guilini et al. (eds.), Springer Verlag, p. 67.

[34] Hameroff, S. R. 1987. Ultimate Computing, North – Holland.

[35] Hameroff, S. R. and Mercer, P. 1998. Quantum computation in brain microtubules? The Penrose –Hameroff 'Orch Or' model of consciousness [and Discussion]. Phil. Transactions: Math., Phys., and Eng.Sciences 356(1743), Q. Comp.: Th. and Exp. (Aug. 1998), 1869 – 1896. The Royal Society.

[36] Schneider, J. 1997. Time and the mind – body problem: A quantum perspective. arXiv: quant-ph/9707056v1, Jul. 1997.

[37] Freud, S. (1953 – 1974). The Standard Edition of the Complete Psychological Works. Translated from the German under the General Editorship of James Strachey in Collaboration of Anna Freud, Vol. I. – XXIV. The Hogarth Press and the Institute of Psycho – Analysis. Vol. XIX., The Ego and the Id. pp. 3 – 66.

[38] Armus, H. L., Montgomerry, A. and Jellison, J. 2006. Discrimination learning in Paramaecia (*P. caudatum)*.The Psych. Record 56, 489 – 498.

[39] Primas, H. 1985. Kann Chemie auf Physik reduziert werden? Chemie in unserer Zeit, Part I.: 19(4), 109 –119., Part II.: 19(5), 160 – 166.

[40] Dyson, F. 1999. Origins of Life, Cambridge Univ. Press

[41] Pattee, H. H. 1974. The vital statistics of quantum mechanics. In Irreversible Thermodynamics and the Origin of Life, Oster, G. F. et al. (eds.), Gordon and Breach Science Publishers, pp. 33 – 43.

[42] Pattee, H. H. 1993. The limitations of formal models of measurement, control and cognition. Appl. Math.Comp. 56, 111 – 130.

[43] Pattee, H. H. 1969. The physical basis of coding and reliability in biological evolution. In Towards a Theoretical Biology, Vol I., Waddington, C. H. (ed.), pp. 268 – 284.

[44] Peirce, C. S. 1932. Division of signs. In Collected Papers II., Cambridge Univ. Press, pp. 134 – 173.

[45] Bodó, Z. 2004. On Symbolic Tensor Calculus. Unpublished results.

[46] Kuhlman, B., Dantas, G., Ireton, G. C., Varani, G., Stoddard, B. L., Baker, D. 2003. Design of a novel protein fold with atomic level accuracy. Science 302(5649), 1364 – 1368.

[47] Conrad, M. 1995. Cross – scale interactions in biomolecular information processing. BioSystems 35, 157 –160.

[48] Pattee, H. H. 1979. The complementarity principle and macromolecular information. BioSystems 11, 217 – 226.

[49] Pattee, H. H. 1973. Physical basis and origin of hierarchycal control. In Hierarchy Theory, Pattee, H. H. (ed.), Braziller, Ch. 4.

[50] Montague, R. 1974. Formal Philosophy: Selected Papers of Richard Montague, Thomason, R. (ed.), Yale Univ. Press

[51] Patel, A. D. 2008. Towards Understanding the Origin of Genetic Languages. In Quantum Aspects of Life, Abbot, D., Davies, P., Pati, A. (eds.), Ch. 10., Imperial College Press; and references cited therein.

[52] Baranov, P. V., Venin, M. Provan, G. 2009. Codon size reduction as the origin of the triplet genetic code. PLoS One (May 2009), 4(5), e5768.

[53] Eschrig, H. 1996. The Fundamentals of Density Functional Theory, Teubner.

[54] Primas, H. 1981. Chemisty, Quantum Mechanics and Reductionism, Springer Verlag.