Concept Paper

The Biological "Invariant of Motion" *vs.* "Struggle for Life"? On the Possible Quantum Mechanical Origin and Evolution of Semiotic Controls in Biology

András Balázs

Department of Biological Physics, Eötvös Lóránd University, Pázmány sétány 1/A, H–1117 Budapest, Hungary; E-Mail: balazsandras2002@yahoo.com; Tel.: +36-23-381-377

Abstract: A novel, alternative and deeper view to the "selfish gene" paradigm is presented, describable as the "selfish code" frame. Introducing it, we put forth a quantum mechanical algorithm as a new description of the intracellular protein synthetizing machinery. The successive steps of the algorithm are, tentatively, semiotic constraints of the well-known quantum mechanical molecular "internal measurement" type. It is proposed that this molecular algorithm mediates a quantum mechanical time reversed dynamics with a primordial special version of this latter molecular measurement type ("mixed measurement") as its origin. It is furthermore suggested that this intracellular regressive algorithmical dynamics is a component of biological "motion", the other, strongly coupled component being the macroscopic phenotypic motion. The biological "invariant of motion" of this hierarchically coupled overall generalized dynamics is suggested to be the evolutionally converged invariant genetic code vocabulary. It forms, possibly, the underlying internal "driving force" of evolution, as being "struggle for life".

Keywords: "abstract" genetic code; time inversion symmetry breaking/restoration; molecular semiotics; invariants of motion; group theory

1. Introduction

R. Dawkins, in his well-known book "The Selfish Gene" [1], opposing the previously widespread view of race-preserving instincts, such as self-maintenance or mating, advocated a paradigm which was claimed to fit better to observable biological facts, chiefly data of ethological nature. According to this, ethological events and relations point to the fact that ethological instincts are servants of the

underlying individual genes, "selfish" as they are; in fact, even humans are merely phenotypic "survival machines" of the genome, striving to perpetuate themselves.

At the outset, this frame is better than race-preservation; however, it has problems of its own. Actually, it is hard to understand how this fundamental framework theory could account for the observation that individually transmitted genes get soon dissolved in the gene-pool of the population. Therefore, the determined, fierce struggle for their transmission is accordingly pointless in the strict sense.

Actually, ever since Darwin's "The Origin of Species" [2] the expression "struggle for life" was used theoretically in two interrelated senses: the (genetic) variability *vs.* phenotypic natural selection by the environment, *i.e.*, the "hardware" of adaptation on one hand and, on the other, the "subjective" phenotypic "struggle for life" in which the organismic "software" constrains the individual organism to fiercely fight for survival and reproduction. While the former sense in its generality seems to be apt for a framework theory, the second, supposedly *implementing* phenomenon refers to a rather curious tacitly assumed mechanism. It is difficult to comprehend *why* there is this kind of stubborn and occasionally frantic, strive on the part of an at least conceptually "physical system". However, it is, anyway, a solid part of our biological empirism. The goal of "selfish" survival and reproduction, possibly, must have a more profound reason than that proposed by the selfish gene theory. The latter has no supporting physical evidence from an ever-changing genetic realm. This nature of such a biological "invariant" of motion indicates that we might possibly be able to detect a real "invariant of motion" with both molecular and physical underlying, hopefully in a strict sense. (The notion "invariant of motion" refers to a mathematical object: scalar, vector, *etc.,* which does not change, is conserved during dynamics and is usually related to an intrinsic *symmetry*, such as, e.g., energy *vs.* homogeneity of time. *Direct* time inversion symmetry, exceptionally, has no such a corresponding invariant [3] but an indirect, real–time *regressive*-recursive dynamics of time symmetry restoring might have one (see Section 3). Tentatively, it must be represented by *quantum correlated*, entanglemented, material molecular wavefunctions of codons and amino acids, as if existed *in vacuo* (see Section 3.2.).

In this paper, we put forth a highly tentative different scheme: a "selfish code" one. According to this, the real biological "invariant of motion" in both onto-and phylogenesis is the converged "abstract" code vocabulary. It is invariant of an internal multi-level generalized biological dynamics of a special kind of time-inversion symmetry restoring. This invariant of this generalized dynamics and the dynamics itself is essentially of a quantum mechanical nature at their origin. Genes are, it is supposed, only special, classical-functional configurations of it, formed exactly for its safe transmission, its constancy.

We show that this frame gives a tentative solution for our central difficult theoretical biological problem of the above rise of the "mysterious" drive of every organism to perpetuate and reproduce itself (see also [4]).

Along this line, we have to discuss the problem of molecular information and molecular semiotics as its carrier, and show that a special unitary symmetry breaking, a code assignment molecular *quantum measurement*, was the birth of this very molecular semiotics. In fact, tentatively it was emerging by a primordial molecular special type of "internal measurement" (see below) as a measurement outcome relation. It was thereby locally coupled to, and globally mapped onto, the whole causal internal macromolecular network of the measuring system. It thus arose as global "abstract" assignment rules, measurement outcomes, as quantum dynamical global *functions* as "software" above the macromolecular sterical record and memory "hardware" states. The abstract molecular semiotics

obeys a global virtual-dual entanglemental dynamics as the ultimate software, lending invariance properties to these fundamental semiotic relations (Sections 2.1. and 3.2.; see Post's assertion on the related problem of symbols as sterical representations of "invariant objects in a time flow" [5]). The time symmetry finally reached corresponds accordingly to the arisal of a space-mapped symmetry as spatial doubling-up (See Sections 3.1.2. and 3.1.3.). In fact, we give a distinct, novel meaning to Pattee's symbol-constrained dynamics concept [6–8]. In this context, we have to discuss to some extent the intracellular semiotics in a necessary relation to its *origin.*

Actually, it is quantum theory as such which is the appropriate physical frame for the description of molecular systems. Fundamental molecular biological processes, as semiotics, are built on both the "virtual dual" semiotic software controls and also on their controlled macromolecular hardware quantal interaction dynamics, hence quantum theory is the proper means to consider them.

It should be noted here, that McFadden introduced a complete theory of intracellular quantum biological processes in terms of quantum measurements in a unitary dynamical background [9]. He deduced a frame similar to ours, which was severely criticized by Donald [10]. Donald's main standpoints are the criticism of applying unitary (pure state) wavefunction dynamics and the "inverse quantum Zeno effect" to biological systems. We acknowledge his criticism of McFadden's concepts, but we put forth our own considerations, differing from McFadden's as follows. We do not use the decoherence picture in connection with the projection postulate. Our "original" ("mixed") and subsequent ("internal") measurements are introduced as having an intrinsic *dynamical* component [11] *not* depending on a Hamiltonian corresponding to the system's interaction with the "environment". Rather, they depend on specific 3D relations lifted to the Hilbert space. This was clear already for Pattee [12]. Also, we consider a *living* cell being of a fully *virtually coherent*, single quantum system (Section 2.). This is meant as a *self-distinctioning* aspect of the cell, a phenomenon well-known higher up on the evolutional ladder. It was probably a prerequisite of a "mixed" measurement (Section 3.1.1.). Any external "not expected" physical disturbance, possibly, would do damage to this virtual coherence, which seems to point to a Bohr-type complementarity relation, as he tentatively applied the concept to biology [13]. It is supported internally by the numerous self-correcting molecular mechanisms. The primary distinction, the protective role is that of the cell membrane, so important in the higher, evolved nervous systems. In fact, the latters are of an *ectodermal*, interface origin. This "*ab initio*", evolutionally holistic, "subjective" property, corresponding to Conrad's vacuum-shadow self-correcting concept [14,15], conforms to a globally maintained entanglement of the assignments of the genetic code (Section 3.2.). This is in relation to the requested underlying global virtual coherence. This permanently, evolutionally maintained internal global virtual coherence invalidates the "fast decoherence" claim of Donald. As concerning the needed "free energy gradient" and the related "entropy-dependent" processes, they are, in our scheme, embedded into an *external energy dependent* "uphill" quantal (external measurement, Section 3.1.1.) dynamics. Here the latter is the crucial, *active* factor. Note again, that "external measurement" here is not meant in the decoherence picture, rather, as a descendant of the holistic orthodox interpretation of quantum mechanics in evolutionally differently evolved forms (Section 3.1.1.).

Complementing the discussion, we infer that the set of "*abstract*" genetic codes, as a vocabulary of signs, by its control-mediating nonlinear molecular hardware, is just an invariant of the above generalized dynamics (Section 2.2.). This is due to the mediating material macromolecular algorithm

of protein synthesis *and* the higher level phenotypic "motion", being actually a biological agent which nonlinearly permanently fixes its own *initial conditions* through the action of the genotype and phenotype (see [16]; also Section 5.3.). In this way, this multi-level nonlinear generalized dynamics might allow, in ultimate terms, the code vocabulary to be a true quantum dynamic group-invariant of a product group of a special supersymmetry Lie-group of the genetic code assignments, and a unique group of a dynamical nature.

2. Preliminary Overview: The Nature of Biological Motion ("Generalized Dynamics")

Our primary concern here is the evolutionary invariance of the genetic code vocabulary in relation to the similarly invariant and also somewhat "mysterious" "struggle for life" phenotypic behavior. In this way, we need to investigate here in an introductory way the origin and evolution of this invariance of the code assignments. Here, we must discuss at some length the biological phenomenon, which might be termed "*generalized dynamics*". The latter encompasses both the quantum mechanical intracellular genetic dynamics and the macroscopic phenotypic biological "motion".

2.1. The Nature of Biological Semiotic Controls in the Intracellular Elementary Quantum Dynamics: Virtuality and Duality

As noted above, we suppose here that the emergence of the genetic code assignments were due to several parallel *special type* of molecular quantum mechanical "internal measurements" ("mixed" measurements, Section 3.1.2.) as their results, measurement outcomes. (See for an early but very competent consideration [17], forming the starting point of our corresponding discussion, also see Section 3.1.2.). We present below a brief tentative discussion, based on these concepts, to preliminarily introduce the special quantal nature of the elementary molecular semiotic controls.

In our case, accordingly, both the quantum mechanical measurement device as primordial protein polymerase enzymes, also the record and memory states (actually, built-up primordial RNAs), together with the object system as primeval RNA oligomers, were macromolecular as is usual in "internal measurement" cases [12,17] (see also [11] and Section 3.1.1.). The protein device was supposedly *internal* to the protobiological system. The object RNA oligomers were, tentatively, *external* to it before the "measurement". *By* the measurement, supposedly, the measured object system as "record and memory" became similarly internal due to its coupling to the internally integrated macromolecular network of the measuring system. It was realized through coupling to the measurement device state of the proto-protein. These record and memory states, encoding the object/device (outcome) relations, must have been concomitantly mapped, presumably, onto the holistic internal causal dynamical network in a global way. This is required by the general processes in a molecular mixed, special internal measurement (Section 3.1.1.). The mappings define, as functions to functions operators, the assignations as quantum mechanically correlated and conserved outcomes of the special object/device (and record and memory) relations; hence we term them "assignation operators". The necessary break in causality, rising in every ordinary, also in mixed measurements (e.g., [18]; Section 3.1.2.), probably had a pay-off in a short period of chemical evolution in favor of *internal causality*. This dynamical causality is following the past history of the molecular assignment process, the macromolecular object/device relations, as the *only causal* time direction. It is eventually amounting to a regressive

(real, positive time) time inversion symmetry restoring as its future. The process may have had a strong selection pressure against unavoidable destabilizing alternative fast decoherence of uncontrolledly arising post-measurement superpositions, in favor of stabilizing causality.

The above global internal assignation-mappings encoded and conserved the measurement outcome, the object/device relations, maintaining the semiotic relations by coupling to the whole internal *causal* macromolecular network system. We term this tentative phenomenon "virtual coherence".

This virtual coherence is that of the whole cellular organization, which accounts for the physically not directly observable holistic, biological behavior of the integrated living cell. This, in fact, acknowledges the internally time-space coordinated global behavior of the living cell as a single correlated dynamical quantum system, tacitly assumed in the biologist's approach. (Even when we use vectors to transform genetically the living cell, we keep integrated the evolutionally intact molecular machinery of the genetic system.) The virtual global dynamic correlation between codons and amino acids was, tentatively, then maintained and mediated through this global virtually correlated macromolecular network. It emerged as the "software" function upon the macromolecular record and memory "hardware", due to the assignment operators (Section 3.1.2.). The latter are the corresponding entities to human "external", "subjective" measuremental outcomes (compare with [19]).

The mediating discrete algorithmical steps (e.g., [20,21]) of the correlations, through the whole intracellular molecular protein synthetizing machinery, can be described by parallel simple diagrams. They are similar to those in use in field theories, specifying different parallel assignment histories of the protobiological system, referring to a specific protein macromolecule. The parallel diagrams consist of a virtual-global organizational codon loop, inward running material ("real") codon and activated amino acid lines and a common outward running real protein polymer line. The vertices are controlling molecular internal measurements in the mediating translational algorithm, referring to codon-codon and codon-amino acid interactions.

Mathematically, "virtuality", as introduced above for the globally-organizationally maintained "abstract" code assignment rules (compare with [22]), is describable by a split affine dual frame. By this, virtuality corresponds to the contravariant "bra" wavefunctions of the codes, while, in parallel, the covariant "ket" wavefunctions correspond to the real material amino acids in the direct product affine Hilbert spaces. This virtually coherent pure semiotic relation, the ultimate software, implies tentatively a virtual quantum entanglemental correlation: it is well known that the object/device relation in "external", thus also in "mixed" measurements emerges as being in such a quantum correlation ([23]; Section 3.2.). In this way, the wavefunctions are quantum correlated, because the result of the assignation operators similarly possesses this dynamical correspondence as acting upon the device/record and memory hardware states. Tentatively, it is this virtual entanglemental correlation between the two molecular species of the code assignments which is maintained and mediated through the virtually fully coherent causal macromolecular network. This reflects the decisive role of the global-virtual network in the interpretation of the assignments [24].

The supposed global control, rules of these semiotic relations above the underlying mediating material dynamics can be introduced formally as the interaction

$$\alpha_i><\beta^i \Sigma \alpha_i> \rightarrow \alpha_i> \; ; \; <\beta^i \alpha_j> = \delta^i_j \tag{1}$$

assuming a biorthonormality relation, where the virtual assignment of the amino acid (α_i>) to the "abstract" genetic code is expressed as due to the virtual code < β^i.

Thus, affine duality of molecular Hilbert spaces is a mathematical representation of the "virtually" existing, in its effects observable, global-organizational assignment relations. This is a prerequisite to the *controlled* local-material quantum dynamics, protein synthesis.

In this way, the central characteristics of the genetic semiotic controls is that they may have emerged by intracellular time inversion restorations in a retrocausated quantum dynamics, with reversed object/device molecular correspondences, *i.e.*, they may have arisen in some primordial special molecular "mixed measurements" and are conserved in a *reverse* object/device form. This means that now it is the code determining the amino acid species, rather than the other way round. It might have emerged in connection with a biased dynamics favoring post-measurement causality against fast decoherence. We devote a more detailed discussion to this tentative mechanism, possibly a turning point in protobiological evolution, in Sections 3.1.1. and 3.1.2.

2.2. The Nature of Phenotypic Motion and the Concept of a Generalized Dynamics

In evolution, there is a certain constancy, as it were, an invariant property of biological "motion": an invariant "struggle for life", a certain constant strive for biological being. It is the *individual realization* of the constant phenotypic macroevolutional adaptational event-chain, so manifest at higher grades on the evolutionary ladder, without which this "objective" adaptational evolution could not take place. As here in this paper we reconsider the source of this highly "mysterious" invariance property of life, we have to consider also global phenotypic motion in addition to the above intracellular genetic dynamics. We consider in this paper the characteristics of homoiothermous Mammals, but keep in mind that the results are hopefully of a more universal nature.

From the ancient concept of Physis, *gross*, phenotypic motion was considered to be an attribute of living systems, down to, e.g., McFadden [9]. In fact, spontaneous internally generated 3D motion, even if only that of growth, is a good indication of a living organism. Modern molecular biology has revealed many internal secrets of life. However, the closer ontological connection between the intracellular molecular dynamics, *i.e.*, the existence and immediate action of the genetic code on one hand, and the fundamental characteristics of *gross* macroscopic phenotypic "motion" on the other, have nonetheless remained largely unknown.

In these terms, there arises the question of the *gross* teleonomy, as that of the invariance of the genetic material, in effect, that of the genetic code, *i.e.*, if the latter could form the material basis of the similar mysterious invariance of the macroscopic "struggle for life". This then might be an objective, material "aim", which teleonomical existence thus needs a more thorough investigation. In fact, it is our supposition throughout this paper that certain invariance of the molecular semiotics, the assignment rules of the genetic code in evolution, has much to do with this also invariant, self-maintaining phenotypic teleonomy of biological "motion". In fact, it is our basic suggestion here that we have an ontological relation between the internal/external teleonomical micro/macro dynamics of the biological organism. By this, we might term this coupled, hierarchical "motion" as a "generalized dynamics".

Actually, on one hand, we have the phenotypic, highly classical intercellular integrated motion of organisms as a whole (or the cell itself, concerning unicellulars, e.g., [25]). On the other hand, we have the above-noted intracellular highly quantal, genetic "motion", quantum dynamics. It is easy to see that the former is based on the latter, and the proper classicality/quantum mechanical nature is due to the fact that phenotypic motion is, in the ultimate analysis, an internally quantally generated external classical process. It does, however, exert also nonlinear controlling effects, as intracellular constraints, on the genetic dynamics, e.g., of hormonal nature. The primary manifestation of phenotypic motion is the well-known classical inhibition/release constraints on the internal genetically (quantally) induced excitatory processes of the central nervous system. They constrain them, through the phenotypic motion, towards fulfillments of self-maintaining and mating behavior.

In this way, we have the local quantum mechanical, ultimately cellular quantal motion, which by its semiotically, *i.e.*, classically highly constrained nature, emerges upon the realm of a yet "uninformed", molecular quantum dynamics. By the control it exerts, through its molecular products, on the classical, phenotypic part of the generalized dynamics, it thus forms also the basis of higher level classical-macroscopic phenotypic motion (compare with [11]).

In fact, global external macroscopic-phenotypic motion itself is, in evolution in a more and more complex way, under the similarly inhibition/release type internal constraints of the quantal semiotic controls. The intracellular semiotically constrained quantum dynamics arises as a characteristic, integrated, autonomic behavior, which property is thus also characteristic of the phenotypic motion. Actually, the global integrated inhibition/release, classical phenotypic biological motion is the result of an underlying fundamental quantum mechanical dynamical coupling of similar internal inhibition/release quantal genetical processes. These coupled cellular time-cycles are evolving to gross organizationally differentiated macroscopicity and classicality in ontogenesis. The *gross* time cycle of this generalized dynamics of a cell-phenotype-cell type derives from the primordially emerged nonlinearity, a mediated self-reference, of the action of the genetic machinery (Section 5.). The overall dynamics, accordingly, in a natural way forms not only a life cycle, but in a more strict way, a "weak", mediated self-referential cycle. It carries out a central, empirically observable, somewhat "mysterious" symmetry restoring process as self-maintaining, also a no less mysterious behavior of "self"-reproduction. The latter is, in the present scheme, a space-mapped attained time symmetry (compare with [26]). This generalized dynamics of the organism eventually amounts to setting its own permanent quantal/classical *initial conditions* (Section 5.3.).

Thus "biological motion", as a two-level, basically nonlinear phenomenon, is tentatively derivable from an internal, elementary autonomic quantum dynamics, where constraints are of a relatively "freely set" nature. This kind of dynamical intracellular-molecular/intercellular-macroscopic evolutionary coupling is easily visualized, e.g., in neuromuscular function, with the autonomic macroscopically controlled phenotype built upon the molecularly controlled genotype as a hierarchy of controls. See for instance the phenomenon of classical muscular innervation and a more fundamental and ancient molecular quantal signal transduction in phenotypic motion (compare with [9]).

In this way, when we discuss "invariants of motion" below, we imply biological motion as a strongly coupled, hierarchical internal/external quantal/classical generalized dynamics. It is in general subject to autonomous inhibition/release internal "freely set" rules of a classical nature, by which they are thus in turn highly constrained. As hinted above, we risk here the assertion that these rules are

descending in evolution from the recurrent autonomical setting of the organism's (the cell's) own quantal molecular initial conditions. The latter are subject to a self-maintaining, "self"-reproductive, teleonomy. That is to say, biological motion is, in the ultimate analysis, at its roots, of a two-level intercellularly coupled nonlinear intracellular genetical-quantum mechanical nature. We suggest that the origin of these semiotic rules were those of the primeval processes of the code assignments.

As C.H. Waddington once remarked, the immediate phenotype of the cellular genome is the enzymatic proteins produced by them, here identified as the products of a regressive semiotically constrained quantum dynamics of the translational apparatus. The range of the effect of this basic teleonomic cellular machinery is magnified and extended, through the molecular products of the process, up to the true phenotypic level, just by the vertically coupled intracellular machineries. Thus, the phenotype, as a mediating structure of the above-noted basic "weak" nonlinearity (see Section 4.) is a macroscopic servant of the underlying intracellular regressive semiotically constrained quantum dynamics. Thus, the phenotype follows, tentatively, in this way, by its phenotypic biological motion, the same teleonomic "aims" which are those of the underlying intracellular genetical quantum dynamics.

This consideration forms the basis of our central discussion.

Thus, the biological time cycle, as a semiotically controlled process, at higher grades on the evolutional ladder is a cell-tissue-organ-organism-cell one, a mediated (weak) self-reference, nonlinearity (see also Section 5.1.). As noted above, Dawkins suggests that they are the genes which create a "survival machine" for them, yet we would rather be inclined to propose that symmetry restoration, as a generalized two-level dynamics, has a molecular software-type dynamical-evolutional invariant, the "abstract" genetic code vocabulary. This invariance as teleonomy determines the similar invariance of the basic patterns of biological motion.

However, we must investigate more closely the special physical source of this internal symmetry-restoring, symmetry constructing autonomic quantum dynamics. It may have emerged in evolution as a sort of internal "freedom", with its special semiotic evolutionary rules, however, and as one which is extending, through its molecular controlling effects, to the phenotypic organizational level.

A note is in order here on the evolutionary role of the "epigenome" and its possible physical modeling as compared to the framework presented here. The term denotes the overall set of epigenetic, *i.e.*, "above the genome" factors. There are, according to theory, a number of routes determined by these factors. The latter may be environmental, dependent on the individual organism, or molecular mechanisms influencing switching on/off of DNA. Along this line, specifically, analyzing epigenetic processes such as the regulation of the glucose/lactose metabolism in *E. coli*, e.g., Asano *et al.* arrive at a "quantum-like" model of the switching processes of the lactose operon [27]. Specifically, analyzing empirical data and evoking an operational formalism of quantum mechanics and quantum information theory (quantum channels), they were able to show that the involved metabolic processes satisfy non-classical (*biased*) probability equations. Most importantly, their "coarse grained" (*gross*) approach could show that there are characteristic *invariants* in the biases (preferences) between *E. coli* strains, describable by the formalism. This latter result must give us a second-thought on the form of dealing mathematically with our "invariants of biological motion" (Section 5.4.). On the other hand, concerning the recent general interest in epigenetic, (neo-) Lamarckian evolution, the required *adaptive dynamics* is again formalized by these authors in a coarse grained operational (quantum channel) framework [28]. They deduced that a crucial decoherence-like *measurement interaction* with the

environment occurs, providing stable "attractors". Thus quantum open-system steady states are deduced in evolution. In this way, a supposed global, cell-dimension pure state is reduced to a diagonal density matrix *via* the decoherence-like interactions. Here, again, the "adaptive interference", dynamics, is crucially dependent, in the quantal operational formalism, on the nature of these interferences. The authors even succeeded in reconciling the epigenetic and (neo-) Darwinian genetic evolution. We, however, chose a different measurement picture, as required by our own framework: the (molecular) measurement depends on internal *virtual coherence* as *self-distinction.* It should be noted, however, that our viewpoint stands on less firm legs at present than that of the alternative one of these authors, adopting decoherence measurement theory.

3. Symmetry Restoring: Biological Quantum-Measurement Control Schemes and a Tentative Scenario of the Possible Advent of Molecular Information

3.1. Quantum Mechanics and Semiotic Controls

As a corresponding scheme, we present below for the emergence of molecular semiotic controls a quantum mechanical frame. We introduce it in relation to the directly observable, *algorithmically*, materially *mediated*, "abstract", genetic code software. We present it as being in direct relation to the origin and contemporary existence of the genetic code-protein synthetizing system. We will find the invariance of the code vocabulary to satisfy the requirements of being a special source of spontaneous, integrative autonomy of a semiotic nature. It also serves as a clue to investigate the integrated causal cellular organization, *i.e.*, the causal macromolecular network. This maintains and mediates the invariant abstract, virtual existence of the code vocabulary.

We note here that time evolution in quantum mechanics is twofold: in between quantum measurements, time evolution is a unitary one, subject to the linear superpositional (paralell evolutionary) dynamical principle of a many-to-many nature on one hand, and the nonlinear, projective, many-to-one evolutionary, quantum measurement nature, on the other. The former is a real quantal process, while the latter is heavily debated but agreed to involve some kind of classical component.

3.1.1. Quantum Measurement Schemes

There are three distinct, but related quantum measurement schemes of biological significance, denoted below by letters *a*, *b*, *c*, having bearings on our scenario of the emergence of semiotic controls in chemical evolution.

These schemes can be classified according to the kind of the arbitrary position of the so-called "Heisenberg-cut" [29], which divides the underlying quantum object and the classical device (and record and memory states), *i.e.*, it specifies *where* the "reduction of the wave packet" occurs. Accordingly, Neumann's infinite regress analysis [20] permits the introduction of the projection operator, along with this cut, to be placed at any level of this regress (the "projection *postulate*").

 (a) *External* ("*orthodox*", "*holistic*") *Measurements*

Here belongs the ordinary case, where the Heisenberg-cut is placed between the consciousness and memory of the human observer and his brain, his body in general. This is the ultimate solution of

Neumann [20]. Later Wigner relaxed the idea to embrace biological organisms in general [30]. Here it is the "subject" of the organism, *depending on its whole body*, which *is* the place of reduction, "projection". All material components: object, device, and the body of the observer form a chain of interacting physical systems. Record and memory states are thus objectively contingently, holistically-organizationally biological. Also, there comes about a mapping of the measurement outcome relations upon the "subject", as the ultimate realization of the reduction of the wavepacket. This stage must have been preceded by "internal"- and, the already strongly related "mixed" measurements, with the biological "subject" identified in the latter as the *global virtually coherent organization* of the "measurer" biological system.

(b) *"Internal" Measurement*

Though this concept was not introduced exclusively in biology, it has shown its primary use in protobiology [11,17].

Here we place the Heisenberg-cut, and the level of projection, between a macromolecular object and its macromolecular measurement device with its record and memory states *within the same system*, so that, e.g., a biopolymer "measures" its "object" biopolymer (see further e.g., [2,4–7]). The basic idea is that a molecular measurement on a larger quantum system cannot be instantenous according to special relativity, *i.e.*, takes *internal* dynamical time. In this scheme, we introduce, accordingly, "internal" quantum measurement and internal quantum dynamics on equal footings. The measurement does not depend directly on an interaction Hamiltonian of the influence of an "environment", rather, on specific *gross* 3D relations. The latter is governed by the fitting of the "device" and "object" subsystems in *internal dynamical* time. In this way, 3D relations are "lifted" to the (composite) Hilbert space. Mathematically, it is a constrained linear combination set of molecular projection operators, yielding a 3D steric *classical* selection *and* specific *quantal* overlaps (compare with molecular projections [31]). The result is a highly constrained time dependence, measurement dynamics, in our context a set of paralell evolutionary many-to-one processes, each resulting in one of a highly limited number of "similar" outcomes. In this way, the dynamics of internal measurement proceeds as

$$\Pi_i \left(\Sigma^L_{\alpha=1} \mathbf{P}_\alpha \Psi_i (t_1) \rightarrow \Sigma^M_{\beta=1} \mathbf{P}_\beta \Psi_i (t_2) \rightarrow \Sigma^N_{\gamma=1} \mathbf{P}_\gamma \Psi_i (t_3) \rightarrow \dots \right) \tag{2}$$

where Π is product, the $\mathbf{P}$'s are the molecular projectors (characterized below), belonging to the same molecular "device", $\Psi(t)$ is the object wavefunction, with $L > M > N$. The limiting expression is the integral

$$\Pi_i \int \mathbf{P}(x,t) \Psi_i(x,t) d\mu = \Pi_i \left(\Phi_i (\mathbf{X}_i, \mathbf{T}) \in \{\Phi_\lambda\}_{\lambda=1}^n \right) \tag{3}$$

where "*n*" is a smaller number. This is a natural expression for a dynamical-measuremental evolutionary *approximate* sterical fitting.

(c) *"Mixed" Measurements*

We introduce this special case of internal measurement as a mediating process between molecular internal and human "orthodox", external, instantaneous measurements. Here, we place the cut between the *external* object and the *internal* device, with the latter being part of the "body" of the macromolecular network "observer", forming an interacting quantum dynamical system. That is, we place the cut at the border between the two worlds. However, *by* the measurement, the projected object

state as *record and memory state* is, through the device state, locally coupled to, and globally mapped onto, the holistic, overall pre-existent *gross* biological organization. Thus, it becomes a part of the same quantum dynamical network. In this way, the setting *internally* represents these *external* measurement characteristics. This type of measurement occurs at the interface of internal/external measurements: the object is essentially external but the measuremental device *and* the following record and memory states are internal. Here, the reduction by projection occurs, finally, by internal mapping operators, mapping the measurement outcomes on the internal causal dynamical network. This completes and fixes the measurements. In fact, these mapping operators fix the object/device relations, the outcomes of the measurements, acting upon the device/record and memory wavefunctions. Additionally, there emerges, as a novel phenomenon an *entangled*, nonseparable state of the measurement device and the object system similarly to pure "external" processes [24]. However, in mixed measurements, this entangled state is internal to the global measuring system.

As to the general nonlinear nature of projection operators, we note that *any* projection operator depends on the specific, projected state of its "object". In our case of biological semiotic control functions, this state is predetermined by the corresponding projection operator, projecting out this specific state from the quantal superposition, the existing possibilities. It satisfies, thus, the specific requirement of internal biological *control*. Quantum measurements, as discussed below, are of this usual control type:

$$\alpha_i ><\alpha_i \sum_i \alpha_i > \rightarrow \alpha_i > \tag{4}$$

3.1.2. The Origin Problem: Chemical Evolution as the Evolution of Nonlinearity

To understand the origin of certain invariant biological semiotic controls and, as their function, those of the informational symmetry breakings/restorations, is basic for the understanding the deeper significance and action of these controls. The fundamental elementary biological semiotic controls are those of the genetic mechanism, the code assignments, forming possibly the basic evolutionary division line between pure chemical and biological systems and their evolution.

The transition from chemical evolution to biological evolution was due to roughly five distinct successive stages, where the evolution of the nonlinear nature of the corresponding processes played the central role. To arrive at our goal, we briefly review these well-known stages of chemical evolution.

   I.   *Symmetry-Breaking Instabilities and Dissipative Structures*

Here belong in chemical evolution those auto-and cross-catalytic networks which were nonlinear in their *concentrations, a statistical constraint* was exerted upon the underlying dynamics [32]. These structures were evidently present in early chemical evolution probably with spatio-temporal periodic patterns [33], subject to statistical closure.

As shown by Kauffman's analysis, in these processes, at "the edge of chaos", *i.e.*, conforming to both stability and adaptability as variance, autocatalysis is more stable than simple catalysis in the polymeric network. Even more important, polymeric *size* in general increases in the evolution of these structures [34].

II. *Dynamical Nonlinearity*

With increasing polymeric mass (length) and complicated 3D structure, conformation and the resultantly evolving higher quantum specificity, *i.e.*, acting on *specific* quantum states of their object in the catalytic process, the characteristics of the process shift towards individual polymers. They shift, in fact, towards *individual* macromolecular quantum dynamics. Here, nonlinearity is a *dynamical* one, its object, in autocatalytic activity, is implied in its time dependent potential energy operator. The system has, accordingly, a *dynamic* closure and nonlinearity; hence, the polymeric dynamical network is *causal* in the quantum mechanical sense of unitary time evolution. With individual large auto-catalytic and cross-catalytic polymers, primeval proteins and RNAs with high quantum specificity, there may have emerged stage III.

III. *Internal Measurement*

Sufficiently evolved enzymes and ribozymes perform internal measurements [11,17,18]. They act as molecular projection operators [18], projecting out specific quantum states of their objects by their 3D classical conformational structure, lifted to the Hilbert space, and their quantum-specific degrees of freedom. The nonlinearity of their action is thus evolved to a pre-informational structural-molecular *projective* one. However, they still do not have real semiotic control on the internal protobiological processes. By the modern *language* of decoherence, the "pointer state" of the "preferred observable", which is least perturbed by the internal measurement, here the state of molecular shape [35], provides a spontaneous symmetry breaking of the unitary time evolution of the quantum dynamic superposition of the "object". There is an informational gain, in open system dynamics. For the first time, coupled to this dynamics, the above projection operators appear [24].

IV. *Pre-Formed Structures towards Internal Semiotic Controls*

Concerning the ultimate step towards the emergence of semiotic controls, we must make a specific supposition. According to this, we have "autocatalytic" *internal measurements* of RNAs on themselves. This supposition is usually made in the "RNA-World" scenarios, as, e.g., in [36], with the difference that we here do not appeal to the usual template-dependent reactions, rather, to a reversal of the self-cleavage function. It emerges as the transition from spontaneously formed oligomers to the build-up of RNA polymers. We also take the further, widely accepted, view of polymerases as catalytically building RNAs [17]. This model amounts to a "strong" ("direct") self-reference, nonlinearity of RNAs dynamics, with the corollary that there was a similar internal measurement "catalysis" by primordial proteins, which in general terms is, in fact, a compromise between the RNA- and Protein-World views.

V. *Mixed Measurements and the Emergence of Invariant Genetic Assignments as the Fundamental Semiotic Controls*

This crucial step may have emerged when the auto-and cross-catalytic network, the proto-organism, the "*measuring agent*", was well developed to "perform" external, holistical measurements. It possibly had internal global virtual coherence ("self-distinction"), and faced externally emerging short ribonucleic acid oligomers as objects (compare with [17,37,38]).

Concerning individual primordial codons, it follows from stage *IV* that ancient, undeveloped polymerases performed "catalytic" internal measurements as measurement devices in a naturally nonlinear projective way. The emergence of primordial longer RNAs may have been the measurement outcomes. Also, these RNAs were involved in strongly nonlinear "*autocatalysis*". This suggested process has certain similarities to Dyson's concept [38] of a two-step evolution as metabolism followed by the internalization of the later informational, macromolecular RNAs(/DNAs). However, in our scheme the coding function is concomitant with the measurement interaction, see also [17,25]. Individual amino acid-codon pairs may have evolved during the gradual, in some aspects dynamical, internal measurements of the molecular shape class. The process was governed by gradual 3D fitting of specific sequence shorter-longer polymers. We do not wish in this paper go into a possible detailed stereochemical argument. Perhaps it is enough here to point out that several alternative mechanisms may have been involved. For instance, the protein *device* may have acted as an envelope around specific shorter RNA oligomers as a stereochemical structure. The stereochemically decisive amino acid residues as loop-producing turning points in the conformations could evolve to code the similarly stereochemically crucial codon units, nucleotide sequences. The chemical evolutional existence of the protein device must have been a statistically and occasionally emerging internal event. This tentative process may have formed the dynamical, "stereochemical" evolutionary aspect, as accompanied by a correspondingly constrained probabilistic quantum transition during the measurement dynamics. The latter random measurement aspect then resulted in a stereochemically "constrained" probability choice outcome, *i.e.*, the probabilistic choice is made from a set of sterically related molecular measurement alternatives. This tentative process of *both* chance *and* 3D dependence in evolution, resulting in a few, "similar", degenerate codons, then may have resulted in a both stereochemical *and* a constrained frozen accident emergence of the code (see originally e.g., Woese [39] *vs.* Crick [40]; for the possibly stereochemical origin of the presumably most ancient coding of *t*RNAs, see [4]).

By mixed measurements, which are contingent upon a clear spatial-causal distinction between the internal and external world (see "Semantic Closure" [41]), the internal macromolecular record and memory electronic wavefunctions, depending on the steric molecular nuclear structural frame, were then mapped onto the underlying global virtually coherent internal causal network by the assignation operators. They were, in fact, encoding the object/device measurement outcome. The *internalization* of the record and memory states was due to the dynamical, internal measurement aspect of mixed measurements. The mapping itself, as the ultimate "reduction of the wave packet", may have been a manifestation of the external measuremental aspect. There thus presumably appeared, by conforming to this external aspect, a set of integrated, global-"abstract" correlation-conserving entities, quantum mechanical global-virtual ultimate measurement outcomes. They were thus internally virtually *representing* the original macromolecular measurement outcome, *i.e.*, the record and memory state. The record and memory states, in this way, were possibly encoding by their steric structures the contingently arisen *reversed* object/device relations. The latter relation, presumably, must have emerged by these *newly internalized*, coupled record and memory states becoming the natural internal *causal predecessor* to the state of the internal device and, through it, to the cycles of the global network.

In this way, the *possibility* of an *internal* reversal of the original object/device relations may have emerged, the two components together forming a retrocausated one-to-many local dynamical process. The splitting into probability branches of the record and memory states post-measurement might have

been then due to an inducing effect of the particular perturbing time-dependent nonlinear interaction Hamiltonian, acting through the protein device state, at the "edge of chaos" *nonlinear* complex case [34]. Thus, the original cause, the protein device realizing a causal reversal, depends on its own future as its own effect, *i.e.*, projected RNA. Its mechanism, thus, is the coupling of RNA to the internal network through the "*ab initio*" internal, dynamically coupled protein device state. In this context, we refer to the kind of reverse case of partial measurements [42].

In this way, the states of the projected RNAs will depend nonlinearly on their protein effects and in general, the global network through the assignment operators, which is our point here: assignation is a function of the global network (compare with [25]).

The resultant fixed global causal entities as outcome functions of the mapping (assignation) operations could be the abstract-virtual, semiotic classical rules, encoding the reversed object/device relations. They may be quantum dynamical correlation functions, global spatio-temporal "software correlations" over the structural hardware, the macromolecular device and record and memory spatial structural states. Actually, these naturally emerging classical semiotic rules, encoding the measurement outcome relations, may have emerged as represented by internal causally maintained quantum mechanical *entanglemental correlations* by a virtually coherent internal dynamical network background. They might have emerged according to the well-known entanglement relation between the quantum mechanical device and its object.

In this way, the measurement phenomenon involved a macromolecular hardware *and* a globally-semiotically interpreted software, assignment. In a natural way, as pointed out above, the latter emerged as a function (representation) of the former, as "self-distinction".

Thus, at this presumed final, rather singular molecular evolutional stage, all components of the set "object", "device", "record" and "memory" was internalized into the system *by* the measurement. It should be stressed, that by the chemical evolutionally emerged mixed measurements, there was a concomitant cause-effect, causal break in the dynamics of the object as is usual in ordinary holistic quantum measurements. (We recall that a many-to-one process cannot be *causally* a predecessor of a many-to-many one. The von Neumann entropy changes during the event [20], see essentially, e.g., [19]. In this case, however, the causal break was mapped to internal *causally reversed* projected object state/device state relations. In this way, semiotic controls could emerge as an internal global *reverse causal representation*. So the causal break was eliminated from the system by a retrocausal dynamics.)

In concrete terms, by the presumed evolutionary, measurement coupling of the two nonlinear molecular "catalytic" processes of Protein→RNA and RNA→RNA, *i.e.*, by the introduction of a certain semiotic *reversal* of the processes, a reversal of the original internal measurement relations happens, leading to an RNA→Protein→RNA dynamics. A time symmetric future is *constructed* by symmetrically following, in a regressive way, the past of the system. (Thus, this reversal does not correspond to simple antiunitarity; the arrows denote "producing".)

The fundamental reason for this *construction* of a time-symmetric one-to-one regressive quantum dynamics is that it is required by "external" quantum measurements in an "internal" context ("mixed" measurements). A continuously *causal dynamics* was being able to come about *only by following the reverse process*, the past, *i.e.*, in a retrocausal way. In fact, this route of the quantum dynamics of the record and memory RNA structures was the *only* continuously causal quantum dynamical future of these ancient, measurement ("catalytically") built RNAs, encoding the assignments. This *choice*

possibility arose as they were coupled to the continously causal quantum dynamical internal organizational network through the protein device state. Thus a dynamically, causally continuous dynamics of the record and memory RNAs was possible to emerge post-measurement, just by coupling to the continuously causal organizational network. It was, in fact, an alternative to a highly unstable post-measurement *acausal* superposition, as supported by possibly strong protobiological evolutional pressure. Its alternative, the acausally emerging superposition was subject to unavoidable uncontrolled random internal fast decoherence.

The necessary continuously causal future of these upbuilt, projected macromolecular RNA record and memory systems was tentatively needed to be *regressively constructed* in a real-time, time-symmetric manner, just as they were coupled to the rest of the macromolecular network. Actually, the process had to be stepwise highly constrained, *i.e.*, constructed from its origin, since it was evolving in a regressive one-to-many way upon the only available retrocausal time direction, not following any special reverse assignment history. The projected, assigned object wavefunctions, here those of *t*RNA-like coding RNA structures, became the projective controlling ones on the wavefunction of the former device protein. Accordingly, the process possibly arose by the many-to-one relation of the original measurement constraint becoming a peculiar underlying energizing one-to-many relation concerning the component macromolecular wavefunctions. In fact, the causal interaction with the global enzymatic virtually coherent network might have resulted in the concatenation of the complementer ("anti"-) N! primordial codons of the tRNA-like structures, yielding a sequence of nucleotide bases, the coding RNA/DNA *polymer*, in an energizing quantum mechanical one-to-many process. (N here denotes the serial, not necessarily different, codons.) The quantal superposition of each ("anti"-) "codon" was then constrained by the control-setting many-to-one projection of the internal assignment rule of the full causal network. Selection might have then favored the emergence of specialized *polymerases*.

Thus the resultant recursive process, as successive projection constraints upon the post-measurement successive time evolutions, right from the very origin emerges as an observable *energized* one-to-one correspondence (rule) chain.

The ambiguity in the post measurement time evolution of the projected object system, hardware RNAs, was so probably having, within a short term in evolution, a pay-off in favor of a semiotically constructed stable internal causality. From this stage on, they were the RNAs *with a global software* which acted as symmetry constructing "internal measurement devices". They were the carriers of the reversed assignments as *t*RNA-like ribozyme species, with the genetic code, carried by them, interpreted by the whole intracellular macromolecular machinery. In this way, the molecular hardware as nucleotide sequence is correspondingly local, while the software as abstract-virtual genetic codes is global. In a natural way, there must have existed systems following the acausal route with undeveloped internal causality conditions.

Accordingly, these evolutionary semiotic constraints are but descendants of the above "direct" assignments, arising from the measurements, as embodying "reversed" assignments. They are, on one hand, fairly arbitrarily set as an evolutional *choice* of retrocausality, while, by their consequent fundamental causality, are strongly constrained. This is what we suggest here as a certain kind of special "biological freedom". This overall process is amounting to the emergence of *semantic nonlinearity* in direct context with the symmetry restoration dynamical cell cycle.

This is, tentatively, how and why physical records and memories of internal measuremental sterical relation origins may have evolved into global-virtual semiotic natural projection operators. They act upon the underlying reversed dynamics, yielding the necessary constructing "initial symbols" of the entanglement correlations in terms of the molecular algorithm, as their projective role. They are existing in relation to the intact cell cycle in a holistic organizationally maintained and mediated, dynamical virtual coherence. Concerning mathematical representation, they are projection operators corresponding to this deeply quantal, if virtual, quantum correlation (Section 3.2.). They are built on (are representations of) internal "coding" record and memory states of RNAs(/DNAs) as the dual wavefunctions of them by the assignation operators, and embody an evolutionally robust, invariant, also global-virtual and self-distinctioning, assignment relation.

In terms of internal chemistry, the origin of the observable protein synthetizing process was in a way natural, taking into account the resolution of direct ("strong") RNA nonlinearity into a "weak", protein mediated one. In fact, the cause-effect relations of a dynamical nonlinearity with quantum specific interactions were opened up by the perturbing effect of the proto-protein, and its *effect* in turn becomes the effect of an other, more stable (*mediated*) nonlinearity (compare with [43]). This amounts to chemical assignments and their semiotic reversal. It comes about by a dynamical change of the object/device relations and, by the nature of the process, it was, and contemporarily also is, a regressive, real positive time, phenomenon.

3.1.3. The Process of Semiotic Symmetry Breaking/Restoring: on the Source of Biomolecular Information

It follows from the above tentative scenario, that the emergence of biological semiotic controls was presumably of a fairly singular, quantum measurement, origin. As was noted above, subsequently to the primeval mixed measurements, the reversedly emerging superpositions contain as branches the different reverse assignment possibilities as alternative histories. The primary "initial symbols" of the following protein synthetizing translational algorithms are the stable entanglemental global-virtual reverse assignment projection operators. They can be conceived grammatically as a simple declarative "sentence" of a virtual language, to be translated to another, molecular, material language. These projections select, as semiotic controls, the proper reverse histories, reverse assignments. They set the right physical initial conditions of the measuremental-dynamical (internal measurement) recursion.

The successive process corresponds to the well-known steps of the genetic translational apparatus, the whole molecular dynamics being comprised of retrocausal, discrete algorithmic steps. These algorithmic discrete steps are thus internal measuremental, recursive-regressive steps where one macromolecule is once a measured, once a measuring entity in the algorithm [11] (compare also with [44]), corresponding to the important phenomenon of "quantum update".

It is a primary result of the above discussion that time-invariant semiotic controls could *only* emerge by a causal break*, i.e.,* breaking of time inversion symmetry, forming a *possibility* of setting the kind of "arbitrary" unitary symmetry breaking special constraints on the post-measurement superpositions, *i.e.*, the process arose as the introduction of the element of *choice*. There emerged in evolution a new, *constructed* kind of causality, at the expense of external physical matter and energy sources, to be gained. It is an emergence from the universal natural history, the universal continuous unidirectional

dynamical time evolution. We consider, thus, biological autonomy, spontaneity and internally controlled causality as the strongest evidence of the above discussed evolutionary vital mechanism.

This special overall symmetry restoring process is in line with similar suggestions in the literature of "perpetual inconsistency-restoration force" schemes [11,14,15,43]. However, it is the primary advantage of our frame, that even if it belongs to this family of concepts, it is special in that it corresponds to the strong requirement to account for this internally generated spontaneous *energized* activity. That these semiotic controls had to be born concomitant with the very origin of life was pointed out long ago by Pattee [6,7,17]. Also, according to the above scenario, this symmetry restoring dynamics of internal origin is a liberated one by the break in causality, providing the *possibility* of the evolution of the aforementioned element of physical "freedom" as choice.

It is implied by the above discussions, that the emerging *information*, in the present context, is defined as the probability measure of the right, projectional choice of the branch in each reverse superposition, belonging to each assignment,

$$I = \sum_i p_i \log_2 p_i \tag{5}$$

Here, p_i is the square of the time dependent probability coefficient of the ith, special unique branch in the proper reverse superposition of assignment histories, summed over the paralell reverse different assignment superpositions in creating a protein macromolecule.

Thus, they are these downward causational, virtual-global, evolutionary semiotic controls which make biological organisms so integrated, spontaneous and distinct in face of the rest of the Universe. In fact, they are these which can account for the *origin* of the internally generated spontaneous activity, corresponding to the internal, liberated efficient cause of biological "motion", generalized dynamics (see also Sections 2.2. and 5.3. and [16]). Actually, it appears that they are these pre-set, organizationally integrated "abstract" semiotic assignment relations which are the central *cause* and at the same time also the nonlinear *effect* of the overall biological generalized dynamics. Possibly, it is this semiotic relation which is often simplified by the concept of "autocatalysis".

The controlling global-virtual quantum mechanical correlation primavelly may have arisen from a *common,* primordial *material origin* of the two molecular species as internal measurement "outcome" relations of codons and amino acids, evolving into mixed measurement outcome relations, as primeval correspondance. There are in this way a chemical evolution maintained coherence, in fact entanglement relation, between codons and the proper amino acids. The measurement assignment operators, corresponding to mixed measurements, may have evolved upon these inherent entanglement correspondances, setting initial conditions for the macromolecular algorithm. As to the contents of these quantum correlations, measuring one molecular species immediately sets the measurement outcome of the other, which is a solid component of our understanding of the "genetic language".

3.2. Epistemology and Physics of the Elementary Projections as the Invariance of the Genetic Code

As Patel [22] also noted, the genetic vocabulary is an "abstract" entity. What actually can be observed is the nucleotide base sequence. This is made spectacularly clear in slipping errors of wrong initiation. It is a set of symmetry breaking, abstract-virtual informational *constraints* as initial symbols,

which is superimposed upon the underlying reversedly arising unitary dynamics. This is what is leading to the observable semiotically constrained dynamical algorithm (compare with [7,8]).

Above we referred extensively to concepts of a "virtual-global" and a "material-local" dynamics, which needs clarification here.

It has been shown by Primas [35] and also, e.g., Man'ko and Man'ko [45] and Elze *et al.* [46], that there are physical systems with both classical *and* quantal properties. Regarding our considerations of Section 2.2., we intend here to include in this class also biological systems, tentatively already at the cellular level, genetical dynamics. The reason is, that *rules*, emerging in evolution, as mediated by quantum measurements, as constraints are in fact generally classical, even if maintained and mediated by deeply quantum mechanical mechanisms. Being concerned here with the invariance of the genetic code assignments during evolution, we consider, as mechanism, certain quantum dynamically induced long-range correlations between the corresponding subsystems of codons and amino acids, which supposedly belong to the family of *quantum entanglement*. As was mentioned above, this approach is based on the well-known entanglement relation of the corresponding states of an ancient system-internal measurement device and its internalized object in "mixed measurements". This relation was conserved globally during evolution till the corresponding system can be considered as "living", *i.e.*, is virtually coherent. Accordingly, we have the deeply quantum mechanical "intra-system" correlations between part-systems, derivable from the von Neumann equation, *and* a classically generated, classical-algorithmic "inter-system" correlation, derivable from the generalized Liouville equation [46]. Our point is the relation between the two correlation dynamics.

Introducing tentatively the two kinds of correlations for the above discussed, coupled codon-amino acid part systems, we have an "intra-system" *nonseparable* quantum entanglement dual dynamics *and* a *separable*, classical product state, "inter-system" dynamical correlation. (For the former, see [47]; for the latter, see [46].)

We suppose, thus, on one hand, a material, local-classical (internal measurement) correlation of the two subsystems in the macromolecular algorithm *and,* on the other hand, a quantum mechanical entanglement, an "initial symbol" quantum mechanical *blueprint* correlation. The latter is a materially stepwise unfolding *semiotic correlation*, projected upon the material components, the post-measurement superposition. It corresponds to the above abstract-global nature of the code assignments, the latter being a virtual, but in its effects observable, global physical relation. It is as if this correlation were acting in perfect isolation, *in vacuo, i.e.,* virtually, not destroyed by the intracellular environment. Rather, it appears as if it were materially maintained by it in a global, mediated way.

The experimentally observed invariance of the genetic code assignments during evolution, in these terms, derives from both a globally, coherently maintained semiotic-virtual assignment in evolution, *and* a similarly robust material-concrete, local algorithmic relation as protein synthesis and the production of new DNA strands. (The latter corresponds to attained space-mapped time symmetry). Inherent invariance thus arose, primordially from a special quantum mechanical (object/device entanglement) relation which emerged upon a stable material sterical macromolecular record and memory states in a past mixed measurement. The latter were mapped onto the similarly stable self-regulating global causal macromolecular network by the assignment operator, as discussed in Section 3.1.2. It was, possibly, the advent of "*natural sign*", "software", from which the two coupled,

hierarchical dynamics of a common material origin, emerged. It may have been, more closely, the birth of the exceptionally stable abstract-virtual entanglement correlations by the action of the assignment mapping operator. What followed probably was the evolutionary emergence of the translational recursive molecular unfolding of these virtual-global projectors ("initial symbols").

Accordingly, concerning the action of this virtual-global assignment correlation, we know, as hinted above, one possible mechanism: the natural *composite projector* nature of the descendant entangled state of codons as ancient reversed internal measuremental device systems "B", and assigned amino acids, object systems "A". We have

$$\rho^{AB} = |\Psi>^{AB} <\Psi^{AB}|, |\Psi>^{AB} \in H^A \otimes H^B \tag{6}$$

where ρ^{AB} is the general density matrix of the entangled system, $\otimes$ indicates the tensor product, the *H*'s are proper Hilbert spaces; thus we have the special projection

$$|\Psi_i(\mathbf{q}_i)>^{AB} <\Psi^{iAB}(\mathbf{Q}_i)| \,|\, \Sigma_i| \Psi_i(\mathbf{q}_i)>^{AB} \Rightarrow |\Psi_i(\mathbf{q}_i)>^{AB}; |\Psi_i(\mathbf{q}_i)>^{AB} \in H^A \otimes H^B \tag{7}$$

with $|\Psi^A> = \Sigma_i c_i^A| i >_{iA} \in H^A$, $|\Psi^B> = \Sigma_j c_j^{,B}| j>_{jB} \in H^B$ as molecular wavefunctions, indices *i, j* belonging to different measurement outcomes; so that

$$\Psi_i^{AB} = c_{ii}| i>_{iA} \otimes| i>_{iB}, \text{ with } c_{ii} \neq c_i c_i' = 1 \tag{8}$$

from where the above introduced nonlinear assignment operator **A**, ensuring invariance, is defined as

$$\mathbf{A}(\Psi^{iAB}(\mathbf{Q}_i)>< \Psi^{i\,AB}(\mathbf{Q}_i))(\alpha_i(\mathbf{q}_i)^A> \beta_i(\mathbf{q}_i)^B>) = \Psi^{i\,AB}(\mathbf{Q}_i)> \tag{9}$$

Here **Q** denotes the global space coordinates. The projection of Equation (7) is what provides a quantum mechanical blueprint selection for the proper material assignment history in the post-measurement arising assignation superpositions. This "initial symbol" depends on the global coordinate **Q**. This virtual entanglement, $|\alpha_i><\beta^i|$ (α: amino acid, β: codon) thus serves as the informational initial, unitary symmetry breaking projection operator, the virtually mediated software projection. It is materially carried out by the whole internal global virtually coherent organizational network. It provides a quantum mechanical blueprint for the molecular recursion as an initial semiotic constraint on the concrete-local molecular, superpositional (unitary) process. The following mediating, materializing mechanism, evolving from this primordial assignment relation, was possibly the origin of the protein synthetizing macromolecular algorithm.

Both the virtual and material processes obey, in a local-material and global-semiotic way, a cellular Semantic Closure Principle [41], and both imply symmetry-breaking informational controls. Thus, mathematically one aspect of the "bra" codon wavefunctions corresponds to the *local* internal measuremental *classical* correlations, which have as mechanism, a time-ordered internal measurement-series. The other aspect is the codon wavefunctions as of quantum mechanical triplets in a *global*, abstractly represented, virtual quantum entanglement correlation. The wavefunctions of the assigned pure physical hardware codons are denoted by $\beta_j(\mathbf{q}_j)>$, while that of the virtual assigned codons are denoted by $<\beta^j(\mathbf{Q}_j)$, with $\mathbf{Q}_j$ being the global space coordinates of the wavefunctions (see Section 5.4.).

The sequence of codons and amino acids in biopolymers thus arose and contemporarily still arises possibly only as a secondarily organized, classically correlated set of these quantum structures. In the above-characterized classical local-material algorithm, the central *correlation-mediating* internal measurement role contemporarily is played by the aminoacyl-*t*RNA synthetase enzymes (see for an overview, e.g., Patel [4]). The last step of the translational recursion is, in a natural way, the sequential internal measurement binding of the individual amino acid-*t*RNA complexes to the proper similarly classically correlated codon sequence(s) of RNA(/DNA).

Thus, the gross state of individual genes and proteins is potentially separable (not entangled), *i.e.*, can be written as a simple product state:

$$\phi = p_i | \Psi_1 ><\Psi_1| \otimes \ldots \otimes| \Psi_N ><\Psi_N| \qquad (10)$$

so the individual assignments can be realized. In this way, proteins and informational nucleic acids are materially formed by specific series of time dependent classical concatenation (polymerase enzymes) operators of the material monomers, the latter produced by the paralell translational assignment algorithms.

4. Internal Teleonomy of Biomolecular Semiotics: The Ontology of the Molecular Semantics in Defining the Phenotype

A probable key to the above characterized, observable algorithmical biological symmetry restoration cellular cycle phenomenon is provided by the observation that it forms stepwise one-to-one informational internal measurement symmetry breakings as a "classical" constraint chain. In fact, without this chain of molecular internal measurements, the proper special reverse assignment relations would get looser and looser in time, according to their being reverse histories. This information conserving evolutionarily fixed functional aspect is due to the characteristics of the internal measurements: the *special* holistic nature of internal quantum measurement (compare with [48]) is realized inside the system by successive molecular shape complementations. This points to the unity of object and device as a physical totality, a universal lock-and-key type system of the classical device and the quantal object. The action of the formers is a chain of unitary symmetry breaking consecutive projections on the stepwise emerging inter-measurement unitary dynamics, superpositions in a virtually coherent background. The quantum measurements preserve the unique information content of the recursion, as set by the "initial symbols". They preserve it by *interpreting* the consecutive sign fuctions of the macromolecular members of the recursion chain. In fact, they carry out this function by complementing molecular structures, *i.e.*, by implementing the software by a unique hardware, which lends to the algorithm a stepwise physical stability. Thus this realized *material-structural unity* of *classical* iconic *sign* and its *information* is peculiar to biological systems: the unity of them is due to just this special chain of symmetry restoration algorithmic steps in the form of classical molecular shape complementations ("law-like iconic" sign, Peirce [49]). The specifically emerging biased change of the dynamic probability of the state of the successive object, receiver system, is just the informational function, the local *meaning* of these molecular signs (compare our symmetry breakings to pragmatic information, e.g., [50]).

In this way, the relevance of the term "local molecular sign", as molecular local *information*, local meaning is made clear by the *global* meaning of the semiotically-controlled dynamical context. Actually, it is the global symmetry restoration *rule, i.e.*, developing towards time symmetry, which *is* the natural objective global *"interpreter"*. Thus, we have the succession of internal measurements, the process progressing along as internal information propagation. It is building up informationally a classical phenotype, which process corresponds to the catalytically enhanced biochemical reactions concept of usual biochemistry (compare with [9]). We have a locally hardware-implemented global software with an irreversible semiotically constrained generalized dynamics. As Sharov noted, "every informational process is teleological" [51]. This mechanism corresponds to the perpetually maintained unique ontological existence, cycling *material renewal*, of the global-virtual assignments in evolution.

In context with this very concept of molecular information as stepwise unitary symmetry breakings, *i.e.*, internal measurement interpreted local molecular signs, it is commonplace in nowadays theoretical biology that the genetic code→protein dynamical system can be formalized in terms of a T-grammar (compare with [21,22]). According to the above discussion, it can also be interpreted as a translational algorithm, naturally emerging in organic evolution. Also, it has been suggested, that closed formal languages are not evolvable [52], only systems are such which allow for the changes of grammatical rules in time. Then the two aspects of the behavior of the system, semiotics/dynamics are defined as being in a self-referential convergence.

Actually, the above discussed semiotically constrained dynamics as a classical molecular algorithm can be defined as an early converged, fixed phenomenological dynamics of a biological molecular language. Here the deep structure [53,54] is being the expectation, *i.e.*, pre-set competence, for the fixed spatial primary, secondary and tertiary structures of RNAs/(DNAs) in the molecular context (e.g., [25]; compare also with [4]). This well-known fact is interpreted here as due to the *gross* cellular organization, since it forms a material system with a *pre-set natural competence*, virtual coherence, for the global projectors as "initial symbols". This is, supposedly, the ultimate underlying reason of the inherently holistic (self-distinctioning) behavior of the living cell.

As to the other aspect, the ultimate ontology of the *global* meaning of the translational algorithm, it is, at its roots, a contextual, relational phenomenon [55]. The above "objective existence" of the *local* meaning is the natural foundation for the ontological-epistemological context in the global meaning aspect. In fact, it is the above lying global meta-rule of the symmetry restoration internal relation which is unfolded by *sign-manipulation* via the local control-chain. This global symmetry restoration is based on the above discussed self-reference, semiotic nonlinearity of a "weak" nature. In fact, it is contingent upon the translational molecular algorithm with protein-enzymes as classical terminal strings and, along this line, generally upon the phenotype. The latter copes with surrounding reality in a code→phenotype→code process (generalized dynamics, Section 2.2.), and forms a nonlinear material cycle. In fact, the basis of this material nonlinear cycle is provided by the molecular algorithm, while the self-referent loop-closing process is the *action* of the phenotype, nonlinearly depending on and *preserving* in its action, the quantum dynamical invariance of the converged code vocabulary itself in evolution (Sections 3.1.2. and 3.1.3.).

In this way, the latter *"mediating global meaning"* of this weak nonlinearity, self-reference emerges tentatively as the ultimate ontology, the *existence* of a *global meaning* of the process. The quantal symmetry restoration semiotic projections have the virtual-global *teleonomy of self-maintainance*,

towards the global goal of space-mapped time symmetry ("self-reproduction"). This result has importance on our discussion of biological generalized dynamical "invariants" *vs.* the phenomenon of the similarly invariant "struggle for life".

It is peculiar that the ontology of the local meaning can be interpreted in global terms, while the ontology of the global meaning can be interpreted in local terms. This self-referential relation is a characteristics of the ontology of the fundamental biological dynamics. It refers to the circumstance that they are mutually interdependent sides of the same ontology.

Above, the tentative suggestions in Sections 3.1.2., 3.1.3. and 3.2. concerned one aspect, the possible molecular-genetical mechanism, trying to deduce the fundamental molecular basis of the problem of the biological evolutionary molecular invariance relations. Below, we intend to pass to more general points on this ground.

5. Discussion: The "Strategy" of the Abstract Genetic Code as a Biological Dynamical Invariant

5.1. Motion, Freedom, Nonlinearity

As shown above in its generality, the assignment control by the genetic code is a highly nonlinear phenomenon: even in its immediate, protein sythetizing function, it depends on its very "phenotypic" specific proteins and nucleic acids, *i.e.*, it depends on an integrated organization consisting of e.g., *t*RNAs, *t*RNA-aminoacyl synthetases, polymerases, *etc.*, these in turn being dependent on the very assignments. This is not a direct, strong, but a weak nonlinearity, self-reference, mediated by the formers [43]. The fundamental biological relation being this nonlinearity, the effect of this mediated self-reference can be observed at every descendant "motions" (generalized dynamics, Section 2.2.), on a multi-level basis at all the accompanying different levels of organization. This is in close connection with the spontaneous setting in a kind of "liberation", a certain free set rules on the internal/external dynamics. It corresponds to a kind of freedom in choice among a set of possibilities at every level. It is in fact observed at every hierarchical level from the bottom up, and is descending from the nonlinear evolutional freedom of choice of the quantum mechanical genetic assignments. In fact, the internal spontaneous *free cause* in the biological internal/external dynamics, *i.e.*, in the biological motion at every level, derives from the quantal, similarly freely chosen nonlinearity of the code assignments. There is a descendant hierarchy of on one hand freely set ("chosen"), on the other hand deterministic, constraints. They are classical "rules upon rules", evolutionally developing hierarchical controls upon controls, at different higher organizational levels. As hinted above, the overall "goal" might be to nonlinearly preserve the underlying invariance of the code vocabulary. The latter, thus, as *molecular* self-maintainance, is, in fact, the very content of this teleonomy.

This apparent freedom in choice of the constraints on motion amounts to a certain nonlinear choice of its own initial conditions by the organism itself, at its different organizational levels, in its teleonomy towards self-maintainance. As Pattee [44] observed, initial conditions are in fact set by molecular/macroscopic internal/external *measurements* (see Section 2.2. above). In a *gross,* global sense, this generalized dynamics, encompassing all biological motions, is ultimately under the nonlinear control of the action of the genetic code. It is under similarly freely set constraints as those

controlling the genetic assignment dynamics itself. The generalized dynamics is, thus, similarly "free" (chosen) in a hierarchical way.

As a summary, now we can pose our fundamental question*: why is the living form of matter so stubbornly preferred, integrated, over the non-living one in evolution*? From where does "struggle for life", this special existence for special existence originate?

5.2. The "Selfish-Code" Paradigm

Opposing Dawkins' "selfish-gene" concept, we put forth a different view of the *gross* evolutionally invariant strive for being, "struggle for life", and the accompanying accumulation of "freedom" (actually, the Kolmogorov-Chaitin entropy [56]) in evolution. We suggested above that it is tentatively due to the abstract-virtual semiotics of the genetic code. The former, the strive for being, is presumably emerging as a similarly "invariant" of motion, a self-maintaining nonlinear (mediated self-referential) function of the underlying invariant code vocabulary. This is manifest at any levels of the biological internal/external generalized dynamics.

At closer inspection, in fact, it appears to us that genes exist for the code, rather than on the reverse. The genome of the individual organism is an object of an organized code assembly, a configuration of individual codons, which ensures, in evolution more and more safely, the transmission of the underlying invariant code vocabulary. As noted above, the basis of this transmission, its constancy, is "self"-reproduction, as time symmetry mapped onto space. From this fact originates the *individual basis* of this process, similarly as it is supposed at the selfish-gene paradigm. It follows that practically all derivations of the latter remain valid for the selfish-code paradigm, too, from parental care to kin selection, but on a more sound ground, e.g., Maynard Smith and Szathmáry [57] conclude that the difference between species is the *way of transmission* of the genetic material. We only add: it is possible that at the bottom there is the quantum mechanical genetic code's special global deeply quantal function, the entanglemental assignment. It is this which perpetuates itself, *i.e.,* initiates a semiotical self-referent self-constraint chain. It is, thus, at its roots of a deeply quantum mechanical nature, controlling the phenotype in order to perpetuate its quantal entanglemental dynamical invariance.

That is to say, a living system is subject to (is a function of) the underlying biological invariance in the *action* of the genetic code. According to the above discussion, the invariance of the robust, abstract-semiotical genetic code actually materializes in the nonlinearity of its function: through the code→amino acids→proteins→phenotype→code, retrocausal, weakly nonlinear, *i.e.,* mediated, self-referential chain. In fact, though the essence of the dynamics is the invariance of the code's global quantal entanglemental function, it is the actual local algorithmical implementation, mediation of the assignments as protein synthesis, which is to build the *best phenotype* to ensure this invariance, the safe transmission. The invariant thus *constructs* itself, so *exists*, nonlinearly, as an invariant. DNA(/RNA) is a mere carrier of the self-organized codons only as joint, quantum mechanically describable individual bases without local internal measurement correlations corresponding to the virtual-global classical assignment rules.

Nowadays, it is generally supposed that RNA(/DNA) implemented the code function secondarily in chemical evolution, being/growing out of, autocatalysis. According to the above discussion, we would advocate an initially highly ambiguous, undeveloped, but code-first, genes-second, view. Genes are

generally supposed to build a "survival machine" phenotype for themselves, yet, should we not rather attribute this fact to the real invariant of motion, to the genetic code? Actually, there is some evidence that the assigned code, the unique global correlation with individual amino acids, evolved very early [58], possibly before the advent of synthetase enzymes. Thus, we propose the reverse, *i.e.*, that they are the codes which, in a "selfish" way, facilitate, determine the transmission of their "*own*" genes, the special unique configurations of them. Actually, the latter are acting as the phenotypic blueprint, exposed to selection. The goal of struggle for life, and of the fierce fight for the "selfish" transmission of competitive genes is, presumably, to maintain and in evolution recurrently provide the best phenotype by which the invariance of the code vocabulary can be *optimized*.

Summarising, we think that the deeply "mysterious" strive for being, the "biological function for biological function" (self-production, autopoiesis, e.g., Zeleny [59]), may perhaps be best interpreted along the above line of the genetic code as a generalized dynamical invariant, without which evolution would be utterly impossible. It is thus leading, in fact is giving a reason to, evolution, *i.e.*, towards the evolutional accumulation of information in its genome and in general, in its phenotypic structure.

5.3. The Tentative Mechanism of the Genetic Code as the Biological Invariant of Motion—Decoupled Initial Conditions in General

Above, we several times referred to the possible role of initial conditions in the permanence of the invariance of the genetic vocabulary in the individual internal/external, generalized biological dynamics. The range of this invariance extends to both onto-and phylogenesis.

In physics, initial conditions are supplement to boundary conditions. In our biological case, the latter emerge as the above discussed structural nonholonomic constraints on the dynamics [6,11]. Equally important, if not more important, are the formers. As we introduced the concept above (e.g., Section 2.2.), once initial conditions are fixed by the system itself, the constrained dynamics proceeds to recurrently fix its same initial conditions, amounting to self-maintainance, self-production. The most ancient and basic "freely set" initial conditions, as discussed above, are intracellular quantal symmetry breaking informational controls by the genetic assignments.

Actually, it was shown in a previous paper, that what the phenotype does, in fact, is an extended permanent fixing its own initial conditions [16]. This type of behavior can be, and often is, conceived as the "restoration of the pseudo state Θ" by special types of reflexive processes as special types of constraints. They are supposed to be imposed upon catalysis, *i.e.*, upon the enhancement of the internal process. This regulation of the internal/external energy flow is thought to result in a "competitive subtraction" of energy from the environment [60].

Our concept of the perpetual reproduction of initial conditions by the very biological organism, however, is well applicable to higher grades on the evolutional ladder, which is not the case for the autocatalytic paradigm. We suggest that evolution of fundamental biosemiotics progresses along a gradual *decoupling* of the initial conditions and the constrained dynamical laws, being in unity in the Universal history of inanimate nature. This decoupling evolves towards kind of *liberation* of the initial conditions, amounting to "arbitrary" internally generated semiotical activity. This kind of liberated, free process, at different organizational levels is fundamentally constrained, however, as discussed above, by the very freely set rules towards the fulfillment of the most ancient biological goal of

symmetry restoration (space-mapped time symmetry), the latter as the basic teleonomy (compare with [8]; for a discussion of this kind of "freedom", see [16]). This can be most easily demonstrated by discussing metabolism. The organism actively searches for its energy rich supply sources, and constrains them to pass down its enzyme chains to produce energy rich phosphate molecules, mainly ATPs, for its self-maintenance. The existence of the latter global "goal" as organismic self-maintenance was shown above to be the prerequisite of the nonlinear global invariance of the code vocabulary. In fact, this kind of nonlinearity concept is an alternative formulation of phenotypic mediating meaning, the essential weak self-reference of the generalized dynamics at all organizational levels (compare with Section 4.).

Actually, taking a multicellular predator as an example, with the same fundamental biological functions as possessed already by unicellulars: supplemented by certain cost/gain evaluations as intermediate, freely set active information processing, *i.e.*, temporarily withholding the choice in the proper inhibition/release way, it finds, kills and utilizes its pray for its own initial conditions. The consecutive coupled intracellular internal dynamics then proceeds to constrain the phenotype to externally repeat the process (Section 2.). In fact, this is one nonlinear way of achieving the fixation of the system's own initial conditions. In our example, it is carried out largely by its modified original ectoderm, teeth, developed in evolution around the entrance channel of the ancient archenteron. The process ("motion", generalized dynamics) fixes then periodically the initial conditions for its constituent cells. (In this context, its prey animal is generally on a different strategy.)

Thus, according to the above outlined concept, embracing both genetical-molecular and phenotypic-macroscopic phenomena, the permanent "struggle for life" tentatively is the phenotypic material expression of the invariance of the genetic code assignments in evolution. The fundamental semiotic informational goal is then, tentatively, the space-mapped time symmetry (doubling-up), which gives the profound underlying reason to self-maintainance as symmetry restoration. Actually, we can extend this view, in the organism-organ-tissue-cellular context, beyond the implementing algorithms, to the underlying code: the fundamental nonlinear biological process can possibly be conceived as the genetic code constructing its own global initial conditions of transmission, "self"-reproduction. It is set by creating and controlling the self-maintaning phenotype, carrying out the task. As to the mediating genes, as noted above, they are only the special configurations of the genetic codes which actually dynamically achieve the very invariance of their constituent codes. In semiotic terms: we have the invariant code words with their highly nonlinear, self-referential, classical sentences of enzyme species in protein synthesis. (This is, of course, a different approach from the above "initial symbol" one.) In other words, they are the genes, built of codes, which nonlinearly, mediatingly *ensure* the invariance of the underlying codes through enzymes and, generally, the phenotype. This very primordial "choice" of the organization of the hierarchy is the reason that evolution acts on the code configuration level, not on the more fundamental abstract-semiotical, classically *interpretable*, in its mechanism highly quantal, individual code *assignment* level.

Also, it should be added that the above considerations remain valid for the vegetation kingdom, too, but the corresponding mechanisms remain much more latent there than in the animal kingdom. In fact, the different vegetation phenotypes also have their own cellular "invariants of motions", ruling the formers, with a different strategy: disregarding exceptions, the strategy is a *direct* utilization of the sunbeam as energy source, therefore there is no need for *gross phenotypic* capability of motion, and

therefore also for secondary (phenotypic nervous system dependent) information processings [27]. What biologically significant is the potential for evolution through the diverse forms of "struggle for life", e.g., to win the (kind of characteristically more passive) competition of having an appropriate sunny growing space or, in this respect, developing different mosaics of leaves for maximal efficiency in an ecological niche, with widely different degree of *activity*.

5.4. Some Preliminary Formal Notions for Future Study

It would be desirable to formalize in future studies the above biological "invariant of motion" concept. We think that the first step towards this goal has been the discovered supersymmetric relation between assigned codons and the corresponding amino acids.

Actually, it can be shown [61,62] that the genetic code vocabulary corresponds to consecutive symmetry breakings of an approximately A(5,0) Lie superalgebra (supersymmetry) with a 64 dimensional irreducible representation (irep), to yield 21 ireps with variable dimensions of members of degenerate codes. The theory has been developed in essence for a code evolutional study. While this might be approximately correct as reflecting actual chemical evolution, we need a representation which expresses the invariance of the developed, *evolutional* genetic code in symmetry restoration, *i.e.*, quantum dynamically. In fact, this is approaching the problem from a perspective of group theory.

Introducing the time inversion operator **F**, in view of the double-stranded DNA, we have,

$$\rho \, (t') \rightarrow \mathbf{F}^{-1} \, \beta_i \, (\mathbf{q}_i) > <_i \, \beta \, (\mathbf{q'}_i) \, (t'_{0,\,in}) \, \mathbf{F} => \alpha_i \, (\mathbf{q}_i) > <^i \, \beta \, (\mathbf{Q}_i') \, (t')$$

$$=> \beta_i \, (\mathbf{q}_i) > <_i \, \beta \, (\mathbf{q'}_i) \, (t'_{fin}) \tag{11}$$

Here $\beta_i >$ is the physical carrier of the codon as quantal nucleotide triplets, while $<^i \beta$ is the abstract-symbolical codon; α is the physical amino acid wavefunction; *in* and *fin* denote initial and final states; t' is the internal cycle-time flow, while $|-\tau|$, the internal time parameter is defined by $t' = |-\tau| - |t|$ with t as an external time reference. This diagonal element of a composite density matrix, $c_{ii} \Psi_i^A \, (\mathbf{q}_i) \Psi^i B \, (\mathbf{Q'}_i)$, this "intra-system" correlation function [46] of the evolved code is *dynamically invariant* under the progressing symmetry restoration and ultimately attained symmetry, both onto-and phylogenetically. The real invariance of the code is thus presumably under the product group $A(5,0)x$ *F*. Thus the fundamental symmetry (ireps) derives from internal symmetry breakings of a A(5,0) Lie superalgebra and also those of a dynamical symmetry (actually, its dynamical restoration). The dynamical symmetry invariants are then, tentatively, the virtual, *assigned* supersymmetric genetic codes in a generalized dynamics progressing along regressive symmetry restoration.

Also, a kind of *affine* description is required by the symmetry restoration dynamics: time reversal of a state evolution can be described by ordinary complex conjugation [3], whereas a *regressive* quantum dynamics, progressing in real-positive time, needs an affine dual description. Both the amino acid "ket" wavefunction ($|\alpha>_i$) and the time-reversed virtual "bra" codon wavefunction ($<\beta^i|$) are then affine basis functions, both of a covariant and a contravariant characteristics. The "biased", controlled material dynamics is a highly constrained one by the proper "bracket" g_{ij}, g^{ij}, g_i^j metric tensor components between basis functions, e.g., $<\beta_i | \beta_j> = g_{ij}$, as subject to the global-virtual constraints. The mathematical formalization also forms the general descriptional frame of the latter (dual dynamics) (see also Section 2.1.).

5.5. Some Suggestions on Possible Experimental Work

According to the suppositions of the above discussions, the most important experimentally available phenomenon might possibly be the global-virtual quantum entanglement relation between (*t*RNA-bound) codons and the corresponding amino acids.

It is, thus, of primary interest, if an evolutional, *in vivo* prepared codon-amino acid complex, a loaded *t*RNA, exhibits such quantum correlations "virtually" (interpreted by us as acting materially *in vacuo*) during spatial separation. To investigate it experimentally, starting from a *t*RNA-amino acyl synthetase-bound, loaded *t*RNA, the complex should be perturbed, e.g., ionized, and detect the electronic structure, charge distribution of the amino acid component *vs.* the electronic structure of the *t*RNA-bound codon in increasing separation. Recombination at the codon-part can be detected by NMR and/or ESR spectroscopy at both systems. If the correlation persists, the measured charge distribution at the distant codon-part effects that of the measurable amino acid-part by its electronic recombination, even in distant divisions.

6. Concluding Remarks

It was shown in this paper that a more natural "selfish-code" concept can be deduced as an alternative to the "selfish-gene" paradigm [1]. This was tentatively achieved by defining the abstract-symbolical genetic code vocabulary as a special elementary biological invariant of the internal/external motion, *i.e.*, of a generalized dynamics.

The well-known observable algorithmical internal dynamics of protein synthesis, in fact, was shown to conform to our virtual-global semiotic symmetry restoration "goal" as a correlative, quantal one-to-one "internal measuremental" chain, realizing a recursive function. It is mediating, unfolding recursively as a translational algorithm the above-lying virtual-global semiotic rules, *i.e.*, the semiotic assignment quantum correlations. The latter appear as "initial symbol" projectors for the translational algorithms. The intracellular invariant of the internal evolutionary quantum dynamics appears to be an entanglement correlation of the "abstract" genetic code with its amino acid, *i.e.*, it is a deeply quantum dynamical feature. This tentative entanglement relation which may have emerged primordially in "mixed" molecular quantum measurements, was introduced on the grounds of the quantum mechanical observation that ordinary measurement device and its object are in such a relation. In this way, the ultimate teleonomy of the dual "abstract" code vocabulary at every organizational level is realized as a nonlinear, *i.e.*, self-referential, generalized dynamics, an implementation by the quantal/classical biological processes. It is, in fact, a material self-maintaining/self-transmissional ("self-distinctioning") process. The underlying intracellular quantal genetical *action* of the code is carried out by evolutional classical distinct organizations, configurations of the codes, *i.e.*, the genetic material and the following phenotype. These do not possess themselves dynamical invariance during evolution.

As we intended to deduce the evolutionary origin of the element of biological choice, "freedom", exhibited by the phenomena of self-maintainance as "struggle for life" and "self"-reproduction, we had to discuss primarily the origin and existence of the genetic assignment rules. Accordingly, we tried to deduce, as the basis of the curiously self-perpetuating phenotype, the underlying quantum dynamics of the code. This was approached by examining the relatively "free" settings of the system's own

permanent local physical (protein synthetizing), and the dual global (semiotic) permanent initial conditions, leading to "self"-reproduction. In fact, ultimately, as symmetry attained, there appear daughter cells as the attained symmetry relation is mapped onto space, recurrently representing globally-virtually the original "mixed" measurement outcome, the invariant genetic assignments.

These chemical evolutionally emerged "free" rules are evolutionally converged at the genetic assignment level, and are effective as the nonlinear controlling basis of the molecular/macroscopic phenotype. From an informational viewpoint, our information measure descends from an ancient, but also recurrent, *unitary symmetry breaking/restoring by quantum measurements.* Along these lines, we proposed that the curious "struggle for life" phenomenon descends, in this context, from the invariance of the converged genetic code vocabulary, *i.e.*, of the assignments.

However, supposing the abstract genetic code vocabulary to be a true "invariant of motion" of the internal/external semiotically controlled quantum/classical generalized dynamics, a more exact mathematical treatment of the abstract assignment is needed in context with its quantum dynamics. Further studies, using group-theoretical methods, which were here considered only very tangentially, are required. Also, we are aware of the highly tentative nature of the conceptual quantal dynamical frame presented. Therefore, careful experimental tests would be required as to the suggested global/local quantal/classical correlations.

Also, while in the ultimate analysis, concerning integrative-, autonomy-"forces", our considerations seem to be in a certain relation to those of Driesch [63], ours differ by taking into account exclusively quantum physical concepts (assignment "quantum entanglemental blueprint" *vs.* "entelechy"; compare with e.g., "cell psychology" [64]).

Conflicts of Interest

The author declares no conflicts of interest.

References

1. Dawkins, R. *The Selfish Gene*, 1st ed.; Freeman & Co.: Oxford, UK, 1976.
2. Darwin, C.R. *The Origin of Species,* 1st ed.; John Murray: London, UK, 1859.
3. Wigner, E.P. Group Theory and its Application to the Quantum Mechanics of Atomic Spectra, Academic Press: New York, NY, USA and London, UK, 1959.
4. Patel, A.D. Towards Understanding the Origin of Genetic Languages. In *Quantum Aspects of Life*; Abbot, D., Davies, P., Pati, A., Eds.; Imperial College Press: London, UK, 2008; Chapter 10, pp. 18–19.
5. Post, E.L. Recursive unsolvability of a problem of Thue. *J. Symb. Logic* **1947**, *12*, 1–11.
6. Pattee, H.H. Laws and Constraints, Symbols and Languages. In *Towards a Theoretical Biology*, 1st ed.; Waddington, C.H., Ed.; Aldine Publishing Company: Chicago, IL, USA, 1972; Volume 4, pp. 248–258.
7. Pattee, H.H. Evolving self-reference: Matter, symbols, and semantic closure. *Commun. Cogn.—Artif. Intell.* **1995**, *12*, 9–27.
8. Pattee, H.H. The Physics of Symbols and the Evolution of Semiotic Controls. Paper presented at the Workshop on Control Mechanisms for Control Systems: Issues of Measurement and Semiotic

Analysis, Las Cruces, NM, USA, 8–12 December 1996; Addison-Wesley: Redwood City, CA, USA, 1997.

9. McFadden, J. *Quantum Evolution*; Harper and Collins: London, UK, 2000.

10. Donald, M.J. A review of Johnjoe McFadden's book "Quantum Evolution". **2001**, arXiv: quant-ph/0101019.

11. Matsuno, K. *Protobiology: Physical Basis of Biology*; CRC Press: Boca Raton, FL, USA, 1989.

12. Pattee, H.H. The Vital Statistics of Quantum Dynamics. In *Irreversible Thermodynamics and the Origin of Life*, 1st ed.; Oster, G.F., Silver, I.L., Tobias, C.A., Eds.; Gordon and Breach Science Publishers: New York, NY, USA, 1974; pp. 33–43.

13. Bohr, N. *Atomic Theory and the Description of Nature*; Cambridge University Press: London, UK, 1934.

14. Conrad, M. Physics and biology: Towards a unified model. *Appl. Math. Comp.* **1989**, *32*, 75–102.

15. Conrad, M. The fluctuon model of force, life and computation: a constructive analysis. *Appl. Math. Comp.* **1993**, *56*, 208–259.

16. Balázs, A. The ontological roots of human science: The message of evolution—the physics of freedom (choice). *World Fut*. **2007**, *63*, 568–583.

17. Pattee, H.H. Can Life Explain Quantum Mechanics? In *Quantum Theory and Beyond*; Bastin, T., Ed.; Cambridge University Press: Cambridge, UK, 1971; pp. 307–319.

18. Belinfante, F. *Measurement and Time Reversal in Objective Quantum Theory*, 1st ed.; Pergamon Press Ltd.: Oxford, UK, 1975.

19. Neumann, J. *Mathematical Foundations of Quantum Mechanics*, Princeton University Press: Princeton, NJ, USA, 1955.

20. Searls, D.B. Formal Grammars for Intermolecular Structure. In Proceedings of the First International IEEE Symposium on Intelligence in Neural and Biological Systems, Herndon, VA, USA, May 1995; IEEE Computer Society Press: Los Alamos, NM, USA; pp. 30–37.

21. Searls, D.B. Linguistic approaches to biological sequencies. *Comput. Appl. Biosci.* **1997**, *13*, 333–344.

22. Patel, A.D. Quantum algorithms and the genetic code. *Pramana* **2001**, *56*, 367–381.

23. Zurek, W.H. Relative states and the environment: Einselection, envariance, quantum Darwinism and the existential interpretation. **2008**, arXiv: 0707.2832v1.

24. Pattee, H.H. How does a molecule become a message? *Develop. Biol. Suppl.* **1970**, *3*, 1–16.

25. Armus, H.L.; Amber, M.; Jellison, J. Discrimination learning in Paramecia (*P. Caudatum*). *Psychol. Rec.* **2006**, *56*, 489–498.

26. Balázs, A. On some evolutionary aspects of the mind-matter problem. *Mind & Matter* **2013**, under review.

27. Asano, M.; Basieva, I.; Khrennikov, A.; Ohya, M.; Tanaka, Y.; Yamato, I. Quantum-like model for the adaptive dynamics of the genetic regulation of E. coli's metabolism of glucose/lactose. *Syst. Synth. Biol.* **2012**, *6*, 1−7.

28. Asano, M.; Basieva, I.; Khrennikov, A.; Ohya, M.; Tanaka, Y.; Yamato, I. Towards modeling of epigenetic evolution with the aid of theory of open quantum systems. *AIP Conf. Proc.* **2012**, *1508*, 75−78.

29. Stapp, H.P. *Mind, Matter and Quantum Mechanics*; Springer: Berlin, Germany, 1993.

30. Wigner, E.P. Remarks on the Mind-Body Question. In *The Scientist Speculates*; Good, I.J., Ed.; Heinemann: London, UK, 1961; pp. 284–302.

31. Balázs, A. On the physics of the symbol-matter problem in biological systems and the origin of life: Affine Hilbert spaces model of the robustness of the internal quantum dynamics of biological systems. *BioSystems* **2003**, *70*, 43–54.

32. Prigogine, I. Symmetry Breaking Chemical Instabilities. In *Irreversible Thermodynamics and the Origin of Life*, 1st ed.; Oster, G.F., Silver, I.L., Tobias, C.A., Eds.; Gordon and Breach Science Publishers: New York, NY, USA, 1974; pp. 11–24.

33. Nicolis, G.; Prigogine, I. *Self-Organization in Non-Equilibrium Systems*; Wiley: New York, NY, USA, 1977.

34. Kauffman, S.A. *The Origins of Order*, 1st ed.; Oxford University Press: Oxford, UK, 1993; Part II.

35. Primas, H. *Chemistry, Quantum Mechanics and Reductionism*, 1st ed; Springer: Berlin, Germany and New York, NY, USA, 1981.

36. Joyce, G.F.; Orgel, L.E. Progress toward Understanding the Origin of the RNA World. In *The RNA World*, 3rd ed.; Gesteland, R.F., Cech, T., Atkins, J.F., Eds.; Cold Spring Harbor Laboratory Press: Cold Spring Harbor, NY, USA, 2006; pp. 23–56.

37. Eigen, M.; Chuster, P. *The Hypercycle: A Principle of Natural Self-Organization*; Springer: Berlin, Germany and New York, NY, USA, 1979.

38. Dyson, F. *Origins of Life*, 1st ed.; Cambridge University Press: Cambridge, UK, 1999.

39. Woese, C.R. *The Genetic Code*, 1st ed.; Harper & Row: New York, NY, USA, 1967.

40. Crick, F.H.C. The origin of the genetic code. *J. Mol. Biol.* **1968**, *38*, 367–379.

41. Pattee, H.H. Physical Basis and Origin of Hierarchical Control. In *Hierarchy Theory*; Pattee, H.H., Ed.; Braziller: New York, NY, USA, 1973; Chapter 4.

42. Elitzur, A.C.; Cohen, E. The Retrocausal Nature of Quantum Measurement Revealed by Partial and Weak Measurement. In *Quantum Retrocausation: Theory and Experiment*; Sheehan, D.P., Ed.; Melwille: New York, NY, USA, 2011; pp. 120–131.

43. Gunji, Y.-P. Global logic resulting from disequilibration process. *BioSystems* **1995**, *35*, 33–62.

44. Pattee, H.H. The complementarity principle and the origin of macromolecular information. *BioSystems* **1979**, *11*, 217–226.

45. Man'ko, O.V.; Man'ko, V.I. Classical mechanics is not the $h{\rightarrow}0$ limit of quantum mechanics. **2004**, arXiv: quant-ph/0407183.

46. Elze, H.-T.; Gambarotta, G.; Vallone, F. Path integral for classical dynamics, entanglement, and Jaynes-Cummings model at the quantum-classical divide. *Int. J. Quantum Inf.* **2011**, *9*, 203–224.

47. Al-Qasimi, A.; James, D.F.V. A comparison of the attempts of quantum discord and quantum entanglement to capture quantum correlations. **2010**, arXiv: 1007.1814v1.

48. Bohr, N. Essays 1958–1962 on Atomic Physics and Human Knowledge; Wiley: New York, NY, USA, 1963.

49. Peirce, C.S. Division of Signs. In *Collected Papers* II.; Harvard University Press: Cambridge, MA, USA, 1932; pp. 134–173.

50. Gernert, D. Incomplete knowledge and the chances of a constructive mastering. *World Fut.* **2004**, *60*, 547–565.

51. Sharov, A.A. From cybernetics to semiotics in biology. *Semiotica* **1998**, *120*, 403–419.

52. Witzany, G. From the "Logic of the Molecular Syntax" to Molecular Pragmatism. In *Evolution and Cognition*; Vienna University Press: Vienna, Austria, 1995; Volume 1 (No 2), pp. 148–168.

53. Chomsky, N. *Syntactic Structures*, 1st ed.; Mouton, The Hague: Berlin, Germany, 1957.

54. Chomsky, N. *Aspects of the Theory of Syntax*, 1st ed.; MIT Press: Cambridge, MA, USA, 1965.

55. Rosen, R. *Life Itself*; Columbia University Press: New York, NY, USA, 1991.

56. Yockey, H.P. *Information Theory, Evolution, and the Origin of Life*; Cambridge University Press: Cambridge, UK and New York, NY, USA, 2005.

57. Maynard Smith, J.; Szathmáry, E. *The Major Transitions in Evolution*; Oxford University Press: Oxford, UK, 1995.

58. Wetzel, R. Evolution of the aminoacyl-*t*RNA synthetases and the origin of the genetic code. *J. Mol. Evol.* **1995**, *40*, 545–550.

59. Zeleny, M. *Autopoiesis: A Theory of Living Organization*; North-Holland: New York, NY, USA, 1981.

60. Popa, R. Between Necessity and Probability: Searching for the Definition and Origin of Life, 1st ed.; Springer: Berlin-Heidelberg, Germany, 2004; Chapter 2.

61. Bashford, J.D.; Tsohantjis, I.; Jarvis, P.D. Codon and nucleotide assignments in a supersymmetric model of the genetic code. *Phys. Lett. A.* **1997**, *233*, 481–488.

62. Bashford, J.D.; Tsohantjis, I.; Jarvis, P.D. A supersymmetric model for the evolution of the genetic code. *Proc. Nat. Acad. Sci. USA* **1998**, *95*, 987–992.

63. Driesch, H. *The Science and Philosophy of the Organism*, 2nd ed.; A & C Black, Ltd.: London, UK, 1929; Section B, Parts I–III.

64. Pattee, H.H. Cell psychology: An evolutional approach to the symbol-matter problem. *Cogn. Brain Theory* **1982**, *5*, 325–341.