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# What does a molecule want? The myth of the self-replicating molecule (comments on the "selfish-gene" paradigm)

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**Abstract**

The non-equilibrium statistical mechanical autocatalytic theory, underlying the "selfish-gene" paradigm, is shown to be at several points insufficient and contradictory for the description of observed facts of biological systems. We analyze at some length these deficiencies as (1) statistical versus individual non-linear self-constraints, (2) the continuous versus discrete cause–effect evolutional transition, and (3) the nature of the emerging aim-directed biological systems. Concerning the latter, it is shown that it can only be described with reference to the origin of the genetic code, which cannot be accounted for by the *continuous evolution* of non-equilibrium statistical mechanical systems. We point out that these deficiencies might be covered by alternative (quantum) theoretical considerations. The theory of evolution according to which may have lead to aim-directedness in the primordeal times in a more consistent way, concerning *both* phenotype *and* genotype. The specific physical model adopted is an affine Hilbert spaces scheme, with a naturally emerging *internal dynamics of measurement*, monitored *internally* by (time-inversion) symmetry restoration. In this context, the physical relation of internal molecular symbolism (semiosis) and internal quantum mechanics is discussed.


*Keywords:* Autocatalysis; Cause–effect relations; Goal-directed phenotype; Affine Hilbert spaces; Internal dynamics of measurement

## 1. Introduction

Force (or energy-driven process) in physics is always *causal* in its root (dynamics) in the final analysis, the variational

$$\delta(Et) = 0 \tag{1}$$

equation (where $E$ is energy and $t$ is time) can, in principle, be always transformed to such a causal picture, characterized by the equations in mechanics

$$\dot{x}_i = f(x_1, \ldots, x_i, \ldots, x_N, t) \tag{2}$$

where $x_i$ is the coordinate of the $i$th particle, and this holds true, in a sense, even for quantum mechanics, where we have, instead of (2), the Schrödinger equation (for dynamic *probabilities*).

The "canonical" version of the origin of life (e.g. Maynard-Smith and Szathmáry, 1995)

(1) Begins with an ancient nucleic acid (presumably RNA) as a "self-replicating" molecule (through template-directed pairs) which we call here "naked" RNA autocatalysis.
(2) The second step is postulated for the latter, by this *causal* physico-chemical mechanism or the other (quantum *dynamics*), to ("*somehow*") "learn" to code (so produce) ancient proto-enzymes which, in turn, catalyze their replication.
(3) As an (even now dominating) ultimate step would then be the whole biological organism being

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similarly "coded" (produced) to play the role of a phenotypic "machine" for the continuation of producing proper conditions for the survival and *self-replication* of the genes (i.e. of nucleic acids).

This line of thought has been by long ago criticized by Commoner (1962) on the claim of "self"-reproduction (and this is our point of departure here, too).

Extension of the general view was provided (e.g. by Dawkins, 1976), in fact sharpening it to a paradigm, shared by now by numerous authors. According to this "selfish-gene" paradigm:

- The ultimate "aim" of the gene is to replicate itself.
- Living (biological) systems (the phenotype) are "survival-machines" of the genes, serving the purpose.

The underlying, tacitly or explicitly assumed physical model is *autocatalysis in the strict sense* (even though the conceived relation of the "replicator" concept to strict autocatalytic physico-chemical theory is more often than not fortitutous and loose).

Thus, paradigmatically:

(1) There is no *in principle* difference from "naked" RNA autocatalysis through coded catalytic "phenotypic" enzyme systems to biological systems with a complex phenotype.
(2) Hence, physical cause–effect relations (autocatalysis of RNAs) are *continuous* in evolution from inanimate template-directed autonomous self-replication of naked RNAs to biological phenotype.
(3) This way, somewhat hazyly, RNA (DNA) "wants" to replicate, the phenotype is a blind machine serving this purpose.

However, closer investigation of the chemical (physical-mechanical) basis of the supposed autocatalysis versus biological systems (the living state), reveals some innocent-looking problems which, when followed up to their very roots, cast some doubt on this paradigm. It is perhaps timely, in view of the rapid development of modern quantum biology, to devote a second-thought to this basic supposition, originated in the 1970s.

In this respect, concepts like statistical—individual "aim"—(optimization goal) relations versus physical cause–effect relations are examined below, and it is hopefully shown that there is a sharp distinction (difference) between "naked" RNA autocatalysis and genetic code-directed phenotype (most elementarily copying enzymes) upbuilding, and that only the latter is capable for "aim-directed" ("information-processing") behavior.

In doing so, we must show that

(1) the coming about of the genetic code cannot be accounted for by continuous evolution of physical cause–effect relations (even those of quantum *dynamic*);
(2) the coming about of the code was a special physical event, encompassing in essence *both* ancient RNAs *and* proto-proteins;
(3) so the biological system's behavior in general depends as much on the phenotype as on the genotype (in a *joint way* genotypically–phenotypically *reversing* the primordeal cause–effect relations);
(4) in this way, "aim-directed" ("optimization dynamic-algorithmic") behavior (Balázs, 2003) is a *genotypic–phenotypic combined* behavior, so the selfish-gene concept, *as autocatalysis of nucleic acids* (in the strict sense of a physical–chemical theory), is invalidated by the available facts.

## 2. Autocatalysis versus internal macromolecular dynamics

The "selfish-gene" paradigm, thus, is an extreme but logical derivative of the biological autocatalytic research program, as it has been laid down most explicitly by Prigogine (e.g. Nicolis and Prigogine, 1977) Eigen and Schuster (1977), Gánti (1979). This theory is introduced for both the origin and essence of the living state, supposedly providing a sufficiently rich mathematical-physical structure to encompass evolutional emergence of more and more developed physical structures/processes, still under the same organizational statistical physical-mechanical (autocatalytic) principle.

The Prigogine–Eigen–Gánti version of the theory of autocatalysis, as applied for biochemical systems, supposes coupled autocatalytic cycles of RNAs (DNAs) and proteins. The supersystem is called by Eigen the "Hypercycle" and by Gánti the "Chemoton" (later in evolution the "Bioton"). (Prigogine had laid down the basis of the underlying appropriate far

from equilibrium non-linear thermodynamics, not definitely for the purpose.) This kind of "downward causation" (Anderson et al., 2000) of probabilistic phenotypic/genotypic connected networks as the origins of (biological) "order" has been summarized, e.g. by Kauffman (1993).

More closely, it is supposed that each sub-cycle is submitted to the common underlying laws of non-equilibrium thermodynamics. According to the latter, elementarily we have (Haken, 1977) the autocatalytic rate equation, with one autocatalytic molecular species,

$$\mathrm{A} + \mathrm{X} \underset{k_1'}{\overset{k_1}{\rightleftarrows}} 2\mathrm{X} \qquad \mathrm{B} + \mathrm{X} \underset{k_2'}{\overset{k_2}{\rightleftarrows}} \mathrm{C} \tag{3}$$

where A, B, C, X are molecules, and $k_1, k_1', k_2, k_2'$ are rate constants.

With denoting the corresponding concentrations

$[\mathrm{A}] \to a$

$[\mathrm{B}] \to b$

$[\mathrm{C}] \to c$

$[\mathrm{X}] \to n$

and

$k_1' = 1$

$k_1 a = 1$

$k_2 b = \beta$

$k_2' c = \gamma$

we have the rate equation for the concentration of the autocatalytic species $X$

$$\dot{n} = (1-\beta)n - n^2 + \gamma = \phi(n) \tag{4}$$

Generally, either with or without diffusion, we have then the coupled equations with the type of relations

$$\dot{n}_i \sim \phi(n_1, \ldots, n_i, \ldots, n_N) \tag{5}$$

where $\phi(n_1, \ldots, n_i, \ldots, n_N)$ is a non-linear (polynomial) function of the concentrations of the $X_i(n_i)$s, expressing that the rate equations depend on a non-linear "potential" $V(n_1, \ldots, n_i, \ldots, n_N)$,

$$\frac{\partial V(n_1, \ldots, n_i, \ldots, n_N)}{\partial n_i} = -\phi(n_i)$$

With searching for far from equilibrium steady-state ($\dot{n}_i = 0$) conditions, or solving generally for $n_i(t)$ in a function of a control parameter (such as rates of concentrations), the concentrations may bifurcate, have stability/instability and chaotic regions, oscillate in space and time, etc. according to the form of the "potential." The usual description then follows as co-operation/competition of these chemical cycles.

However, these are *macroscopic-statistical* considerations. Living matter, as it is generally acknowledged today, is characterized by *microscopic individual-dynamic* self-production, non-linearity, concerning *macromolecules*.

Cause–effect relations are statistical in the former theory, so the rate Eq. (5) corresponds only to a *statistical constraint* on $n_i$. This is even more evident in the (more involved) stochastic formulation of the reaction equations, where we have the *probability* of the *number* of the "birth" and "death" of molecules. Transcription into a microscopic (quantum mechanical) formalism *of these fundamental suppositions* does not improve much the situation, as we have then, *according to the premises of the analysis*, no better than the time-dependent *quantal* averages (expressible by the proper time-dependent Green functions). This holds true, in essence, for *any* coupled autocatalytic hypercycle ("supersystem").

RNA(/DNA)-protein non-linearity, as indirect self-reference of RNAs (DNAs) *mediated by the coded protein molecules* (Balázs, 2003), is constraining their own production on an *individual-dynamical* basis. As we will see, this is a fundamental difference in relation to the evolution of physical cause–effect relations (non-linearity).

Autocatalytic non-linearity is also *mediated* (by the product molecules) as "*self-reference*," but *only in a statistical sense*. However, large a DNA molecule might be, it is still an individual molecule, whereas without macroscopic concentrations, the above type of analysis breaks down. Mathematically, large-amplitude "fluctuations," *in the stability region*, will become the rule, rather than there occurring only small-amplitude perturbations, as $n_i(\boldsymbol{r} = 0, t = 0) \to 0$ (here $\boldsymbol{r}$ equals the space coordinate and $t$ is time), and this spoils the analysis.

Thus, as we have no *macroscopic statistics* in RNA(/DNA)-controlled protein production, we have no "autocatalysis" in a *strict sense*. If we had, even the

question why only *one copy* of the gene is produced in the time- (cell-) cycle, instead of a multiple amount, could not be answered. (In fact, it would require the ad hoc additional supposition that (elementarily) the cell cycle (division) equals the *autocatalytic duplication* of RNA(/DNA). This would be, in fact, far from being a trivial supposition, as is actually made (e.g. by Gánti, 1979).)

This, however, is not all.

Space–time initial conditions $n_i(\boldsymbol{r} = 0, t = 0)$ are in autocatalysis *statistically averaged* for reactant molecules (Pattee, 2000), whereas they are individually— *dynamically chosen* (determined) in the RNA (/DNA)-protein system, the formers (RNA(/DNA)) exerting *semiotic controls* on the latters, not derivable directly from the underlying quantum dynamics (Pattee, 1995, 1997). Autocatalysis is a statistical simple physical cause–effect relation, whereas RNA(/DNA)-protein production *is not*, and *cannot be understood without some investigation concerning its origin rooted in the origin of the genetic code*, as the primary evolutional semiotic control subsystem (Pattee, 1997).

## 3. Alternative approach to the problem: the physical "aim" ("goal") of life

As we have shown elsewhere (Balázs, 2003), it is *probable* that codeless pure chemical evolution lead to the ("naked") autocatalysis of RNA-type molecules, but that it is equally probable that there was a *sharp border* between pre-code (chemical) and post-code (biological) systems. That is, evolution was most probably, *not continuous* between chemical autocatalysis and code-directed protein production. This concerns, first of all, the evolution of physical cause–effect relations.

If external physical–chemical conditions (e.g. matching of diffusion and internal rate constants, so emphasized by Prigogine (e.g. Prigogine, 1974)) are insufficient, autocatalytic activity ceises. Biological systems, on the other hand, *actively solve*, in poor external conditions, *against* external cause–effect relations (for instance) their metabolic functions, by proceeding *against* concentration gradients, as it can be observed already with unicellulars (e.g. Kung, 1979). Observations of this kind (being even more evident higher up on the evolutional ladder) point to an *internal optimization goal relation* which, however, can be traced back to the origin of the genetic code, the latter *decoupling* the pre-code physical cause–effect relations. In fact, the *physical necessity* of the unity of serial initial conditions and physical law (the physical cause–effect relations) of the controlled subsystems are *liberated*, and control is exerted as *choice* (of initial conditions) (Pattee, 1995, 1997; Balázs, 2003, Philosophy of Biology, to be published). This transition from inert physical cause–effect relations to internal goal-relations must have been, necessarily, a discrete one, not a continuous evolution of autocatalysis, and could evolve solely on an individual-quantum dynamical basis. (Usual theories of the coming about of the genetic code generally acknowledge this latter circumstance, *in itself running in the face of strict statistical mechanical autocatalytic theory*, yet, the supposed mechanisms still fall short of the requirement of evolving semiotic (informational) controls over initial conditions of the phenotype.)

We have put forward a general scheme of *one gross qualitative* possible mechanism elsewhere (Balázs, 2003).

The origin of the code may have been an internal quantum mechanical self-measuremental event during chemical evolution, between pre-biological proto-" enzymes" ("object") and their *dynamical effect*, pre-biological (tRNA-like) RNA molecules ("measuremental records," carrying *classical symbols*, the semantic codes).

This supposed self-measurement may have resulted in an internal (observerless, "endophysical," Primas, 1992, 1993, 1994) *split* in the system into measured "object" and "measuremental molecular records," with the *dynamical* time-inversion symmetry *broken*, as it is generally known concerning quantum measurements (e.g. Bohm, 1951; Belinfante, 1975). Simple physical (chemical evolutional, quantum dynamical) cause–effect relations were then internally split up. As we have shown (Balázs, 2003), there probably arised an internal *reversal of cause–effect relations* in order to restore the time-inversion symmetry, reversing the internal dynamical cause–effect relations, most elementarily the reversal of the protein → RNA cause–effect relation to RNA → protein, i.e. reversing the relation of ancient RNAs being catalyzed by proto-enzymes, to *producing proteins* by the formers.

(It was this reversed dynamical-algorithmic time process which gave rise later in evolution to generally the "phenotype.")

This internal time process *for* restoration of time-inversion symmetry, amounting to a "molecular drive," *is* the "internal goal-relation," and is characteristic *only* of biological systems. It could arise only, as its origin, dependent on *both* proto-protein (enzymes) *and* ancient RNA—*as a global quantum mechanical self-measurement* where "apparatus + record" and "object" played equally important roles, and was as unresolvable as quantum measurement in general is. As the manifestation of this internal goal-relation, a "*phenotype*" (such as copying enzymes) is, (*and has ever been*), a priori indispensable. *This irreducible coupling of genotype and phenotype is the paradigmatical difference between our analysis and autocatalytic theory.*

No evolution of a "naked" RNA autocatalysis could possible lead to these systems, as it requires a *splitting-up* and *reversal* of pre-biological physical–chemical dynamical cause–effect relations. This reversal thus naturally accounts for the above-stated "liberation" (internal choice) of initial conditions, elementarily of those of protein molecules by RNAs, autonomously determining them by their internal measuremental (semiotic) control *function*, and *this condition of discontinuous evolution cannot be deduced from autocatalysis*. The ability of successively determining the internal initial conditions of the controlled (macro-) molecules in an internal quantum measuremental chain, that is, the difference between *statistical* non-linearity and the *dynamical* cause–effect *split* and *reversal*, had to be present from the earliest biological systems, i.e. the origin of the genetic code (Balázs, in preparation-a). Thus, there is no continuous physical transition even from (inert) quantum scattering (dynamical interaction) between the (premeval chemical) system and environmental "food molecules" (Wigner, 1961), to "selfish-genes." Not only the theorem holds that there is no in principle route from dynamical description to a statistical one, but similarly, there is no route back from a statistical one to a (constrained) microdynamical description.

In this way, the crucial step, the *discontinuous* transition from "naked" template-dependent autocatalysis to *indirect* (coded phenotypic) self-reference cannot be in principle accounted for by the usual theory.

In our scheme, on the other hand, the internal goal of time-inversion symmetry restoration leads to the fixed point of an algorithmic quantum mechanical time process as duplication (as the ultimate time symmetry *mapped onto space* Balázs, 2003). *Thus, we also have the fundamental "aim of replication," but without the problems raised by usual autocatalytic ("self-replication") theory.* This "aim of replication" is characteristic jointly of the phenotype and genotype: this essential life process encompasses both subsystems and explains their coupled nature as elementary division (the cell-cycle).

Biological systems are of a *special* (*self-observing*) *exophysical* nature (entailing itself as observer), yet originating inherently from an *observerless endophysical* existence (Primas, 1992, 1993, 1994), and this is the underlying reason of their having a simultaneous backwards goal-directed time process (time-inversion symmetry restoration), following from a primordeal quantum mechanical self-measurement.

*Biological phenotype* is truly an optimizing information-processing, goal-directed "machine," which *postpones* duplication in order to protect and sustain it in reaching optimum conditions, originally evolutionally dependent on the genotype.

This process, by its very nature, however, has little to do with autocatalysis: it does it by controlling ("liberating") internal/external dynamical initial conditions (or, in other words, forming internal quantum mechanical measuremental chains), additional to (*above* the) underlying quantum dynamics (Balázs, 2003; Philosophy of Biology, to be published). This is the essence of *biological* (*genotypic–phenotypic*) *information*: optimum searching by liberating internal/external initial conditions *is* what we call purposeful behavior or "will." Neither subsystem (RNAs or proteins) possesses any sense of "will" without the other, either onto or phylogenetically.

In this way, "will" is an attribute of the indirect, mediated self-referential optimum searching genotype–phenotype *jointly*, having its roots in the very origin of the system (as quantum mechanical self-measurement, depending on both "object" and "record"). In physical terms: it is the attribute of the split and reversed internal cause–effect relations, the (regressive) *time-reversal* (symmetry restoring quantum mechanical internal/external measuremental) *process*.

Thus, the genetic code *does not function autocatalytically, and, presumably, did not come about that way*. Subsequent robust evolvability was due to the integrative local-global symbolic (semiotic control) process, having arised in the primordeal global internal measuremental event.

The involved broken cause–effect relations, corresponding to a splitting between dynamical law and its initial conditions (or ability of undergoing "semiotic displacement," Pattee, 1997) might be, in a wider sense, considered as being "wanted" to be restored (see also Matsuno's and Conrad's "equilibrating" and "restoration force" quantal theory Matsuno, 1989; Conrad, 1989, 1993); however, this was, and ever since is, dependent on both genotypic–phenotypic systems.

A molecule (such as DNA) in itself does not "want" anything; *autocatalytic* "self-reproduction," as applied for biological systems, appear to be either a convenient physical *allegory* or, taken literally, a pure *myth*.

## 4. Attempt for a solution: the affine Hilbert spaces model of an information-driven dynamics

So far we have dealt with some well-recognized qualitative aspects of the problem, presented from the special point of view of continuous–discrete, causal–acausal development (evolution). Below we try to put forth a more coherent and pointed scheme as a possible physical way out of the problems discussed above. In this connection, the semiotic aspect versus ordinary quantum dynamics, proposed above, active inside biological systems, needs a more deeper consideration. The latter, in fact, is closely related to a proposed special quasiclassical internal dynamics.

### 4.1. Molecular symbolism

First we note that there is a third possibility characterizing a dynamical system, besides macroscopic classical and detailed quantum mechanical, that of *quasi classicality*, which conceptually lies between the two if defined properly, and the evolutional emergence of a *molecular symbolism* is approached from this quasiclassical molecular *measuremental* (projection) view (with reference to the only known physical process producing symbols (records)), as *quantum specificity* (*function*). Our definition descands from the relaxed (with *quasi* classical *internal* molecular measuremental devices) Copenhagen interpretation of quantum mechanics of *internal measuremental constraints* (Pattee, 1995, 1997). We thus define ("second order") constraining (functional symbolic) relations on the ordinary quantal uncertainty equations, necessary for the right introduction of the *internalized dynamics of measurement*, discussed below. It is important to emphasize here that the ultimate (*local*) "quasiclassicality," the symbolic *aspect* of biological macromolecules, originating from *previous* internal measuremental interactions in a serial way, dating back to the origin of the genetic code, is understood in the sense that the (locally collective, evolutionally contextual) coordinate distributions and the conjugate momenta of their *logical units*, having evolved *above* their pure quantal structure satisfy, for both nuclei and electrons,

$$\Delta Q_i(\Delta P_i) \sim h_{ii} = h \to 0.$$

These quasiclassical (symbolic) observables are the variables of a corresponding *symbolic* wavefunctions of biological macromolecules, forming their *additional* symbolic degrees of freedom. (An informational macromolecule, such as $RNA^{store}$ or the evidently later developed DNA/mRNA system can, in principle, subdivided in a unique way into such quasiclassical symbolic (logical) local units (e.g. codons and amino acid residues).) The closer meaning of $\Delta Q_i(\Delta P_i)$ in connection with internal quantal information is briefly discussed in Balázs (in preparation-a). For the present, suffice to state that they are defined as evolutionally contextual, locally collective coordinates and momenta for the logical physical units, with $\Delta$ referring to uncertainty *within* quasiclassicality (substitutions, permutations, etc. of atoms and intramolecular groups) in the logical units. These considerations point to the fact that the special physical relations, i.e. the "second order" (*constraining*, symbolic-controlling) relations, presented below, must have come about by the internal split to quantal "object" and classical record-conveying quasiclassical structures ("apparatuses"), exerting internal constraints in the original global internal measurement. "First order uncertainty" places a constraint on *certainty*; "second order" (symbolic *functional relation*), in a similar irreducible way, places a constraint on *uncertainty*. This introduction of "internal information" (symbolic constraint, internal function) *defines struc-*

*ture internally to an extent beyond that permitted by the external uncertainty relations*. External uncertainty relations are *internally constrained* and express complementarity of the biologically fixed internal measuremental (informational) coupling of internal "object" and "apparatus" in the dynamics of internal measurement (function) *and* the external accessibility of the detailed (quantal) nature (as opposed to gross classicality) of the components (structure).

Tentatively, the result of this derivation can be accomplished, in formal terms, by introducing the irreducible coupling of *two* Planck's action constants $h$, (one for the "object," one for its internal "measuremental device") instead of one (characteristic of the arbitrary object-apparatus separability of external description) in the internal measuremental situation, corresponding to a special form of the Bohr–Elsasser Generalized Complementarity relation (Bohr, 1934, 1958; Elsasser, 1962, 1969). In a compact form,

$$(\Delta q_j - \Delta Q_i)(\Delta p_j - \Delta P_i) \sim (h - h_{ii}) + (h - h_{jj}) - 2h_{ij} = 0$$

i.e.

$$h_{ii} + h_{jj} = 2h - 2h_{ij} < 2h \tag{6}$$

Here $h_{ij}$ is a coupling action constant, $h_{ii}$ is defined above, and

$$\Delta Q_i \Delta p_j = \Delta q_j \Delta P_i \sim h_{ij} < h$$

$$\Delta q_j \Delta p_j = h \to 0$$

Here $i$ and $j$ are the indices of the coordinates and momenta of the local units of the molecular "measuremental device" and its pure quantal "object." The first equation expresses the gross (external) conservation of the integrity of Planck's action constant $h$ in the internal measuremental interaction (functional symbolic constraint) and the last relation follows from the measuremental constraint exerted by the quasiclassical "molecular measuremental device," the symbolic wavefunction side of each biological macromolecule on the subsequent "molecular object." (This notation is a shorthand form of the description of the coupling of many corresponding action cells in phase space.) $h_{ii}$ not necessarily equals $h_{jj}$, corresponding to the concept of the *degree of quantal specificity* of internal information (the measuremental interaction). (The $q_j$'s and $p_j$'s are the corresponding quantal observables of the "object," controlled quantum system.)

The two (symbolical-controlling $\leftrightarrow$ quantum mechanical, controlled) subsystems are, then, measurementally (functionally) in a stable (robust) way *coupled*, as expressed by the coupling action constants $h_{ij}$, with a measuremental *disentanglement* between them (e.g. Primas, 1981), however. Usual *external* complementarity now is between the *individual action cells* of the composite system *and*their *coupling action constants*. Constrained quantum probabilities (dynamics) ($h_{ii}, h_{jj} \to 0$) correspond to large symbolic coupling (control) ($2h_{ij} \to 2h$), while more definite (constraint-free) quantum dynamics ($h_{ii}, h_{jj} \to h$) corresponds to weak symbolic (functional) control ($2h_{ij} \to 0$).

Physics has successfully used the $h \to 0$ condition for the description of approaching classical behavior in the *external* context as *above detailed quantal* behavior. In our internal scheme, there are two (usually different degrees of) *internal* quasiclassicality with a different meaning: it describes classical behavior *beyond* quantum probabilities. *This leads to semiotically-controlled autonomy and purposeful action, where, however, the quantal details of the structure are accordingly externally simultaneously less well specified. Internal* quantum specificity (quasiclassicality) can only be observed in terms of *external* quasiclassicality (loss of quantal details, compare Pattee, 1973).

By inspection of Eq. (6) it follows in a simple derivation, that

$$\Delta q_j = C_{ji} \Delta Q_i \tag{7}$$

where $C_{ji}$ is a dimensionless constant characterizing the specific internal measuremental interaction, which is to be expected at an informational-symbolic constraint.

Thus, we associate the symbolic (internal "measuremental device," controlling) aspect of a biological macromolecule with its proper $h \to 0$ *quasiclassical* "bra" wavefunction, preformed to be in a *duality relation* (constraining specific overlap) with the ordinary quantal ("ket") wavefunction aspect of *another* macromolecule. It is easy to see (Pattee, 1971) that the symbolic wavefunction originally characterizes an ancient molecular record of the original (internal) quantum measurement (the genetic code).

In general terms, the essence of this internal dynamic symbolism can be properly characterized in the Post sense ("symbol is a time process mapped onto space," Post, 1965): *the pre-code primordeal quantum statistical time process was dynamically mapped onto space* by the first natural internal measuremental symbol (the genetic code), possibly by a distinctedly (dynamically) self-constrained (non-linear) amino acid residue—mesoscopic RNA interaction time evolution, emerging from the mesoscopic-statistical self-constrained system. The newly formed time-invariant space (molecular record) structure was the internal classical symbol of its *own* individual-dynamical *past* as a spatial macromolecular *effect* of the past quantum dynamic chemical evolutional proto-enzymatic process (i.e. its quantum dynamical *cause*). The singular splitting of the total system into two *space*-complementing subsystems (e.g. Shimizu, 1982, 1983) with quantum disentanglement between them is, in the model adopted, *space representation* of the singular *time*-complementation, i.e. the splitting-up of the two opposite time directions, *ordered to each other*. Subsequently, then, the original self-measuremental classical symbol, in turn, acts reversedly as *classical cause* (setting initial conditions) in the subsequent discrete, reversed dynamics (as space-mapped internal time-inversion process, i.e. through space-like *classical* internal measuremental *constraints* on space-like "objects," in a serial way). It appears then, that in accordance with the above Post-definition of symbol, *the genetic code is the space-like classical constraining symbol of time reversal*, conveyed by a quasiclassical (macro-) molecular structure.

The fact that we have jointly the basic and dual state spaces of subsystem A (proteins) and of B (RNA) ordered to each other, representing the object system and its symbolic representation is, within the general formalism of quantum mechanics (i.e. the conjugate spaces), in accordance with the coexistence of the two *inequivalent* time evolutions (corresponding to *affine Hilbert spaces*), of which the spontaneously arising inner, backwards process dominates the external, forward one (see below).

### 4.2. The internal dynamics of measurement

"Dynamics of measurement" is a relatively novel notion in theoretical physics. Its basic concept is (Altenmuller and Schenzle, 1993) the "inverse quantum Zeno effect." It states that by frequently following external measurements (of spatial coordinates) on the system, we can orient a *quasiclassical* "trajectory" of the system into any arbitrarily chosen direction, eventually even parallizing its time evolution. In our internal case, we have the internal spontaneous time-inversion symmetry restoration, along the cyclic internal time parameter $t'$ (defined below), monitoring the direction of the "trajectory." (Note again that some kind of symmetry restoration is generally introduced in related internal measuremental schemes, too, (e.g. Matsuno, 1989; Conrad, 1989, 1993).) Generally, it is the description of the internal *dynamics* which defies analysis, e.g. why individual (macro-) molecules retain their individual identity, instead of entering a statistical ensemble. *Instead of an energy-driven dynamics, we have an information-driven dynamics.*

In our scheme, individualization of the macromolecules is accomplished by having their individual-"measuremental apparatus" side (characterized by the quasiclassical "bra" wavefunction in an individual-symbolic aspect) of an affine Hilbert spaces description. Here the symbolic-measuremental and ordinary structural (quantum mechanical) wavefunctions are introduced on equal footing, with definite 3D (specific constraining matching overlap) relations ("duality relations") between subsequent molecular Hilbert spaces in the internal dynamics, at the same time naturally accounting for time-inversion symmetry restoring (Balázs, 2003) (affine spaces instead of the usual conjugate pair). These 3D (matching) relations, *lifted to the Hilbert spaces*, provide a well-defined connection between symbolic and structural aspects: as has been described above, biologically active macromolecules as quasiclassical internal measuremental devices consist of quasiclassical, locally collectively describable, evolutionally contextual symbolic logical units, e.g. with their quasiclassical Born–Oppenheimer (internal coordinates) nuclear frames and localized (geometrical) electronic (quasiclassical) orbitals, having their contributing quasiclassical wavefunctions, yet in a complementer way being pure quantum mechanical entities, too. *It is the primary attribute of a measuremental apparatus that it never enters a statistical ensemble, is always individual, just as is the result of a quantum measurement.*

The affine Hilbert spaces model thus accounts for these 3D matching relations between symbolical and quantum mechanical wavefunctions at the level of Hilbert spaces, consecutively projecting out from the dynamic product Hilbert spaces, in an internally monitored internal dynamics of measurement,

$$\boldsymbol{H}_{\mathrm{A}} \otimes \boldsymbol{H}_{\mathrm{B}} \otimes \boldsymbol{H}_{\mathrm{C}} \ldots$$

the proper time-dependent diagonal (reduced) product as

$$\boldsymbol{H}^{i}_{(\mathrm{A})} \otimes \boldsymbol{H}^{j}_{(\mathrm{B})} \otimes \boldsymbol{H}^{k}_{(\mathrm{C})} \ldots$$

(We do not specify here in details the actual duality relations, this is done in Balázs, in preparation-a,b). The latter process can be described as being built on consecutive isomorphisms of one subsystem's Hilbert space $H_{\mathrm{A}}$ to the non-trivial (affine) dual (defined as the *symbolic H*-space) of the other in the series, $(H^{\mathrm{dual}}_{\mathrm{B}})$, $H_{\mathrm{AB}} = H_{\mathrm{A}} \otimes H^{\mathrm{dual}}_{\mathrm{B}}$, where $\otimes$ denotes the tensor product, the tensor product space $H_{\mathrm{AB}}$ restricted to the subspace spanned by the diagonal terms. Introducing

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

where $-\tau$ is a fixed internal parameter (in general inversely proportional to the turnover rate of the metabolism of the organism), the consequent dynamics, following $t'$, will be a self-constrained (Pattee, 1969, 1972) ("self-projected") unidirectional quantum dynamics, and corresponds to the above noted theory of internal symbolism (regressive time evolution).

In fact, time will be a locally cyclic parameter, evolution according to which from one doubling-up (fixed point) to the other, demands a classically behaving (deterministical) recursive, non-invertible projector operator formalism (algorithm). The discrete irreversible dynamical time series will consist of spontaneous measuremental quantum transitions of a "measuremental quantum automaton" (Albert, 1983; Deutsch, 1985) which are *classically coupled* in the converging projection algorithm.

The resultant projection algorithm, as internal dynamics of measurement, can be written in a compact form, quoting Eq. (3) from (Balázs, 2003), using the RHS of Eq. (6) in the time–energy picture,

$$\begin{aligned} & g^{i\prime}_{j}\, g^{j\prime}_{k}\, \Psi_i(\boldsymbol{q}_i) \\ & \quad > \mathrm{e}^{i(\varepsilon_{ij}\Delta_{ij}t' + \varepsilon_{jk}\Delta_{jk}t') = 2\pi i(\overline{h}(\nu_{ij}\Delta_{ij}t' + \nu_{jk}\Delta_{jk}t') - 2\overline{h}_{ik}\nu_{ik}\Delta_{ik}t')} \\ & \quad < \Psi^{k}(\boldsymbol{Q}_k, t'_k) \ldots \end{aligned} \tag{8}$$

Here $i, j, k$ are specific quantum states of specific consecutive subsystems (macromolecules), the $g'$s are constraining scalar products between subsequent amplitudes of symbolic and quantal states belonging to the subsequent subsystems, $\boldsymbol{q}_i$ and $\boldsymbol{Q}_k$ are the pure quantal and quasiclassical (mesoscopic) coordinates (defined in Balázs, in preparation-b), the $\nu_{ij}$s are transition frequencies, $\overline{h}$ is Planck's constant divided by $2\pi$, $\overline{h}_{ik}$ is the coupling action constant, and the $\varepsilon_{ij}\Delta_{ij}t'$s are action expressions (see also Balázs, in preparation-b).

That is, there arises a secondary dynamic coupling between quantum states, as that between quantum *transitions*, in accordance with internally fixing of a *quasiclassical trajectory* for the system. This is one implementation of the notion of a symbol-constrained, *purposeful, information-driven internal dynamics.*

## 5. Concluding remarks

In the above arguments, the physical underlying theory of the "selfish-gene" paradigm has been criticized briefly and a possible physical solution was proposed. We have pointed out that the underlying autocatalytic frame, if taken in the strict sense, cannot account for the life process (cycle) in three fundamental ways:

(1) The basic interactions within biological systems (most elementarily, the cell) are individual-dynamical (concerning *macromolecules*), and *not statistical*.
(2) Cause–effect relations, as compared with primordeal physical–chemical ones, are *split up* and *reversed*.
(3) These reversed *dynamical* cause–effect relations are in connection with semiotically controlled ("liberated") initial conditions of and (subsequently) by the phenotype, and is reflecting the *cause–effect split* in the primordeal system.

Concerning these problems, it is suggested that an alternative concept, that of an internal *time-inversion symmetry restoring*, originating from a primordeal

global quantum mechanical self-measurement, as an internal "goal-relation," might eliminate these contradictions. In this respect, it is pointed out that internal goal-relations (reversal of premeval cause–effect interactions) pertain to the phenotype and genotype *jointly*, their coming about having been inherently coupled at the original primordeal self-measurement as molecular "object" and macromolecular "measuremental apparatus + memory" (records and symbols). This then may have induced an internal *quasiclassically constrained* (in the $h \rightarrow 0$ sense) internal "relaxation dynamics" (self-measuremental chain) in subsequent evolution, cyclically with the fixed point of self-replication (as time-symmetry mapped onto space), describable by an affine Hilbert spaces physical scheme. The basic idea of the latter is that a split dual *quasiclassical* (symbolical-measuremental) wavefunction is ordered to each biological macromolecule, originating serially from previous internal measuremental interactions (eventually dating back to the origin of the genetic code), endowing them with an individual-internal measuremental device aspect, in an internalized Copenhagen interpretation of quantum mechanics. This then possibly circumvents the dynamical-statistical "gulf," so emphasized, e.g. by Pattee, and helps to introduce an *internalized dynamics of measurement*. The latter follows a (time-inversion) symmetry restoration internal monitoring scheme, which seems to fit naturally into these considerations, locally accomplished by a molecular duality ("matching") principle at the level of Hilbert spaces.

It can easily be seen, finally, that the whole problem discussed in the present paper naturally leads over to the difficult conceptual problem of "*existence for existence*" or the *unexplained robustness of biological evolution*.

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