

Emergence of information patterns: in the quantum and biochemical realms

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Abstract

Convergence is observed between quantum and molecular descriptions of the emergence of information and of organization from initially disorganized states. The superposition property of quantum mechanics implies that probability waves add and do not interact unless mediated by the interaction with matter. Molecules and associations such as enzyme-substrate or protein-ligand are formed from elements, which interactive sites are freely moving and interacting fugaciously with a variety of other elements from their environments, abundantly manifesting free energies or interactive potentials. At the moment the partners meet and a stable association is reached, the free energies are mutually dampened, tamed in complementation. The mutual adjustment of the free energies into a stable configuration of the interactive sites of the partners is the process of emergence of information. Information structures can be seen to reside somewhere in between the partners, as an organized pattern of interactions that glues components together, giving origin to organized ensembles: a particle originating from quantum waves, a molecule from atoms, or molecular aggregates. In interactions at a distance, along the evolutionary process from e. g. bacterial chemotaxis to human communication, it may be said that a source organism releases messenger molecules or other kinds of products that carry the potentials for developing the informational process when they associate with the receptors. The low energy level involved in biological information processes is probably constitutive, in view of the critical quantum conductivity state of the reactants. In this article I survey literature in both biology and the physical sciences, showing that the well accepted statement - that life is characterized by the ability to create order from chaos - is applied to all biological processes at all scales.

Key Words: Information, Disorder-order, Quantum concepts, Protein structure-function, Genetic code.

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Introduction

The concept of information enriched the discussion of biosystems, but at the same time provoked some conflict due to the different authors not always utilizing the term with equivalent meanings.

A simple way of interpreting the term says of an action (-ation) that gives (in-) forms (-form-) to things.

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The majority of biologists are satisfied with the already trivialized statements that the genomic DNA is a store of information that dictates the sequences of RNAs and protein, and guides its own replication (Guimarães, 2007); the job of construction of the cells and their collectives resides in those latter kinds of molecules (Guimarães, 2015a).

It's not among their worries to further dwell into other semantic complexities that accompany the term, remitted to philosophers. Their main job in the practicality of the field or of the laboratories may go on well without

involvement of the finesse of the information talk.

Otherwise, biology is increasingly becoming more sophisticated due mainly to the opening of various fronts of sequences of macromolecules are now commonplace. These studies brought in some surprising refinements pointing to the involvement of particularities typical of the areas more traditionally involved with information sciences and technologies, such as linguistics and many other branches of the cognitive field. A typical case is the concept of the gene that was thought clear from the Mendelian tradition but became completely changed and still unresolved in the molecular and bioinformatic era; it is becoming increasingly evident that the plasticity that characterizes all components of biosystems also applies to the construction of the functional genes (Guimarães, 2007). More drastic were the numerous cases, probably the rule more than exception, where the change in one amino acid may affect a great number of characters in an organism, showing network and cascade effects analog to some situations of linguistic text building. The book analogy is illustrative: a book can change the behavior of a population that reads it, as much as a change in a protein can affect profoundly an organism. The change in a letter (amino acid) affects not only the word of which it is part but may spread dramatically in the system because the sentence (statement, protein) has its meaning (function, which may be plural and applicable to diverse contexts) changed and all the systemic consequences of its insertions in different subnetworks will be also modified (Hart et al. 2015). More complicated still are the subtleties in the expression of the consequences that may vary in different individuals, sexes or even ages of an organism. Information talk has become an integral part of biological discourse. I will not delve deeply into the concepts of the information area but will only attempt to help making them useful to the biochemist.

Informational structures and utilization modes may be arranged according to evolutionary scales. The process concerns

investigation with utilization of molecular tools.

Genomic analyses and evolutionary and physiological studies based on interactions of the most diverse kinds. A zero-interaction background physico-chemical scenario envisages freely moving dispersed elements that experience encounters or bumps with each other but don't have specific affinity or other kind of adequate surface properties so that the encounter does not result in any kind of exchange; it will be of minimal duration and the elements would just follow directions of their movements dictated by elasticity of the partners and the mechanical impact angles. Mere gravitational interactions are also near zero with respect to chemistry since only masses are involved and effects are negligible in the range of bulk matter of laboratory experiments. Some elements do not get close to each other due to being surrounded by fields with incompatible or repulsive characters; these may contribute to the production of forms in the nearby context and possibly help in setting some characteristics of contours of shapes.

Information talk tends to leave aside the plain biochemical reactions, the field of metabolism, with biosynthesis - anabolism and degradation - catabolism. This area would be too crude, involving too high energy levels, working with more or less equilibrated bulk of the reactants and actions usually spanning short distances. Nonetheless, this area fits adequately many of the necessary components of the information concept. A molecular and macroscopic approach to the concept of information, which serves as a basis for and an introduction to the present paper, is presented in Guimarães (2015a).

This text considers some aspects where molecular and quantum-informational reasoning fit mutually quite well, and may enrich the discussion in both domains.

Phenomena that are privileged in the informational studies are characterized more generally by a disparity between the causal forces, which may be weak, and the magnitude of the effects obtained.

Furthermore, when the connection between source and receiver, the sender of the signal and the organism affected, is a well-known chemical messenger, the phenomenon remains in the biologic realm, such as the hormonal, pheromonal and chemotactic. They tend to concentrate on phenomena that are more difficult to explain, such as how a piece of thought or an idea can produce efficiently strong material effects (Pereira and Gonzalez 1995). Most enigmatic and in search for clarification are the classical problems of the qualia, some of the basic and fundamental feelings, artistic manifestations etc., involved with consciousness.

A nearly vexing conflict arose when many scholars in the epistemology and related areas decided that biological theory and results would not have much more to contribute to the information and the consciousness problems; they turned to quantum physics, instead. Biology is now in the post-genomic effort era and in the middle of a decade focused on the neural system. Of course the latter is a much more difficult task. While experimental neuroscience necessarily advances more slowly, modeling has become a major tool via computing, starting with the artificial neural networks and going to other branches of complexity studies. Present day empirical and experimental biology for sure suffer from heavy technological and time limitations, while computing may advance more speedily. At the same time, a second intriguing area with high appeal, quantum physics, was rescued to be joined to the neurosciences studies. We are now facing the strange dilemma of having to make compatible the rapidly growing neuroscience with the informational area that is heavily dominated by mathematicians and physicists, and the quantum area that also contains various 'strange' propositions. The appeal of the latter succeeded in finding support among the information community possibly in view of the convergence of both working with elemental units - linguistic letters, computer bits, quantum particles, quarks and qubits - which can be utilized with various kinds of formal and combinatorial

procedures. This text tries to bridge the gap from the quantum to the biomolecular domain.

1 - Convergence

A biologist's reading of the quantum physics concepts is of course superficial but the similarity of some of its statements with our work on the formation of the genetic code is impressive. A clear analogy could be perceived between the description of (1) quantum physics, that 'describes the world differently when you measure it, than when you don't. When you don't measure it, when you don't look at the world, it's described as waves of vibrating possibilities, buzzing opportunities, promises and potentia.

In some ways it's not quite real, and it's all vibrating. All these oscillating possibilities; then when you look, it's perfectly normal. The possibilities change into actualities, and these actualities are point-like. They're called quanta, quantum jumps; the world changes from possibility waves to actual particles, from possibility to actuality, from waves to particles. So no one ever sees this quantum world directly, the vibratory possibilities, because we have ways of making measurements'. (Herbert, 2013; Manning, 2014), and (2) the indication of our studies on the origins of the genetic code that proteins started as 'disordered' peptides that acquired ordered states at the interactions with their producer prototRNAs (Guimarães 2014, 2015b). Serious consideration of the homomorphism in the disorder-to-order arrows - emergence of order at associations - prompted the expansion of its exploration in wider contexts, now undertaken. It is considered significant that the transition is not from (a) an ordered state of well-behaved waves to the new state of well-defined particles, only changing the wave-to-particle forms while maintaining order in both states, but (b) from a disordered vibration or probabilistic, restless agitation of 'free energies' that develop organization or order in the act of interaction with other entities, be they of the same kind or of compatible kinds, such as the measuring probes. In spite of the utilization of

different terminologies, both realms converge as to the explanatory schemes. In the case of proteins, many functional structures emerge from initially disorganized states, the functional organization being derived from their interaction with other elements such as the ligands or substrates, at the formation of the ensembles, which is, when the informational structures are formed and the communication between the partners established.

Observation of such convergence arising from distinct realms of thought brings up mixed feelings. We could be just happy with the possibility of one field reinforcing or giving support to the other but I consider that we should as well get suspicious: are we approaching some kind of 'truth' or would the convergence only indicate limitations in the range of our creativity, as if our minds being capable of traveling only a few kinds of pathways? We may be reminded of the Jungian archetypes or of different versions of the Anthropic Principle (Meissner, 2015); it may happen as with the question on the continuum of movements – is it real or a construction, as in cinema, from the superimposition of photograms obtained by our vision or other measuring instruments? In case the limitation is real then the convergence – 'informational closure' – should come as an obligatory consequence; even when taking long times to be reached, the theoretical body would eventually uroborically turn back upon itself.

The biologic background introduces the theme of adaptive processes. Could the theory-to-nature adjustment be more than an analogy, as a result of ecological adaptive evolution? Our theories would be constrained in range or scope, not as widely free as we might wish, by characters of our brains and minds that had to pass through strong filters of adjustments fit for survival. It is still to be evaluated how intense was the expansion of the 'degrees of freedom' in our minds in consequence of the neotenic developmental mechanisms and of the social learning (Bjorklund, 1997). Would our theories contain high degrees of originality and

freedom, as if profiting from exaptation processes, or would they be mainly results from more intensely constrained preadaptations of our brains and minds? Otherwise, such considerations might not be real worries because they refer only to the mechanisms; what matters the most is the correctness of the theory-to-reality adjustments or fitting, in spite of the possibility of some kind of circularity being obtained; we could as well consider that there would be more benefits than problems with the theoretical closure in the circularity.

2 - Rationale

Our examination of the process follows the reasoning that initial states of the partners in interactions should be of high flexibility and plasticity, so that the unknown future partners could be searched and chosen among a variety (Whitford, 2013, Simon, 2014). What is observed in nature is mainly the world of stable objects, which is the result of a few of those choices. Some results are of high specificity such as some pure crystals, others of less specificity that may give rise to the formation of 'families' of objects with some degree of similarity among them, which is more typical of the biologic realm. Maintenance of degrees of flexibility would be a biological requisite, necessary for the adaptive processes. A clear practical example is the working of drugs and medicines, where a molecule with interaction possibilities similar to the physiological effector or agonist is utilized to modulate or change the activity of the target molecule or system. The similarity has to be precisely chosen so that it may allow for its acceptance by the target molecule, replacing the physiological agonist, and at the same time provoking a modification of its activity. It is now possible to point out some specific molecular processes at the basis of what Robert Rosen attempted to characterize as typical of living systems, the overall organization of the metabolic networks (Mikulecky, 1999). It is also indicated that the origin of biological information should be looked for in the mechanisms that establish the flow in metabolism, which

runs from (a) an internal sink at protein synthesis to (b) the surface receptors that are linked to (c) the sustaining environment (Guimarães, 2014, 2015b).

3 - Receptors

The workings of a membrane receptor molecule – the same would apply to other types of binding sites, including those of enzymes – may be described as follows. Receptors are presented in (a) extended states, exposed to the outside of cells, relaxed and with the interactive sites open and showing atoms with the reactive elements pointing out, in agitation because they are being contacted by a great diversity of molecules that are not cognate to them, therewith not fitting their reactive sites' complementarities; the contacts are of short duration and may be followed by repulsions. The 'free energies' remain in agitation waiting and searching for the correct agonists. (b) The receptor site enters the closed state when an agonist makes contact and an informational complementary cognitive interaction occurred. The interactive sites in the partners dope and tame each other, with buffering, dampening and calming of the agitations. The free energies are not anymore free but busy with the sites occupied. (c) Following the receptor site closure at the joining of the effector (agonist), other components of the receptor protein structure (that may be distant) are changed, meaning that the informational effect is transmitted from the receptor site to other sites and the conformation of the protein is modified. As occurs with receptors in membranes, the receptor function is a trigger that is associated with forwarding of the information to the inside of the cell. The protein structure and activity is now retracted from the outside to be exposed in the inside, and the agonist or a signal derived from it may be delivered to the inside. (d) The receptor site is now empty and the protein goes back to the (a) initial extended and exposed state, directed to the exterior. A cycle of extension-retraction, exposure-binding-delivery is configured (a-b-c-d-a). The act of retracting, delivering and going back to the exterior is fast and automatic so that the

receptor site will be empty, open and exposed most of the time. It happens 'as if' the cell would be manifesting avidity or a 'desire' for being satisfied or completed, virtually seeking for a portion of the environment 'on which to hang to'. Of course just having empty receptors exposed is a weak biochemical correlate of the psychic manifestation of desires but it may be a somewhat better correlate of the avidity behavior. When we have no way of talking with molecules, will we forever be impeded of taking the analogy seriously?

4 - Information as shared proteinformation

The term information is examined here through the mutual sharing perspective, more or less like an adhesive that binds or joins partners together at the construction of organized ensembles. It refers to 'the exchange process that occurs at an interaction', in the example above, at the binding of the effector to the receptor site, and to 'the pattern that is formed' by the composition at the meeting of the elemental sites coming from the partners. In the typical cases of receptors, binding between macromolecules and catalytic sites, each elemental site interaction is weak, e. g., through hydrogen bonds, therefore dynamic (the bound and unbound states are in continuous interchange). The necessity for being dynamic, in the living systems, is adequate to the system that is intrinsically and continually following the movements of metabolic flow, with extensive regulatory and adaptive behavior. This concept also says that there is no information freely floating by itself. When two systems are communicating at a distance they are not sending pieces of information one to the other but sending objects that can develop the information process when they reach the receptors.

5 - Experimental

Interactive properties that remain interesting for the production of forms - informational proper - are (a) the classical physicochemical: the strong and the weak nuclear (in the atomic realm), and the electromagnetic, this most important for

the molecular realm, which is the dominant process in the construction of biosystems; and (b) the surface and shape adjustments via their complementariness that, in biosystems, acquires the form of hydrophobicity; this is greatly dependent on the exclusion of water from the interactive interfaces and by external pressure from environmental water, including the internal milieu's, possibly also involving some kind of resonance-sharing in the partners.

The matter that composes the interactive rugged surfaces in the plaques that are formed in the slits or clefts between the partners is peculiar due to the scarcity in atomic nuclei. It is built mostly by electrons moving from one to the other interactive site that shares them, but forming a cloud occupying the positions where the electrons would tend to traverse most frequently so that it becomes more electron dense than the surroundings. Present day atomic force or scanning tunneling microscopy technologies are able to generate pictures of this material (Heath, 2013, Pool, 2014). It may occasionally contain molecules that participate in some types of informational exchanges, such as water molecules or some ions, among other possibilities of bridging elements. Furthermore, this kind of substrate would acquire a highly organized state, which is responsible for giving form to the ensemble of the interacting partners. It is possible that these characters could also inspire studies that propose a material substrate for consciousness (Tegmark 2014).

To inform refers to the process of generating a new form; in the case shown above, the empty receptor became filled to completion and activated in its function. The interactive sites in each interacting segment of a molecule contain possibilities of wide range, when different combinations of elemental (atomic) sites and states may be at work at a moment. The really occurring interactions are only a few from an enormous combinatorial space. It is interesting to consider only those which trigger some effect in the receptive system; these may be called cognitive because the system recognized

them in such a way as to react demonstrating some new behavior, be it augmented, diminished or modified. The other interactions pass along non-perceived because they did not cause modifications, did not call the attention of the potential partner or observer, and can be called non-cognitive.

6 - Plasticity

The low energy levels involved in most of the informational interactions in the biologic realm are indicated to be constitutive to their molecular composition. The work of Vattay et al. (2015) is just a start of investigations in the field (Hewitt, 2015) but already points to a fundamental explanation that is applicable even to the basic character of the living, which is plasticity (Guimarães, 2013, 2014). They described that many molecules of biosystems, from micromolecules to proteins, but not the nucleic acids behave, with respect to electrical conductance, as critical state molecules, poised at the intermediate position between insulators and conductors. They interpreted that this situation would be optimal for the quick spread of information through the whole system. Our interpretations add the rationale that when the interacting elements are in critical states the energy levels necessary for their modulation or regulation are low, which is of high value for the adaptive and plastic character of biosystems. In the same way that happens with the work of enzymes, controls of intensity (e. g. avoiding avalanches) and directionality (avoiding reversed or futile reactions) of the conduction are obtained from the context, that is, the section of the metabolic flow where the molecules are inserted. This should be the biochemical basis for the process of Environment-Assisted Quantum Transport (ENAQT); (Vattay, 2015) and for the long time famous 'Maxwell's Demon', which combines enzyme specificity (choice of kinds) with the flow directionality.

They also highlighted that the process of evolution with selection for this specific kind of constituents would have been very strict since the set of critical

state molecules is a tiny fraction of the space of possible molecular types. This process would have been long, highly iterative and nearly paradoxical due to the self-adjusting reflexive (self-referential) character. The amino acids are produced through the activities of enzymes in biosynthesis pathways, which are themselves proteins made of amino acids; the exact kinds of biosynthetic products have to be adjusted to compose the producers with properties well suited to the productive activity. Precise measurements of electronic states for calculations of criticality are not possible for small molecules but estimates indicate variety for which there are no generic explanations. Among the 20 amino acids, the majority is indicated to be in critical states, there being seven non-critical (Ala, Asp, Asn, Glu, Lys, Tyr, Val) and two (Gly, Gln) without a conclusive definition. Indications are for the criticality being positively related to metabolic or otherwise dynamical roles of the molecules in cells or organisms. Proteins in critical states are e. g. myoglobin, apolipoprotein E and profilin while the strictly structural silk fibroin is not, presenting the insulator behavior. Therefore, the property in proteins is also sequence-dependent.

Considerations on the various kinds of small molecules examined also do not indicate easy generalizations. The list of critical state molecules includes vitamins (e. g. D₃, B₁₂) and nucleobase-related metabolites (xanthine) or mediators (adenosine), but the polycyclic sterols (e. g. the hormonal testosterone and progesterone) are good conductors. It may not be surprising to find that nucleic acid chains (DNA, RNA) belong in the category of insulators, a property that, together with the stability derived from the template replication ability, fits the rationale of the function of genetic memories having been attributed to them, forwarding the more plastic and metabolic functions to the critical state proteins.

7 - Prebiotic realm

The most elementary kinds of informational events occur in the quantum level. Vibrating waves would contain the

interactive possibilities (protoinformation) that will be realized at the actual interactions (information proper) therewith defining some kind of particle or object (a new form). This description fits well the Triple-Aspect Monism proposition (Pereira Jr, 2014). The vibrating waves can interact between themselves or with the measuring systems; at the informational events, new forms get realized or actualized as particles and these can therefore be measured. The usual terminology says of cognate interactions, when productive or stable for some adequate duration, at the same time reserving cognitive for the biological realm. Non-productive interactions, transient or repulsive etc., may also contribute as portions of larger systems that contain other portions formed by productive interactions.

The proto-informational elements in each potential partner would have the duration or half-life of the wave, particle or atom that bears them; the same applies to the informational patterns formed in the ensembles, molecular or of higher degrees. They might be conserved to some extent, albeit suffering changed identities according to contexts, e. g., due to temperature, pH, ionic strength etc. They might be called eternal or perennial in case they would follow the energy-conservation regime, or more fugacious in case they are subjected to wear-and-tear or thermodynamic degradation processes.

The dynamics of such systems installs a process of physicochemical evolution; its description may contain series of complexity starting from the particles and going to atoms and molecules plus its compositions. Among the most complex objects in this realm would be various crystals, others being composites such as enchain reactions in flow systems and the formation of gradients etc. In the organic abiotic realm, molecular sizes reach the oligomeric chains or the highly branched tangles of the kerogens. Polymers are typical of biotic systems.

8 - Mutuality

The lock-and-key metaphor for the description of the interactions of macromolecules with themselves or with other molecules is outdated, now substituted by the process of 'mutually-induced fitting'. In the interactions, the reactants adjust one to the others gradually, in a succession of elemental interactions that finally compose a complex set. The substrate of an enzyme slowly accommodates itself 'in the lap' of the catalytic cavity, while this also adjusts to its contents. It is possible to extend such description to the inorganic interactions, in spite of eventual specificities and of the apparent macroscopic rigidity of crystals.

A character added by biopolymers is the network-like behavior of their soft and plastic 3D conformations. Changes in one site may spread to distant places of the 3D structure and modify (increase, decrease, change etc.) the functions of those places. In a metabolic pathway, activation of a function due to the interaction in one site may facilitate the activity of next steps in the pathway, which are called cooperative effects. There are so many variations in this theme that the general property, called allostery, is of wide applicability also in regulatory pathways (Buchli, 2013), such as genetic activation-repression cycles.

The fundamental theme is that mutual adjustments generate organization (Cerchiari, 2015). The partners would be unstable and indefinite before the interactions. They acquire identity at the interaction, which derives from the encounter with the other; if there are many others possible, the other in one specific interaction may be an important component of the definition of the identity at that context. The sense in such rationality is that in the indefinite or unstable state there is some degree of freedom; there are some possibilities open for interactions with partners that are not always unique, predetermined and singular - the unknown future. The benefit is obvious for the openness to regulation or modulation; an enzyme or a receptor needs not to be strictly specific but may accept some alternatives; this is one of the bases for adaptivity, evolvability, plasticity,

and also what allows for the efficacy of medicines and drugs in general. This rationale makes sensible the chronology of development of protein structures in the origins of life, as described by the self-referential model for the formation of the genetic code (Guimarães, 2014, 2015b). The start with disordered proteins would be adequate to facilitate encounters with a variety of 'others', until a partner is apt for producing an ordered and functional ensemble, which was a pre- or protoRNA in the origins of the biotic system. Starting with ordered structures would have constrained excessively the possibilities; therefore, this was not the actual option taken for the origin of the genetic code.

The interactive sites of proteins, from catalytic cavities to binding and adherence sites in general (Podgornaia and Lamb, 2015), can be placed in the same category of the 'intrinsically disordered regions of proteins'. It is understood that the protein segments that are structured as helices or strands and sheets are devoted to promote the architectural details of the 3D conformations that are important for constructing the catalytic cavity from the outside. Amino acids that compose the inside of the surface of the cavity need not be contiguous in a sequence but may be brought from sites that can be distant in the sequences (Duarte, 2014). They will stay there waiting for the cognate-functional interactions, while testing many other encounters that may be regulatory but mostly non-cognate, fugacious or repulsive.

9 - Evolution

Biological evolutionary thinking tends to focus on the single-trunk tree model of Darwinian origin that together with the main frame of physics that centers on the Big Bang singularity, converge on the propositions of monist character. Not being a philosopher, I accept that a theoretical corpus that starts from something that is primitive and eternal - the trunk, the protomatter at the singularity - would be sitting on solid grounds. Nonetheless, I dare to remain cautious in view of both another

convergence with the Abrahamic monotheisms of the western civilization (possibly mixing mythologic thinking with science) and a possible divergence with the tree metaphor, which has to rely upon many roots to obtain sustainability. The 'many roots to one stem' aspect of the tree metaphor applies well to the origins of biosystems, recalling that geochemical protobiotic systems would have been probably rich in different kinds of reactants necessary to build the early sets of biomolecules and that the early cells would have probably formed highly interactive communities with rich 'horizontal' interchange of constituents, pathways and genetic novelties among them, forming syntrophic and symbiotic networks.

I wonder if the quantum physicists community's thought is homogeneous enough to give support to a purely monist proposition, in spite of knowing that many of them keep trying to reach something like a unified theory. In one side, there is the baryonic world with wide compatibility and interchangeability of the vibrating waves and the particles, which can be clumped together in the concept of matter or decomposed into mass and energy. Mass particles are only recently being identified while energies still resist the attempts at unification. The most careful physicists even resist to the appeal of talking about the reality of 'forces', noticing that what is observed are movements derived from interactions between particles or between them and the measuring instruments; forces are elaborations for explanation and their talk is of the strong and weak nuclear interactions, the electromagnetic and the gravitational interactions. The interactions would be described as mediated by fields, surrounding and emanating from the particles, and I would tend to think of such fields of the quantum world as the correlates of the volumes, shapes and surfaces of the mesoscopic world, which also emanate their own energies and form other fields. The topological or spatial structure model of gravity further complicates the notion of force, as well as the van der Waals optimal distances

between atoms in molecules – if too close there is repulsion, if the distance is somewhat higher than the optimal, there is attraction but this also vanishes with the increase in distance. In the other side, some observations and the theory say that there are the dark or obscure entities, surprisingly about 19-fold more abundant than the baryonic. Would those be original and distinct from the latter or would they be resultant and derived from the latter, which could be accumulating along the evolutionary time?

Information emerges at interactions but can be considered a bona fide component of primordial or fundamental entities. It may be fugacious in some transient interactions, but is most conspicuous in the interactions that reach stability, producing new objects and forms with their own volumes, shapes and surfaces, plus the energetic radicals and other kinds of reactivity. Information at the same time enables and constrains the further interactive and evolutionary possibilities of the objects. If the interactive potentials of the initial reagents are extensively tamed or buffered and neutralized at an interaction, the object formed will lose further potentials and become of low interactivity and evolvability, such as the noble elements and gases, perhaps also some of the dark matter. The entropic directionality suggests that information will follow a path of degradation or dispersal.

10 - The Human

Consciousness remains as enigmatic for a biologist as it is to other branches of sciences. It is full flourished in humans while some hints at its occurrence, probably not as rich as in humans, in preceding or collateral organisms are available but of difficult investigation; how to compare other species' feelings with ours, how to talk with them? The evolutionary rationale allows the proposition that consciousness may have started already in unicellular organisms as an whole-body reactivity, and the associated behaviors, to both the physicochemical and the biotic environment – recall that cells are always

parts of populations, intercommunicating and interchanging communities of organisms. Bacteria have already developed mechanisms of evaluating the intensity of the crowding in their environments (quorum sensing) (Goo, 2012; Marshall, 2013) and can make biofilms, sometimes highly structured – tissue-like or organism-like (O'Loughlin, 2013). The first appearance of the neural system, with identifiable neurons and glial cells is among the coelenterate and cnidarian animals (corals and relatives), as a subsystem of cells 'inserted' in the larger body and devoted to promote rapid communication (integration) between distant parts of the body. Various components of the neural system's workings, such as neurotransmitters, are detectable in the diverse branches of the evolutionary range from bacteria to plants (Garzón, 2007), enforcing the conclusion that the neural system is just a specialization of the body and that consciousness continues to be a function of the whole body. Each species would have its own modality or kind of consciousness, its own mode of organizing, in a totalizing and fully systemic network of feelings and reactivity, the internal and external interactions. I don't feel it is safe to evaluate propositions that some kind of non-biotic consciousness would exist.

A big novelty in our branch of the evolutionary tree was the adaptive immune system, starting in fishes, which profited from combinatorial genetic rearrangements in its somatic cells, with important contribution of nearly randomized modes of generation of diversity. It may be said that this, together with the other new degrees of freedom developed by the neural system, depicted by its wide plasticity, would have been preconditions guaranteeing adaptivity and evolvability to the organisms while most of their other organs were developing very tightly controlled internal organization, as reflected in their loss of protein polymorphisms (Guimarães, 2008; 2015a). Highly organized and more rigid bodies could be obtained with the background support of the immune and the behavioral diversity and plasticity.

Besides these generalities common to our evolutionary branch, there are the human specificities of neoteny, well expressed by our relative 'prematurity' at birth (Bjorklund, 1997), plus the strict societal dependency, which should be considered in the investigation of consciousness as a circular and recursive function in our individuality that builds societies and is built by them.

11 - In the Beginnings

Research on the origins of life has to envision the states of the components in the early macromolecular associations, before the rise of specificities such as the enzymatic or the structural, which would be involved with the metabolic flow. The most basic description is of the macromolecules presenting dynamic states and movements that can be called spontaneous, due to the interactions of the globules with the internal milieu or the environmental watery solutions (Podgornik, 2012; Mentré, 2012; Bianco, 2012). The biopolymer structures may be considered robust, dynamically stable and (paradoxically?) at the same time unstable, under the continuous activities of breaking and rejoining the molecular bonds, dissociation-association. Most dramatic and also the most ancient and primordial tension of instability derives from the diversity in the interactions with water. The strongest is in the polymerization reaction: in the making of a peptide or nucleotide bond, a molecule of water is expelled from one -H and one -OH of the monomers, while this reaction may be reversed due to the attack of the abundant water molecules in the surroundings. This would be the primordial tension or danger, in the cycles of dehydration at the synthesis and polymerization, and hydrolysis that destroys the polymers.

Metaphors are unavoidable; if not adequate for the transposition of concepts from molecules to psychology, they are at least appealing to make the learning easier and to introduce some fun in our arid works. The tension anabolism-catabolism, construction-degradation, would be a molecular counterpart of the basic 'existential anxiety' of all organisms. The

dynamic trembling of biomolecules in water (Kasas, 2015) is an image that finds a nice parallel with the title of Pedro Almodóvar's movie 'Carne Trémula [Live Flesh]'. One factor is that water molecules are polar +OH₂- and continuously challenging the exposed radicals in the biomolecules with interactions that may be of different polarities at each moment. Stability of a certain state means that the molecule visits more frequently that state versus other states or remains in that state for longer periods than other states, which leads to the statistical measures. The stability of the double helix of nucleic acids depends strongly on temperature, ionic strength of solvents and base composition of the sequences, so that in a long molecule there are always some open and other closed regions, which is called movements of molecular breathing (such as the expansion-contraction of the thorax). Such events are much more frequent in proteins and are widely utilized for regulation and modulation of activities. Plasticity is a rule in biology (Guimarães 2013), as a complement to the rigidity of the specificities; both are necessary, specificity for conservativeness, plasticity for adaptivity and change; the relative rigidity of nucleic acid interactions is complemented by the protein high plasticity.

How could the metabolic flow start before structures and specificities were developed? The early nucleoprotein globule behaves like a compartment demarcated from the environment due to (a) the biopolymers being self-adhesive or sticky and to (b) presenting the trembling movements just described. The globular structure works like a sponge that gets imbibed with water and, through the trembling dynamics, is able to promote exchanges with the environment. The interior is mechanically agitated as if possessing a pump that starts the establishment of the in-out distinction. Micromolecules coming in are nutrients and those brought out are excreta; the flow may work even when concentration gradients are weak.

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